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(54) Title: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

(57) Abstract

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

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METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a 5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

The present invention relates, first, to DP178 15 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability, 20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4+ cells, or an ability to modulate intracellular processes involving coiledcoil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids 30 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion 35 capability, antiviral activity, or the ability to

modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein 10 DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, noncytotoxic inhibitors of HIV-1 transfer to uninfected CD-4 cells. The invention is further demonstrated by Examples wherein peptides having structural and/or 15 amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral 20 activity.

2. BACKGROUND OF THE INVENTION

2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly 15 degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science <u>224</u>:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et 20 al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of 25 each of these types. Infection of human CD-4 Tlymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

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replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early 10 replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 15 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, qp41 and qp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains noncovalently associated with gp41, possibly in a 20 trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalgleish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4* receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4* cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

HIV is targeted to CD-4+ cells because the CD-4

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2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991, FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptasetargeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been developed which have been shown to been active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989, 20 Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4⁺ T-cells by some HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,

recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

Attention is also being given to the development 15 of vaccines for the treatment of HIV infection. HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore, 20 these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system. See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

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3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

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The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1 LAI, but found in viruses and/or organisms other than HIV-1_{LAI}. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1 ALI, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1_{LAI} transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

DP107 peptide sequence present within the gp41 protein of HIV-1_{LAI}, but found in viruses and organisms other than HIV-1_{LAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

15 The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of 20 the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4+ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides. 30

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-asociated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs . in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

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Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4+ cell-cell fusion (i.e., syncytial formation) and infection of CD-4+ cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

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3.1. **DEFINITIONS**

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as

15 follows:

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- A (alanine)
- R (arginine)
- N (asparagine)
- D (aspartic acid)
- C (cysteine)
- Q (glutamine)
 - E (glutamic acid)
 - G (glycine)
 - H (histidine)
 - I (isoleucine)
 - L (leucine)
 - K (lysine)
 - M (methionine)
- 25 F (phenylalanine)
 - P (proline)
 - S (serine)
 - T (threonine)
 - W (tryptophan)
 - Y (tyrosine)
 - V (valine)

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4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIVLA; DP178 homologs derived from HIV-1sp2 (DP-185; SEQ ID:3), HIV-1gr (SEQ ID:4), and HIV-1wo (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{red} (SEQ ID:6) and HIV-2_{NIHZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEO ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

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FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC₅₀ refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC₅₀: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{SP2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

- FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.
- FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1)
 and DP-116 (SEQ ID:9) on CEM cells. Cell
 proliferation data is shown.
- and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM.

 The proteins are more fully described, below, in Section 8.1.1.
 - FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.
- FIG. 9. Abrogation of DP178 anti-HIV activity.

 Cell fusion assays were carried out in the presence of
 10 nM DP178 and various concentrations of M41Δ178 or
 M41PΔ178.
 - FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.
- FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally though gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other: In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the 15 fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α -helix. conformational change positions the fusion peptide for 20 interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

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the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♠): PLZIR; Diamonds (♠): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program designed to search for such peptide regions). Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and in bold. DP107 and DP178 sequences are marked, and

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

additionally double-underlined and italicized.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations are as in FIG. 20.

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FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data.
FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D:

Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

"-", negative antiviral activity;

"+/-", antiviral activity at greater than 100µg/ml;

"+", antiviral activity at between 50-100µg/ml; "++", antiviral activity at between 20-50µg/ml;

"+++", antiviral activity at between 1-20 μ g/ml;

"++++", antiviral activity at $<1\mu$ g/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

"-", no helicity;

"+", 25-50% helicity;

"++", 50-75% helicity;

"+++" 75-100% helicity.

 ${\rm IC}_{50}$ refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

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containing no peptide. IC₅₀ values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC₅₀ are as in FIG. 27A-D. IC₅₀ values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3
F1 DP107-like region. Peptide antiviral and CD data.
Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀
values, except where the values are marked by an asterisk (*), in which cases, the IC₅₀ values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3

F1 DP178-like region. Peptide antiviral and CD data.

Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀

values, except where the values are marked by an

asterisk (*), in which cases, the IC₅₀ values were

obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

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FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined

by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian

Mason-Pfizer monkey virus, enveloped (TM) protein

10 qp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for Pseudomonas aerginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for

Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human cfos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC_{50} values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amidoand acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. IC50 is as defined in FIG. 27A-D, and IC50 values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC50 was obtained using a crude peptide preparation. 15

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC₅₀ as defined in FIG. 27A-D, and IC₅₀ values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC₅₀ was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The

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length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

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intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent 15 anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. In the HIV protein, gp41, DP178 corresponds to a putative α helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal 20 site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It 25 is of interest that mutations in the C-terminal α helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral 30 protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal α helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virusinduced membrane fusion.

On the basis of the foregoing, two models are proposed of qp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for qp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of 10 gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within 15 intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form 20 the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one 25 assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane 10 region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides --15 the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. transformation may result from liberation of the potent DP178 domain from a molecular clasp with the 20 leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1_{LM} isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH2-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH2) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not 15 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or 20 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred 25 "X" or "Z" macromolecular group is a peptide group.

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TABLE I DP178 (SEO ID:1) CARBOXY TRUNCATIONS

X-YTS-Z X-YTSL-Z X-YTSLI-Z X-YTSLIH-Z X-YTSLIHS-Z X-YTSLIHSL-Z X-YTSLIHSLI-Z X-YTSLIHSLIE-Z X-YTSLIHSLIEE-Z X-YTSLIHSLIEES-Z X-YTSLIHSLIEESQ-Z X-YTSLIHSLIEESQN-Z X-YTSLIHSLIEESONQ-Z X-YTSLIHSLIEESQNQQ-Z X-YTSLIHSLIEESQNQQE-Z X-YTSLIHSLIEESQNQQEK-Z X-YTSLIHSLIEESQNQQEKN-Z X-YTSLIHSLIEESQNQQEKNE-Z X-YTSLIHSLIEESQNQQEKNEQ-Z X-YTSLIHSLIEESQNQQEKNEQE-Z X-YTSLIHSLIEESQNQQEKNEQEL-Z X-YTSLIHSLIEESQNQQEKNEQELL-Z X-YTSLIHSLIEESQNQQEKNEQELLE-Z X-YTSLIHSLIEESQNQQEKNEQELLEL-Z X-YTSLIHSLIEESQNQQEKNEQELLELD-Z X-YTSLIHSLIEESQNQQEKNEQELLELDK-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWA-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWAS-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASL-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWN-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IA DP178 (SEO ID:1) AMINO TRUNCATIONS

```
X-NWF-Z
                                                    X-WNWF-Z
                                                   X-LWNWF-Z
                                                  X-SLWNWF-Z
 5
                                                 X-ASLWNWF-Z
                                                X-WASLWNWF-Z
                                               X-KWASLWNWF-Z
                                              X-DKWASLWNWF-Z
                                             X-LDKWASLWNWF-Z
                                            X-ELDKWASLWNWF-Z
                                          X-LELDKWASLWNWF-Z
                                         X-LLELDKWASLWNWF-Z
10
                                        X-ELLELDKWASLWNWF-Z
                                       X-QELLELDKWASLWNWF-Z
                                      X-EQELLELDKWASLWNWF-Z
                                     X-NEQELLELDKWASLWNWF-Z
                                    X-KNEQELLELDKWASLWNWF-Z
                                   X-EKNEQELLELDKWASLWNWF-Z
                                  X-QEKNEQELLELDKWASLWNWF-Z
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                                 X-QQEKNEQELLELDKWASLWNWF-Z
                                X-NQQEKNEQELLELDKWASLWNWF-Z
                               X-QNQQEKNEQELLELDKWASLWNWF-Z
                              X-SQNQQEKNEQELLELDKWASLWNWF-Z
                             X-ESQNQQEKNEQELLELDKWASLWNWF-Z
                            X-EESQNQQEKNEQELLELDKWASLWNWF-Z
                           X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
                          X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
20
                         X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                        X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                       X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                      X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                     X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                    X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                   X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP178like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some / conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. 10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to 25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, 10 as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate 15 intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

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5.2. <u>DP107 AND DP107-LIKE PEPTIDES</u>

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1_{LAI} transmembrane (TM) gp41 protein, as shown here:

NH₂-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH (SEQ ID:25)

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In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group $(-NH_2)$ and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "2" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred 20 "X" or "Z" macromolecular group is a peptide group.

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TABLE II DP107 (SEO ID: 25) CARBOXY TRUNCATIONS

X-NNL-Z X-NNLL-Z X-NNLLR-Z X-NNLLRA-Z X-NNLLRAI-Z X-NNLLRAIE-Z X-NNLLRAIEA-Z X-NNLLRAIEAQ-Z X-NNLLRAIEAQQ-Z X-NNLLRAIEAQQH-Z X-NNLLRAIEAQQHL-Z X-NNLLRAIEAOOHLL-Z X-NNLLRAIEAOOHLLO-Z X-NNLLRAIEAQQHLLQL-Z X-NNLLRAIEAQQHLLQLT-Z X-NNLLRAIEAQQHLLQLTV-Z X-NNLLRAIEAQQHLLQLTVW-Z X-NNLLRAIEAOOHLLOLTVWO-Z 15 X-NNLLRAIEAOOHLLOLTVWQI-Z X-NNLLRAIEAQQHLLQLTVWQIK-Z X-NNLLRAIEAQQHLLQLTVWQIKQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQL-Z X-NNLLRAIEAQOHLLQLTVWQIKQLQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z X-NNLLRAIEAQOHLLQLTVWQIKQLQAR-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z 20 X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z 25 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA DP178 (SEO ID:25) AMINO TRUNCATIONS

```
X-KDQ- Z
                                                    X-LKDQ- Z
                                                  X-YLKDO- Z
 5
                                                 X-RYLKDQ- Z
                                                X-ERYLKDQ- Z
                                               X-VERYLKDQ- Z
                                              X-AVERYLKDQ- Z
                                             X-LAVERYLKDQ- Z
                                            X-ILAVERYLKDO- Z
                                           X-RILAVERYLKDO- Z
                                          X-ARILAVERYLKDQ- Z
10
                                         X-QARILAVERYLKDQ- Z
                                        X-LQARILAVERYLKDQ- Z
                                       X-QLQARILAVERYLKDO-.Z
                                      X-KQLQARILAVERYLKDQ- Z
                                     X-IKQLQARILAVERYLKDQ- Z
                                    X-QIKQLQARILAVERYLKDQ- Z
                                   X-WQIKQLQARILAVERYLKDQ- Z
15
                                  X-VWQIKQLQARILAVERYLKDQ- Z
                                X-TVWQIKQLQARILAVERYLKDQ- Z
                               X-LTVWQIKQLQARILAVERYLKDQ- Z
                              X-QLTVWQIKQLQARILAVERYLKDQ- Z
                             X-LQLTVWQIKQLQARILAVERYLKDQ- Z
                            X-LLQLTVWQIKQLQARILAVERYLKDQ- Z
                           X-HLLQLTVWQIKQLQARILAVERYLKDQ- Z
                          X-QHLLQLTVWQIKQLQARILAVERYLKDQ- Z
20
                         X-QQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                        X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                       X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                      X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                     X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                    X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                   X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
25
                  X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                 X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
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The one letter amino acid code is used.

Additionally,

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"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid 20 conservation is of a periodic nature, suggesting some/ conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of 25 the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid 30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to 25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.

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Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiquous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

5.3. DP107 and DP178 ANALOGS

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Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1_{LAI} enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (<u>i.e.</u>, other than HIV-1_{LAI}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41 peptide region of other (<u>i.e.</u>, non HIV-1_{LAI}) HIV-1 isolates may include, for example, peptide sequences as shown below.

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NH₂-YT<u>NTIYTLL</u>EESQNQQEKNEQELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH2-YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF-COOH (SEQ ID:4);

 NH_2 -YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV- $1_{\rm SF2}$, HIV- $1_{\rm RF}$, and HIV- $1_{\rm MN}$ isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding position in the DP178 (SEQ ID:1) peptide. One such

DP178 analog, DP-185 (SEQ ID:3), is described in the-Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV- $2_{\rm NIHZ}$ isolate has the 36 amino acid sequence (reading from amino to carboxy terminus):

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NH2-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations of the HIV-2_{NHZ} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group.

Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a

covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE III

HIV-2_{NUM7} DP178 analog carboxy truncations.

X-LEA-Z X-LEAN-Z X-LEANI-Z X-LEANIS-Z X-LEANISQ-Z X-LEANISQS-Z X-LEANISQSL-Z X-LEANISQSLE-Z X-LEANISQSLEQ-Z X-LEANISQSLEQA-Z X-LEANISQSLEQAQ-Z X-LEANISQSLEQAQI-Z X-LEANISQSLEQAQIQ-Z X-LEANISQSLEQAQIQQ-Z X-LEANISQSLEQAQIQQE-Z X-LEANISQSLEQAQIQQEK-Z X-LEANISQSLEQAQIQQEKN-Z X-LEANISQSLEQAQIQQEKNM-Z X-LEANISQSLEQAQIQQEKNMY-Z 15 X-LEANISQSLEQAQIQQEKNMYE-Z X-LEANISQSLEQAQIQQEKNMYEL-Z X-LEANISQSLEQAQIQQEKNMYELQ-Z X-LEANISQSLEQAQIQQEKNMYELQK-Z X-LEANISQSLEQAQIQQEKNMYELQKL-Z X-LEANISQSLEQAQIQQEKNMYELQKLN-Z X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z X-LEANISOSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV HIV-2_{NDHZ} DP178 analog amino truncations.

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X-NWL-Z
                                                    X-TNWL-Z
                                                   X-FTNWL-Z
                                                  X-VFTNWL-Z
 5
                                                 X-DVFTNWL-Z
                                                X-WDVFTNWL-Z
                                               X-SWDVFTNWL-Z
                                              X-NSWDVFTNWL-Z
                                             X-LNSWDVFTNWL-Z
                                            X-KLNSWDVFTNWL-Z
                                           X-QKLNSWDVFTNWL-Z
                                          X-LQKLNSWDVFTNWL-Z
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                                         X-ELQKLNSWDVFTNWL-Z
                                        X-YELQKLNSWDVFTNWL-Z
                                      X-MYELQKLNSWDVFTNWL-Z
                                      X-NMYELQKLNSWDVFTNWL-2
                                    X-KNMYELQKLNSWDVFTNWL-Z
                                   X-EKNMYELQKLNSWDVFTNWL-Z
                                  X-QEKNMYELQKLNSWDVFTNWL-Z
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                                 X-QQEKNMYELQKLNSWDVFTNWL-Z
                                X-IQQEKNMYELOKLNSWDVFTNWL-Z
                               X-QIQQEKNMYELQKLNSWDVFTNWL-Z
                              X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
                             X-QAQIQQEKNMYELQKLNSWDVFTNWL-Z
                            X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                           X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                          X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
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                         X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                        X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                       X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                      X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                     X-ANISQSLEQAQIQQEKNMYELOKLNSWDVFTNWL-Z
                    X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                   X-LEANISQSLEQAQIQQEKNMYELOKLNSWDVFTNWL-Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV).

Primary amino acid sequence homology between HIV-1 and

Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for

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identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within Dp107. It does, however, identify a region within Dp178 beginning eight amino acids N-terminal to the start of Dp178 and ending eight amino acids from the C-terminus. The Dp107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the Dp107 coiled-coil region. Conversely, the Lupas algorithm identified the Dp178 region as a potential coiled-coil motif. However, the peptide derived from the Dp178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4,
ALLMOTI5 and PLZIP motifs, were designed and
engineered to range in stringency from strict to
broad, as discussed in this Section and in Section 9,
with 107x178x4 being preferred. The sequences

identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first 10 position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed 20 or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

The ALLMOTI5 is written as follows:

{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, ... G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino a cid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

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The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four consecutive heptad repeats (thus the repeat of—the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in Table VII, below at the end of this Section, being preferred.

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The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.

19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, PICTLZIP and P2CTLZIP search motifs, Table XI lists viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII 1sts viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

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The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178, above, in Section 5.1. For example, these peptides

may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory 20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX 25 presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and 30 Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped 35 according to the specific virus which they inhibit,

including respiratory syncytial virus, human parainfluenza virus 3, simian immunodeficiency virus and measles virus.

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TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

PCCTVE	АПЛАЮПЯ	ser (no bacterioghages)	Т	T	100	100	ABEA	ABFAG		1 1 1 1 1
FILERAME			3:] } !!	70-100	Ī	Ţ_	:		
PINK TAVPS	POTENTIAL I TO KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PSU)	Ţ.	14.20	191 446	614.678	1045.1079	113:1176	115.13h	- Section in
PINK TAVSY	POTENTIAL IN KD PROTEIN	TOBACCO MATTLE VIRUS (STRAIN STAI	T				1-		:	
PSSKD HSV6U	55 B KD PROTEIN	HERPES SINDLEX VIXUS (TYPE 6 / STRAIN GLANDALIUS)	1	100-144						:
PAAMT HOVAN	DELTA ANTIGEN	IEPATITIS DELTA VIKUS (ISOLATE ANIEKICAN)		90-144						:
PAANT HOVD)	DELTA ANTIGEN	HEFAILIS DELIA VIRUS (ISOLATE DISO)		100-144						
PAANT MOVIT	DELTA ANTIGEN (ALPHA ANTIGEM)	HETAILIS DELIA VINOS (1905A) E LIAMANA	1							_
PAANT HOVIL!	DELTA ANTIGEN	HEPATITIS DELIA VIKUS (1301.A1C LENANOV.1)		100.144						:
PAANT KOVHI	DELTA ANTIGEN	IEPATITIS DELTA VIRUS (ISOLATE JAPANISE ALI)								:
PAAMT HDVA?	DELTA ANTIGEN	REPATITIS DELTA VIRUS (ISOLATE JAPANENI: NI-3)								
PAANT HDVNA	DELTA ANTIGEN	IEPATITIS DELTA VIRUS (ISOLATE NAURU)		100-144						
PAANT KOVSI	DELTA ANTIGEN	IEPATITIS DELTA VIRUS (ISOLATE JAPANESE 5·1)	9-1	8						1
A A VET	DEI TA ANTIGEN	IEPATITIS DELTA YIRUS (ISOLATE JAPANESE S-1)	1.49	100-144						
	OELTA ANTIGEN	IEPATITIS DELTA VIRUS (ISOLATE WOODCIIUCK)	1-48	100.144						:
TOWN TOWN	ANTITUD CAREN JII HOMOLOG	FOWLPOX VIRUS (ISOLATE ID-438)	11.10							: :
משלים ומיים	A KD A. TVPE INCH LISION PROTEIN	VACCINIA VIRUS (STRAIN WR)	14.57	420.564	170-625					:
2000	ALTYPE INCLUSION PROTEIN	VAUOLA VIRUS	425-535	531-565	\$11-628					_
117.00	AT BUT TO ANCIDENCE FACTOR	HERPES SIMPLEX VIRUS (TYPE I)	104.345							
LVIIIZ HSVII	ALTA INVISITIONING FACTOR	HERPES SDAPLEX VIRUS (TYPE I)	107-139	104.145						-
PATIZ HSVII	ALTA INVESTIGATION FACTOR	FOLIME HERPESVIRUS TYPE ((STRAIN ABAP)	101-147	264-331	L.					
PATTI HSVEB	ALTHA IRANS-INDOLING FACTOR	VACCINIA VIRUS (STILATA COPENHAGEN)	79-134	319-363						
PATI) VACCE	PUTATIVE A-1 TPE INCLUSION PROJECT	VACCIONA VIBILE	79-134							
PATES VACEV	PUTATIVE A-TYPE INCLUSION PROTEIN	TOTAL PARTER WATER COMPANY DIRECTOR	204.161	101.420						<u> </u>
PATI2 VZVD	ALPHA TRANS-INDUCING FACTOR	VAUCELLA-LOSIER VIROS (SIRAIR DORIAS)	10.13							
PATU VACCV	PUTATIVE A-TYPE INCLUSION PROTEIN	VACCINIA VIXUS	9	100 700						
PATTIV HSV3)	ALPHA TILANS-INDUCING PROTEIN (YANNES)	HEAPES SOULEX VINUS (TYPE 2)		100-076						: : :
PATTN MSV2H	ALPHA TRANS-INDUCING PROTEIN (VAWES)	HEAPES SIMPLEX VIRUS (TYPE 1)	171.222	184-381						· · · · · · · · · · · · · · · · · · ·
PATTN HSVBP	ALPHA TRANS-INDUCING PROTEIN	BOVINE HERPESVIRUS TYPE I	195.256							
PATTN MSVEB	ALPHA TRANS-INDUCING PROTEIN	EQUINE HEMPESVIRUS TYPE I	241-289							
PATTY VZVD	ALPHA TRANS-INDUCING PROTEIN (VANICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	206-252							;
PATT COMPX	A. TYPE DACLUSION PROTEIN	CONFOX VIRUS	14-57	428-526	112-566	\$72.629	103-939	8	-	: :
Part 1 FRV	PROTEIN BOLF2	EPSTEIN-BARR VIRUS (STRAIN 895-1)	90-131							
Pari I FAV	TRANSCRUTION ACTIVATOR BALF!	EPSTEIN-BAJA VIRUS (STRAIN D95-8)	150-117							: : !
PCOAT POVIEA	COAT PROTEIN VP	POLYOMAVIRUS BK	107.141							1
PCOA! POWE	COAT PROTEIN VP	POLYGMAVTRUS BK	107.141							
TOTAL POWER	COAT PROTEON VP	HAMSTER POLYOMA VIRUS	159.195						-	
PCOAT EVAN	COAT PROTEIN VP1	SIMILAN VIRUS 40	13.143					İ	1	
PCDA1 BFDV	COAT PROTEIN VP3	RUDGENIGAR FLEDGLING DISEASE VIRUS	141:313						1	
PCOA3 POVIIA	COAT PROTEIN VP2	POLYOMAVIRUS DK (STRAIN AS)	14-64	11:11						
PCOA1 POVBK	COAT PROTEIN VP2	POLYOMAVIRUS DK	14-64	117-338						:
PCOA3 POVBO	COAT PROTEIN VP2	BOVINE POLYONIAVIRUS	35.76	2.28					-	
PCDA2 POVICE	COAT PROTEIN VP3	HAMSTER POLYOMA VIRUS	7:48	12.20						:
PCOA3 POVIC	COAT PROTEIN VP3	POLYOMAYTRUS JC	4.64	333.267						
PCOA2 POVLY	COAT PROTEIN VP3	LYNCHOTROPIC POLYGNIAVIRUS	14.78	26-20					-	
PCOA2 POVAD	COAT PROTEIN 172	MOUSE POLYONIAVIRUS (STRAIN 1)		3						
PCOA2 POWA	COAT PROTEIN VP2	MOUSE POLYONIAVIRUS	5:32	33.13						
PCOA3 POWAC	COAT PROTEIN VP3	MOUSE POLYOMAVIRUS	5.72	<u>=</u>						
PCOAS POWER	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	15.56	=======================================						
200	COAT PROTEON VP3	SDAIAN VINUS 40	14.62	221.262	118-352					
PONT ABLOW	COATPROTEIN	ABUTILON MOSAIC VIRUS (ISOLATE WEST MDIA	180-214							
VALUE ACTIVATION	COATPROTEIN	APPLE CHLOROTIC LEAF SPOT VIRUS	154-110							
PCOAT AFTEV	COATPROTEDIVE	AEDES DENSONUCLEOSIS VIRUS	141-114						-	-
POAT AMOV	COAT PROTEIN	ANTICHOKE MOTTLED CRIMKLE VIRUS	76-70	8						
MAT BIRV	COAT PROTEIN	BEAN LEAFROLL VIAUS	12:13							
Down and									-	

138 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		T	AB Virgin (no bacteriophogra)								
DOUR POINT DOUGLE VILLOW NO. 19.11 DOUGLE VILLOW NO. 19.11		IALLANDIIS		Ţ	Т	T	1	<u>)</u>			4
COAT POOLEN DALEY TILLOW POARA VINIS 16-171 COAT POOLEN DALEY TILLOW POARA VINIS 16-171 COAT POOLEN DALEY TILLOW POARA VINIS 16-171 COAT POOLEN 15-17 16-171 COAT POOLEN 15-17 16-17 COAT POOLEN 15-17 17-17 COAT POOLEN 15-17 17-17 COAT POOLEN 15-17 17-17 COAT POOLEN 15-17 17-17 COAT POOLEN 17-17 17-17	THE MANUE	PROTEIN	BROADE MOSANC VIRUS	1	1						4
COLT FOOTEN COLT FOOTEN 164-179 164-17	VII. 1	COAT PROTEIN	SALES VELLOW DWANT VIRUS	101							4
OOL PROTECT	IAGA ATOM	COAT PROTEIN	SALES SELECTION DWARF VIRUS	161.197	†						-
COAT PROTECT COAT	PCOAT BYDYA	COAT PROTEIN	AARI EV VELLOW DWANT VIRUS	100.198	+						-
COLY FROTEIN COLGING CHARGE (VILL) 15.90 18.21 COLY FROTEIN COLGING CHARGE (VILL) 5.90 18.21 COLY FROTEIN COLA FROTEIN 5.90 18.21 COLY FROTEIN COLA FROTEIN 5.90 18.21 COLY FROTEIN COLA FROTEIN 15.91 18.21 COLY FROTEIN COLA FROTEIN 15.21 18.21 COLA FROTEIN COLOMBER ROSAIC YNUS 18.21	PCOAT BYDY	COAT PROTEIN	BASE EY YELLOW DWALF VIRUS								4
COAT FROTEN COLUNT GOAT ROUTE 15.79 18.71 COAT FROTEN COLUNT GOAT ROUTE 15.79 18.71 COAT FROTEN COLAT FROTEN 15.73 18.73 COAT FROTEN CALATICO MI ROTAL VINUS 18.73 18.73 ROAT FROTEN CALATICO MI ROTAL VINUS 18.73 18.73 COAT FROTEN CALATICO MI ROSAC VINUS 18.73 18.73 COAT FROTEN	PCOAT BYDYA	COAT PROTEIN	CALL DWER MOSAIC VIRUS (STRAIN	Ī							-
COAT FROTEN COAT FROTEN SAPON 18-121 COAT FROTEN COAT FROTEN SAPON 18-121 COAT FROTEN CAAL FROTEN SAPON 18-121 FROM FROTEN CAAL FROTEN SAPON 18-121 COAT FROTEN CACAL FROTEN SAPON 18-121 COAT FROTEN SAPO	SCOAT CAMVC	COAT PROTEIN	CALL THE CASE ANDSAIC VIRUS	T							-
COAT FROTEN CLAMITO STATE (VILLE) 15-15	PCOAT CANOD	COAT PROTEIN	CAULITICALES NIOSAIC VIRUS	1							-
COLT FROTEN CALLITOWER NOONE VIRIS 13-34 113-34	2010	COAT PROTEIN	CAUCITICATE ADEAIT VIRUS		117						· -
COLT FROTEN COLT FROTEN 19-11	VO. 1	COAT PROTECT	CAULIPLOWER PROSPIC VIETE		2						_
COLATIONER COL	MOAT CANY	COAT BOOTER	CAULIFLOWER MOSAN, VINCE	15:51							!
COAT FROTEIN COWER A GROONIC STORE LA VARIS 181-218 181-21	PCOAT CAMYS	731041	CARNATION MOTTLE VIRUS	49.170							!_
	PCOAT CARMY	COATTRUE	COWPEA CHLOROTIC MOTTLE VINUS	103.326						-	!
MAJOR CAPID FOOTEN	PCOAT COAV	COATPROTEIN	CARNATION ETCHED RING VIRUS								÷
AUTORICATION CASSAVA LATERY VIRUS COAT PROTEIN CASSAVA LATERY VIRUS 131-187	PCOAT CERV	PROBABLE COAT PROTEIN	PARAMECIUM BURSANA CINCORELLA VIRUS I								
COAT PROTEIN COAT PROTEIN 13-117	PCOAT CHIVE	NIAJOR CAPSID PROTEIN	CASSAVA LATENT VIAUS							-	-
COAT PROTEIN CUCHARE NOSAIC VINUS COAT PROTEIN	PCOAT CLVK	COAT PROTEIN	CASSAVA LATENT VIRUS								<u>-</u>
COAT PROTEIN CUCABBE HOSAIC VINUS 113-187 COAT PROTEIN ELIPE CALICIVARIS 113-187 COAT PROTEIN FELINE CALICIVARIS 114-189 COAT PROTEIN FELINE CALICIVARIS 114-189 COAT PROTEIN FILLA MIDESCERY VINUS 113-181 COAT PROTEIN GALICIVARIS 113-181 COAT PROTEIN ALLES STRAK VINUS 113-181 COAT PROTEIN FILLA MALES STRAK VINUS 113-181 COAT PROTEIN FORALVA PROVINUS 113-181 COAT PROTEIN	PCDAT CLVN	COAT PROTEIN	CINTIAMER MOSAIC VIRUS				-				_
COAT PROTEIN CUCKABER NOSAIC VIRUS 113-181 COAT PROTEIN CUCKABER NOSAIC VIRUS 114-181 COAT PROTEIN CUCKABER NOSAIC VIRUS 114-181 COAT PROTEIN CUCKABER NOSAIC VIRUS 114-181 COAT PROTEIN CUCKAR PLATE LOSAIC VIRUS 114-181 COAT PROTEIN EGGELANT PLOSAIC VIRUS 114-181 COAT PROTEIN FELINE CALICIVARIS 114-181 COAT PROTEIN ALLES TRACK VIRUS 114-181 COAT PROTEIN ALLES TRACK VIRUS 114-181 COAT PROTEIN ALLES TRACK VIRUS 114-181 COAT PROTEI	PCOAT CALVIC	COAT PROTEIN	CICIAMER MOSAIC VIRUS					-	_		
COAT PROTEIN CUCUMBER NOSAIC VITUS 113-111 113-1	200	COAT PROTEIN	COCOMBED VOCATO VIRUS	133-107						_	_
COAT PROTECH CUCUMBER NOSAIC VILUS 113-181 113-1	100	COAT PROTEIN	COCOMBER PLOS AND	133-167					-	-	_
COLVERGE NOSALE VINUS 191-187		COAT PROTEDY	CUCURIBER PIOSAIC VINOS	1133-187				-	-		-
COAT PROTEIN CUCUABER MOSAIC VRUS 19-391	NOAT CAN	COAT PROTEIN	CUCUMBER MODAIL VINOS	133-147		i		1	1	 -	: -
COAT PROTEIN CICLOMBEA PECKOSIS VINUS 184-318 18	PCOAT CHAME		CUCUMBER MOSAIC VIRUS	136.165					1	-	+
COAT PROTEIN COLONE STRAITE MOSAIC VRUS FI-100 COAT PROTEIN CITUST PROTEIN 163704 COAT PROTEIN CITUST PROTEIN 163704 COAT PROTEIN COAT PROTEIN 163704 COAT PROTEIN FELINE CALLICIVRUS 16370 COAT PROTEIN FELINE CALLICIVRUS 16470 COAT PROTEIN FINAL IAM BEDESCENT VIRUS 16470 CASTO PROTEIN JALLES FIRLE WANDS 1741 COAT PROTEIN PORTAC PROVINUS 1741 COAT PROTEIN PORTAC PROTEIN 1741	PCOAT CANY	COAT PROTEIN	CUCUMBER NECROSIS VIRUS	116.311						1	-
COAT PROTEIN CITTUS FRASTEA, VARUS 1972 HODE COAT PROTEIN COAT PROTEIN 60-74 COAT PROTEIN COAT PROTEIN 60-74 COAT PROTEIN 60-74 COAT PROTEIN 60-74 COAT PROTEIN 76-70 COAT PROTEIN 77-70 COAT PROTEIN 77-70 <td>PCOAT CHV</td> <td>COAT PROIEIN</td> <td>CHEORUS STRUATE MOSAIC VIRUS</td> <td></td> <td></td> <td></td> <td>-</td> <td></td> <td></td> <td>-</td> <td>T</td>	PCOAT CHV	COAT PROIEIN	CHEORUS STRUATE MOSAIC VIRUS				-			-	T
COAT PROTEIN CLOVER YELLOW MOSAIC VIRUS 40.74	PCOAT CSMV	COAT PROTEIN	CITRUS TRUSTEZA VIRUS	2				-			-
COAT PROTEIN EGGPLANT MOSAIC VIRUS 40.146	PCOAT CTV36	COAT PROTEIN	CLOVER YELLOW MOSAIC VIRUS	207.701			-				<u> </u>
COAT PROTEIN FELINE CALICIVRUS 403.466 COAT PROTEIN FELINE CALICIVRUS 403.466 COAT PROTEIN FELINE CALICIVRUS 116.533 166-600 COAT PROTEIN FELINE CALICIVRUS 116.533 166-601 COAT PROTEIN FIGURIA FORTAL MOSAIC VRUS 164-130 26-134 COAT PROTEIN FITTULA RIDESCENT VRUS 164-130 96-134 COAT PROTEIN STRUC LASSO PROTEIN 164-130 96-134 COAT PROTEIN MALES STRUE VIRUS 17-14 17-14 COAT PROTEIN MALES STRUE VIRUS 18-131 16-131 COAT PROTEIN MALES STRUE VIRUS 18-131 16-131 COAT PROTEIN MALES STRUE VIRUS 18-131 16-130 COAT PROTEIN MALES STRUE VIRUS 18-131 16-130 COAT PROTEIN MALES STRUE VIRUS 18-131 16-130 COAT PROTEIN POPLAM MOSAIC VIRUS 18-131 16-130 V COAT PROTEIN POPLAM MOSAIC VIRUS 18-130 V COAT PROTEIN 16-	PCOAT CYNY	COATPROTEIN	ECCEL ANT MOSAIC VIRUS	2	35, 55						i
COAT PROTEIN FELINE CALICIVINUS 102-330 105-330 COAT PROTEIN FELINE CALICIVINUS 116-137 506-247 COAT PROTEIN FIGWORT MOSAK VARUS 164-370 164-370 FROGABLE COAT PROTEIN FONTAL MUDESCENT VARUS 164-370 164-370 CAPSID PROTEIN TITULA RUDESCENT VARUS 17-36 164-370 CAPSID PROTEIN GALLO RUDESCENT VARUS 17-36 164-310 COAT PROTEIN GALLE STREAK VARUS 17-36 164-311 COAT PROTEIN MALZE STREAK VARUS 187-31 167-31 COAT PROTEIN MALZE STREAK VARUS 167-31 167-31 COAT PROTEIN MALZE STREAK VARUS 167-31 167-31 COAT PROTEIN FEA EALY BROWNING VARUS 167-31 167-31 VO COAT PROTEIN FEA EALY BROWNING VARUS 167-31 167-31	PCOAT EPMY	COAT PROTEIN	FEI DE CALICIVIRUS	T	38		1	-			+
COAT PROTEIN FELNE CALICIVIRUS 19-533 185-503 COAT PROTEIN FELNE CALICIVIRUS 164-199 206-347 COAT PROTEIN FIGWORT MOSAIC VRUS 164-199 206-347 COAT PROTEIN FIGWORT MOSAIC VRUS 164-130 106-134 CA-SID PROTEIN GHLO RUDESCERT VRUS 16-134 11-35 COAT PROTEIN ALLY STRUE VRUS 17-36 14-131 COAT PROTEIN ALLY STRUE VRUS 18-21 18-21 COAT PROTEIN ALLE STREAK VRUS 18-21 18-21 COAT PROTEIN DODORTOGLOSSURA RINGSFOT VRUS 18-21 24-440 COAT PROTEIN POTALA WOSAIC VRUS 18-21 24-41 COAT PROTEIN POTALO WOSAIC VRUS 18-21 18-21 COAT PROTEIN POTALO WOSAI	POAT FOVO	COAT PROTEIN	TEL INT CALICIVIRUS	7	200-000		-	-	_		
COAT PROTEIN 144-199 204-247 PROBABLE COAT PROTEIN FIGWARD CHAIL 144-199 204-247 PROBABLE COAT PROTEIN FIGWARD CHAIL 100-134 100-134 CAST FROTEIN STATUL MADDESCENT YRUS 11-13 11-13 CASTO FROTEIN GALLO FROTEIN 11-13 11-13 CAST FROTEIN GALLO FROTEIN 11-13 11-13 COAT PROTEIN JALLE STRLEK YRUS 11-13 14-140 COAT PROTEIN JALLE STRLEK YRUS 11-13 14-140 COAT PROTEIN JALLE STRLEK YRUS 11-13 14-140 COAT PROTEIN JALLE STRLEK YRUS 11-13 14-13 COAT PROTEIN POPLAR BOSHIC YRUS 11-13 14-13 COAT PROTEIN POPLAR BOSHIC YRUS 11-13 14-13 COAT PROTEIN POPLAR BOSHIC YRUS 11-13	TO THE	COAT PROTEIN	TELLING CALL COMMENTS	٦	189.603			-			
TOO ALLE COAT PROTEIN TOWARD, VILLE COAT PROTEIN TOO ALL COAT PROTEIN TOU ALL RUDGESCENT VRUS 19-13	1	COAT PROTEIN	PELINE CALIFORNIA	144-199	206-247		-			-	
COAT PROTEIN ITOMARL MADESCENT VIRUS 90-134 CLASSID PROTEIN SINGLIAM RADESCENT VIRUS 13-36 13-36 CLASSID PROTEIN GHLO INDESCENT VIRUS 13-36 13-36 13-36 COAT PROTEIN LAY STAPFORLESS VIRUS 13-36 14-131 14-131 COAT PROTEIN MAZES STREAK VIRUS 187-231 187-231 187-231 COAT PROTEIN GOAT PROTEIN 187-231 187-231 187-231 OCAT PROTEIN POTATO YELLOW NOSAIC VIRUS 187-131 444-440 V COAT PROTEIN POTATO YELLOW NOSAIC VIRUS 187-236 187-130 V COAT PROTEIN ALSPREANT VIRUS 187-236 187-130 V COAT PROTEIN	100	PROBABLE COAT PROTEIN	FIGWORI MOSAIC VINOS	161-130				1	1		-
CAPSID FROTEIN ITPULA MUDESCENT VIOUS No.134 CAPSID FROTEIN GINGLAND ROBESCENT VIAUS 17-15 17-15 17-16 17-16 17-16 17-16 17-16 17-16 17-16 17-16 17-16 17-16 17-16 17-17 17-16 17-16 17-17	1502	National Nat	POXIAL MOSAL VINCE	90-134				-			T
CAPSID PROTEIN SINULIAM MURESCENT VINUS 11-15 15-219 15-	MOAT FOR	CARTO BOTTEN	TIPULA MUDESCENI VIRUS	90-124					1	1	+
COAT PROTEIN CHILD RIDESCENT VARUS 12:10 215:219	PCOAT DIVI	National Parties	SINDLING INDESCENT VINUS	31.5				-	+	1	+
COAT PROTEIN LATY SYMPTOMLESS VINUS 13-131 14-131	PCOAT DAZ	Costorio	CHILO INDESCENT VIRUS	17.70	155-289					1	+
COAT PROTEIN MAZES STRAK VRIUS 187-221 COAT PROTEIN GOAT PROTEIN 187-221 COAT PROTEIN PRA EALVOYRUS 197-131 COAT PROTEIN PRA EALVOYRUS 13-114 V COAT PROTEIN POTATO VRIUS 16-81 V COAT PROTEIN ALSPBERAY BUSHY DWAK VIRUS 16-41 R COAT PROTEIN 16-41 14-41 R COAT PROTEIN 16-41 14-41 </td <td>POOAT DAVE</td> <td>CASIL FROITER</td> <td>LALY SYMPTOMALESS VIRUS</td> <td>1.76</td> <td>16-121</td> <td></td> <td></td> <td></td> <td></td> <td>1</td> <td>+</td>	POOAT DAVE	CASIL FROITER	LALY SYMPTOMALESS VIRUS	1.76	16-121					1	+
COAT PROTEIN MAZES STREAK VRUS 187-221 COAT PROTEIN VP1 CAMPE PARVOVRUS 180-114 444-410 D COAT PROTEIN VP1 CAMPE PARVOVRUS 180-114 444-410 T COAT PROTEIN VP1 POPLAA MOSAIC VRUS 18-31 16-31 V COAT PROTEIN POTATO VRUS 16-31 16-31 T COAT PROTEIN POTATO VRUS 16-31 16-31 T COAT PROTEIN POTATO VRUS 16-31 16-31 T COAT PROTEIN ASPREANY VRUS 16-31 16-31 T COAT PROTEIN <t< td=""><td>PCOAT LSV</td><td>COALTROITIN</td><td>MAIZE STRIPE VIRUS</td><td>103.331</td><td></td><td></td><td></td><td></td><td></td><td></td><td>+</td></t<>	PCOAT LSV	COALTROITIN	MAIZE STRIPE VIRUS	103.331							+
COAT PROTEIN MAZE STREAK VIRUS 167-221 167-221 167-222	PCOAT MSTV	COALTROIEN	MAIZE STREAK VIRUS	187							1
COAT FROTEIN WAZE STRAAK VIRUS 105-139	PCOAT MSVK	COALFROIEIN	MAIZE STREAK VIRUS	163.331					-	1	1
COAT PACTEIN ODONTOGLOSSUA RINGS FOT VIRUS 100-114 (44-440	PCOAT MSVN	COAT PROTEIN	MAIZE STREAK VIRUS	91						-	1
COAT PAGTEIN BOVING PAAVOVIAUS 491-114	PCOAT MSVS	COAT PROTEIN	ODONTOGLOSSUM RINGSPOT VIRUS		037.777		_				1
OCAL PROTEIN V2 CANTRE PARVOVINUS 497-231 7 COAT PROTEIN V21 FEA EALY BROWNING VIRUS 13-11 7 COAT PROTEIN FOFFER MID MOSAIC VIRUS 16-41 7 COAT PROTEIN FOFFER MID MOSAIC VIRUS 16-41 7 COAT PROTEIN FOFFER MID MOSAIC VIRUS 16-41 7 COAT PROTEIN FOFFER VIRUS 16-419 7 COAT PROTEIN ASTRAIN 140-199 8 ASTRAIN 140-199 140-199 8 ASTRAIN 16-419 140-199 9 ASTRAIN 16-419 140-199 10 COAT PROTEIN 16-419 140-199 10	PCOAT ORSV	COAT PROTEIN	BOVINE PARVOVIRUS	7-087							1
COAT PROTEIN VI PEA EARLY BROWNTHG VIRUS 13-114	PCOAT PAVBO	COAT PROTEIN VP2	CANINE PARVOVIRUS	497.531			-				1
COAT PROTEIN POPLAR MOSAIC VRUS 16-81 COAT PROTEIN POTATO VRUS 10-13 COAT PROTEIN POTATO VRUS 10-13 COAT PROTEIN POTATO VRUS 10-40 COAT PROTEIN POTATO VRUS 10-40 COAT PROTEIN RED CLOVER NECROTIC MOSAIC VRUS 1712-106 V COAT PROTEIN NCES TRUE VRUS 1712-106 V COAT PROTEIN NCES TRUE VRUS 14-64 SQUASH LEAT CURL VRUS 19-21	PCOAT PAVCT	COAT PROTEIN VPI	SEA FARLY BROWNING VIRUS	3:1:4			 		_		
COAT PROTEIN PEPPER MILD MOTTLE VINUS 104-131 151-192 COAT PROTEIN POTATO VRUS 19-134 151-192 COAT PROTEIN POTATO YELLOW MOSAIC VINUS 104-134 140-193 COAT PROTEIN AASPBEINY BUSHY DWALK VINUS 10-48 140-199 V COAT PROTEIN ALED CLOVEL NECOTIC MOSAIC VINUS 171-106 18-130 V COAT PROTEIN SQUASH LEAF CURL VINUS 18-64 18-130	PCOAT PEBV	COAT PROTEIN	SORI AB MOSAIC VIRUS	16-81			-		-		
COAT PROTEIN POTATO VILUS 18-130 18-131 181-132 18-130	V100	COAT PROTEIN	Transce And District Figure	104-138			+	+	-		
COAT PROTEIN POLATO VELLON MOSAIC VIRUS 196-124 / COAT PROTEIN LASPBEANY BUSHY DWALF VIRUS 10-44 140-197 COAT PROTEIN LASPBEANY BUSHY DWALF VIRUS 273-306 273-306 V COAT PROTEIN LACE STRUE VIRUS 34-64 31-130 COAT PROTEIN SQUÁSH LEAF CURL VIRUS 190-234 19-130	SOLUTION S	COAT PROTEIN	TEFFER MALE TO THE TERMS OF THE	31:33	25-332		+	+	+	 -	
V COAT PROTEIN RASPBEARY BUSHY DATA VIRUS 10-44 140-197 COAT PROTEIN KED CLOVEA RECROTIC MOSAIC VIRUS 273-106 373-106 V COAT PROTEIN ACE STRUE VIRUS 34-64 31-120 COAT PROTEIN ACE STRUE VIRUS 16-274 11-120	200	COATPROTEIN	POLATIC VINCE	190-124			1	1		-	
COAT PROTEIN ALSPELLY BUSH DWAS AIC VIRUS 171-106 11-110	LOAI TO	T.	POIATO TELLOW RIGARIC VIRGO	1074	140-199						
V COAT MOTEIN LED CLORL WELKOTK. 114-41 131-130 V COAT MOTEIN IQCS STARE VINUS 14-41 181-130	MOAT PINY	Ŧ	RASPBERAT BUSHT DWANG VINUS	272-306			1	1	1	1	1
COAT MOTEIN SQUASH LEAF CUAL VINUS	AGY VO	T	RED GLOVER MELKOLIA MUSIK	34-64	83-120	39.39	-	+	+	-	
	PCOAT ALCAM	T	MCE STRUE VINOS	190-224			-		1		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NOAT IS	Name of the Party	SQUASH LEAF CURL VIRUS								

		All Virger (as batteriophages)					П	П	П	
ETT P NAME	PROTEIN	YTRUS		ABLAL	AREA?	AREA!	AREAS	AFA F	147	AREA!
POAT BANTA	COAT PROTEIN	SATELLITE MAIZE WHITE LINE MOSAIC VIRUS	66-100							
PCDAT SOCIAL	COAT PROTEIN	SOYBEAN CIE.OROTIC MOTTLE VIRUS	128-166							
PCDAT STAVI	COATPROTEIN	SATELLITE TOBACCO NECROSIS VIAUS I	1.50							
PCDAT STRV2	COAT PROTEIN	SATELLITE TOBACCO NECROSIS VIRUS 2	11.72							
PCOAT TANV	GENOME POLYPROTEIN	TANKALLO MOSAIC VIRUS	7.55							
PCOAT TAV	COATPROTEIN	TOMATO ASPERMY VIRUS	14.48							
PCOAT TBSVB	COATPROTEIN	TOMATO BUSHY STUNT VIRUS	1.33	43-77						-
PCOAT TBSVC	COAT PROTEIN	TOMATO BUSHY STUNT VIRUS	44.78	180						:
PCOAT 1CV	COAT PROTEIN	TURNIP CRINKLE VIRUS	12.46							
PCOAT TOMV	COAT PROTEIN	TOMATO COLDEN NOSAIC VIRUS	166-320							:
PCOAT THOMP	COATPROTEIN	TOBACCO MILD GREEN MOSAIC VIRUS	103-137							
PCOAT TACY	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							!
POOT TANK	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							İ
PCOAT TANCO	COAT PROTEIN	TOBACCO MOSAIC VIRUS	76-138							
PCOAT TANDA	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
PCOAT TANKER	COAT PROTEIN	TOBACCO MOSALC VIRUS	103-137							
PCOAT TANAM	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
100 P	COATEN	TOBACCO MOSAIC VIRUS	103-133							
COVE TOOL	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
COAL INVOK	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
COAL IMAIO	CONTROLEN	TORACCO BATTLE VIRUS	71:100							
PCOAT TRYCA	COALTROILEIN	SOBJECT STATE VISITS	40.101							
PCOAT TRVTC	COAT PROTEIN	TOBACCO VELLOW DIVAGE CIBILS	4							-
PCOAT TYDVA	COAT PROTEIN	TOBACCO TELECOM DIMAGE VINOS								
PCOAT TONY	COAT PROTEIN	TOTAL TELLOW PIOSALL VINOS								!
PCOAT_TYNAVA	COAT PROTEIN	TURNIP YELLOW RIOSAIC VIRUS								1
PCDAT WCLAYO	COAT PROTEIN	WHITE CLOVER MOSAIC VIRUS	167.197							
PCORA HPBGS	CORE ANTIGEN	GROUND SQUIRREL HEPATITIS VIRUS	94-135							
PCORA HEBVE	CORE ANTIGEN	HEPATITIS B VIRUS	11.140							
PCORA WHY!	CORE ANTIGEN	WOODCHUCK HEPATITIS VIRUS I	43.106					1		
PCORA WHYS	CORE ANTIGEN	WOODCHUCK HEPATITIS VIRUS I	10.10				!			
PD250 ASTB?	PROTEIN DISOR	AFRICAN SWINE FEVER VIRUS	198-233						:	
PDINET ADEAT	EARLY ELA DNA-BINDING PROTEIN	HUMAN ADENOVIRUS TYPE 2	91.138							
PDMB1 ADE05	EARLY ELA DNA-BINDING PROTEIN	HUMIAN ADEMOVIRUS TYPE 5	291.334						:	
PONBI EBV	MAJOR DMA-BINDING PROTEIN	EPSTEIN-BARR VIRUS	215-222	718.752	974. 10%	10:7:1061				
PONBI HONVA	PALAION DNA-BINDING PROTEIN	IRAKA CYTONEGALOVIRUS	136-172	101:103			į		: : :	
PONTE HEALT	MAJOR DNA-BINDING PROTEIN	HEAPES SIMPLEX VIAUS	557.595	9.66	769.80)	1039-1140		-		
PDMBI HSVIF	MAJOR DNA-BINDING PROTEIN	HERPES SIMPLEX VIRUS	383.585	197.6-10	764.803	1079-1140			· · · · · ·	
PONB! HSVIK	MAJOR DNA-BINDING PROTEIN	HEAPES SIMPLEX VIRUS	187.191	377.640	769.80)	1079.1140	-			
POWEL HSVB2	MAJOR DNA-BIYDING PROTEIN	BOVINE IERPESVIRUS TVPE. 2	552-501	599.633	1941.131				:	
PONBI HSVEI	MAJOR DNA-BINDING PROTEIN	EQUINE IREAPESYIRUS TYPE I	273-114		ļ			-	:::	
PONEI HSVES	MAJOR DNA-BINDING PROTEIN	EQUINE IGRPESVIRUS TYPE I	617.658	1103-1148					-	
POND! HSVSA	MAJOR DHA-BINDING PROTEIN	Herpesvirus sadiiri	222-259	330-367	506-557	17).707				
POWE MONYS	MAJOR DNA-BINDING PROTEIN	MURINE CYTOMEGALOVIRUS	584-618	987.1125			1	j	-	
PONEI SOUNCE	MAJOR DNA-BINDING PROTEIN	SINITAN CYTOMEGALOVIRUS	525-562							
CVZV IENOT	MAJOR DHA-BINDING PROTEIN	VANCELLA-ZOSTER VIRUS	613-650	1043-1077						•
PONEJ ASPA	DNA LIGASE	AFINCAN SWINE FEVER VIRUS	73.106							:
POR I VACCO	DNA LIGASE	VACCINIA VIRUS	395-436							
PDM J VACCV	DNA LIDASE	VACCIMIA VIRUS	195.436							
PDIALI VARV	DNA LIGASE	VARIOLA VIRUS	195-416							
POPOL ADES	DNA POLYMERASE	HUNAN ADENOVIRUS TYPE 2	667.743							
POPOL ADEOS	DNA POLYMERASE	HIDAAN ADENOVIRUS TYPE S	667.743							
POPOL ADEDI	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE ?	733.800							
									-	

PCGENE	A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A STANKE (#0 Becter Open III)						1		
				ALEAL	ANTA	999	-		-	
Trans.	WATASE	TOXIOPOXVIRUS	2) 64	:03::40		1				!
POPOL ADELE			247.384							
POYOL CBES		CHACKELLA VIXOS PITTA	247-284							
POPOL CHYPA		UNDARIA CIII. CALLECTI	17.51	10.114	171-412					
POPOL CHAPI			183.787	1033-1034						:_
POPOL FOWTY		(0) (3) (3)	5.					-	į	
POPOL HOMA			5.34							.
DIO. HOROS		DUCK IRPATITIS B VIRUS (STRAIGH BUCK ISOLATE ST	5.39	367-138		-	-		1	
POPOL HOTOC		WCK IEPATITIS B VINUS (WILLS	291-325				\downarrow			
POPOL HOTOW		IIIs vinus	5.39	34.365	157.595	4				<u>-</u> -
POPOL POPOS			201-235							:
POPOL HORNE			201-105			_				: :
POPOL HOSVY		0	95 113			L			j	
POPOL HPBVZ			200						İ	. :
POPOL HSVII		HERPES SAPLEX VIRUS (TYPE I / STRAIN ANGELOTTI	211-320			 -				
MAN HIVIA		TERRES STATE EX VIRUS (TYPE 1/STRAIN KOS)	511-559			+				
POPUL HEVIE		STRAFF STATE ST VIRIUS (TYPE 1 / STRAFN SCIS)	911-559			+		-		·
POPOL HSVIS	DHA POLTMERASE	HERPES STAPLEX VIRUS (TYPE 2/STRATH 186)	22.00							:
POPUL HSV21	DNA POLYMENASE	- ALTER DE DE COURTS TYPE I (STRATH APP)	494.528			96, 360	158-101	_		
MAYES	DNA POLYNEILASE	CHANNEL CATHIST (CHANNEL CATHISH VIRUS)	13.67	2. 2. 2. 2. 2. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3.						
537	DNA POLYNERASE	COLOR OF THE PRINCE AND EAR POLYIEDROSIS VIRUS	395-646			-	-			_
200	DNA POLYNERASE	AUTOMATIA CETTA AN COPENIAGEN	627-683	770-118	126-162	1				<u> </u>
	DNA POLYNERASE		627-683	770-111	128-862		-	-	_	ļ ļ_
	DAY POLYACIASE	VACCINIA VIAUS (31 PAIL)	626-682	769-817	827-861		1			<u>:</u> _
אסים יאררי	CANA POR YAGERASE	VARIOLA VIXUS	473-533					-		
POPOL VAN	CNA POLYMERASE	VANCELLA-ZOSTEA VIRUS (STRAIN ZOTTE)	205.336				+	1	1	
DAG VEND	PAIN POI VACERASE	WOODCHUCK HEPAIIIIS VINUS I	160-051					1	1	ļ.
DOLO WINE	TWA POLYNORASE	WOODCHUCK HERAIIIIS VINCES	290-331						-	
DAG WHAS	DAY BOLYMORASE	WOODCHUCK HERAIIIIS VINGS	289-330					1		- -
POPOL WHY	DAY BOT WERASE	WOODCHUCK HERAIIIIS VINUS & WOODCHUCK CLOSE)	160-062							! !_
PDPOL WHYS	SALA BOX WATERASE	WOODCHUCK HEPAILIS VIAUS LINE COLOR	201-235						-	-
POPOL WHY	DAY FOR THE BASE	HEPATITIS & VIRUS (SUBITYE ATW)	2 2 2 3 1 6 3							1
POPON HOBY	DAM SOCIETY OF THE MOCLEOTIDORY	EQUINE HERPESVIRUS TYPE I (STRAIN ABY)	139.223		L					:
POUT HEVED	DEOXTURBING STRIPHOSPHATE MUCLEUTIDOHY		107.141							; -;-
POUT HSYSA	DECATOMORE STREET	HUMAN ADENOVIRUS TYPE 41	771.00			-				+
PEIA ADEAI	EALT EIA 27 TO PROTECT	KUMAN ADENOVIRUS TYPE 40		-	-					_i
PEIBL ADEAD	EIB PROTEIN, LANGE I-ANTIOCA	HIMAN ADEMOVIRUS TYPE 2	20.70		-		 -			-
PEIDS ADEOL	EIB PROTEIN SMALL I ANTIGEN	HUMAN ADENOVIRUS TYPE S		1	-		-			1
PEIBS ADEOS	EIS PROTEIN, SMALL I-MINEY	HUMAN ADENOVIRUS TYPE 12		-						-
PEIBS ADEI3	EIB PROTEIN, SMALL I ANTICES	HUMAN ADEMOVIRUS TYPE 40	1	-			-			<u> </u>
PEIBS ADEAD	EIB PROTEIN, SMALL I-MILIOEN	HUMAN ADENOVIRUS TYPE 41		\downarrow	-	-	_			-
PEIBS ADEAL	EIB PROTEIN, SMALL I ANTINCE	MOUSE ADENOVIRUS TYPE I		-	\ T	-	-			-
PEIBS ADEMI	EIB PROTEIN, SMALL I-MAINSEN	HUMAN ADENOVIRUS TYPE 2		1	-	-				4
PEDIA ADEM	EARLY EIB 14 KD PROTEIN	HUMAN ADENOVIRUS TYPE 3								-
PEDIA ADEDI	EALLY ED 15.3 KD PROTEIN	HUMAN ADENOVIRUS TYPE S		1	1	-				-
PESIA ADEBI	EALTY ED 14.5 KD PROTEIN	HUMAN ADENOVIRUS TYPE 7		+	-					4
PESIA ADEO!	EALTY ED 15.3 KD PROTEIN	MINAAN ADENOVIRUS TYPE 15		1	1					
PELYO ADELS	EALLY ES 30 3 KD GLYCOPROTEIN	MAMAN ADENOVIAUS TYPE 15	3:10	1	+		-	-		.
\$130V 1630	EALLY EJ 70 6 KD GLYCOPROTEIN	LANGAL ADENOVIRUS TYPE 2	10-44		1	+	-			
PEA11 ADE02	PROBABLE EARLY E4 11 KD PROTEIN	LEGICAL ADENOVIRUS TYPE S	3	-	+					
10 ADEDS	PROBABLE EASLY E4 11 KD PROTEIN	EDUTE IN MARK VIRUS (STRAIN B93-9)	2	1	+	+	-			
VEA ENV	EALLY ANTIGEN PROTEIN R	EPETERLIARR VIRUS (STRAIN B93-9)	2		1	+	-	-		Ц
VIE SA	EBNA-4 MICLEAR PROTEIN	12.31 EAT 10.20 A VIBILE	13-71	307.34						
VERN 254	EXTER CASE OFFI	TO A CARLO								

PCCENE	АШМОПІЯ	wer (ne bacterlophages)	T	Т		T	Т	1014	100	1 100
TILE HAME	PROTEIN		J	No.	DE POR	1	T T T T T	Τ	1	
PENI FISTY	ENV POLYPROTEIN PRECURSOR		2/1-1/2				†	Ī	-	
PENNY FREEV	ENV POLYPROTEDN PRECURSOR		341-378							:
	ENV BOX VPROTEIN	AVIAN RETICULOENDOTIELIOSIS VIRUS	420-472							-
אוניי איניי	ENV POR VEROTERA	AVIAN SPLEEN NECROSIS VIRUS	436-478							
VENY AVISA	THE PARTY OF THE P	TRAIN MI)	190-456							į
PENV BAEVI	TAN IN VISITION PRECIENCE	BOVINE INAUMODEFICIENCY VIRUS (ISOLATE 106)	10-44	11.122	221-255	019-015	169-519			
MAIN BINGS	CAN POLITACIEM PACCONOS	BOVINE INSUINODEFICIENCY VIRUS (ISOLATE 137)	10-44	11:13	159-193	130-284	339.639 6	664-124		
TENA BIASI	ENVIOLENTEN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE FLK)	304.379							
A PLAN	SAN POLITACION		104-379							
PENY BLVAU	ENV CALIFOLDIA	BOVING I STREAM VIBILS (AMERICAN ISOLATE VDA)	304.379				- 			
PENV BLVAV	ENV POLYFRUIEIR	MOVING I EINERLIN VIDIG MET GILLA (SOLATE LEZES)	304.379							
PENV BLVB2	ENV POLITIMOTEUR		104.179							:
PENV BLVBS	ENV POLYPROTEIN		200				-			:
PENV_BLVI	ENV POLYPROTEIN	Ţ			111.11	100	i i	-		
PEHV CAEVC	ENV POLYPROTEIN PRECURSOR		2	2013-150						
PENY CAEVO	ENV POCYPROTEIN PRECURSOR	CAPRINE ARTHRITIS ENCEMIALITIS VIRUS (STRAIN GA))	134.193	11:11	11.41	1	-			: :
PENV EIAVI	ENV POLYPROTEIN PRECURSOR		39.76	436-525	359.303	908.710				
PENV ELAVI	ENV POLYPROTEIN PRECURSOR		19.76	436-525	559.393	658.692				
PENV ELAVI	ENV POLYPROTEIN PRECURSOR		39.36	436-525	189-801	658-716				!
PENO ELAVS	ENV POLYPROTEIN PRECURSOR	1	38-76	437-526	\$10.504	659.693				
2 A 1 A 1 A 1 A 1 A 1 A 1 A 1 A 1 A 1 A	ENV POLYPROTEIN PRECURSOR		19.76	416-515	150.503	658.716				:
PEND CIANT	SNV POLYPROTEIN PRECURSOR		39.76	416-525	139-503	658-716				
TOTAL STATE	ENV POLYMENTEN PRECURSOR	2	39.76	436-535	159-563	658-71A				
PENT ELAVE	ENV POLYMENTEN PRECINSOR	MING	39.76	416-525	\$59-563	914-359				
100	SAV BOL VECTER PRECIENTATION		\$63-555	\$67.604						
TENY TENY	CANCEL CARE AND WESTERN PRECIDENCE	S (ISOLATE PETALUNIA)	069-019	119.756						
STATE AND A	ENVELORE BOX VPROTEIN PRECIENCE	Γ	199-109	113.734						
CALL AND	ENVELORE BOX VEGOTEIN PRECIPEOR	Γ	66-123	619-609	314-355					
SENV FI VICE	DAY POLYMOTERN PRECURSOR		497.549	\$61.195						
אלא נו אנו	ENV POLYMOTERY PRECURSOR)W-()	431.530	342-576						
PENV FLVLS	ENV POLYTROTEIN PRECURSOR	٨-٥١)	496-550	562-596						
PENV FIVEA	ENV POLYPROTEIN PRECURSOR	FELINE LEUKEMIA VIRUS (STRAIN SARMA)	415-517	130.573						
PENV FOALO	ENV POLYPROTEIN		141	154.205	121-155	\$63.693	866.903			
PENV PSVČA	ENV POLYPROTEIN PRECURSOR	DNER-ARMSTERN)	491-550	562-596						
PENV PSVCB	ENV POLYPROTEIN PRECURSOR		476-530	\$42-576						İ
PENY FSVSM	ENV POLYPROTEIN PRECURSOR		481.524	\$45.579						1
PEN FSVST	ENV POLYPROTEIN PRECURSOR	IN SNYDER-THEILEN)	496.532							
PEN GALV	ENV POLYPROTEIN PRECURSOR		523-575	387-621						-
PEN HILIA	ENV POLYPROTEIN	HUMAN T-CELL LEUKENIA VIRUS TYPE I (STRAIN ATK)	21:12							
PENV HTLIC	ENV POLYPROTEIN	HUMAN I-CELL LEUKEMIA VIAUS ITTE I (CAUGBEAN ISOLATE JIE-JIE								
PENV HILLIM	ENV POLYPROTEIN						1			
PENV HTLV3	ENV POLYPROTEIN PRECURSOR	HUMAN I-CELL LEUKEMIA VIAUS ITTE II	26.716		344 946					
PENV HVIAS	ENVELOPE POLYPROTEIN GP160 PRECURSOR	HUMAN INGRUNODERICIEMOT VINOS LITE I (ARVINATO)	705 705	11/-910	700-043		+			
PENV HVIBI	ENVELOPE POLYPROTEIN GP160 PRECURSOR	T	205-294	11.010	10.10/		+			
PENV HVIBE	ENVELOPE POLYPROTEIN GP160 PRECURSOR	Т	300-384	907-101	104-501					İ
PENV HVIBN	ENVELOPE POLYPROTEIN GP166 PRECURSOR (COM	3	T	DA :- 100	909-108	161-10/	†			
PENV HVIBA	ENVELOPE POLYPROTEIN GP160 PRECURSOR		T	/1/-(10		, , ,	1			
PENV HVICA	ENVELOPE POLYPROTEIN GP160 PRECURSOR		142.376	\$10.606	676-774	77.133	1			
PENY HVIEL	ENVELOPE POLYPROTEIN GP160 PRECURSOR	T	255.296	502-591	101.70	761.129				.
PENV HVIHI	ENVELOPE POLYPROTEIN GP140 PRECURSOR	Т	505-594	610.712	767-636					
PEN HVIED	ENVELOPE POLYPROTEIN GP160 PRECURSOR	_	505-594	610.712	767.443		+			-
PENY HVID	ENVELOPE POLYPROTEIN GPI00 PRECURSOR	Т		317.603	622-223	100	1	T		
PEN HVIR	ENVELOPE POLYPROTEIN GP160 PRECURSOR	HUMAN MAKUNODEFICIENCY VIRUS TYPE I (FICSF BOLATE)	374.363	497-386	FO)-/GE	239-413	1]		

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FIGENE FILE NAME FEW HVIKS	A 1 1 NO 119	All Virgini in a second								
V HVIKB		21105	TVIN	1	200		115-817	1 118	773-645	
V HYIKB	PROTEIN	31	T	1		Г				
******	ENVELOPS POLYPROTEIN GP166 PRECURSOR		٦	Т	T					
	ENVELOPE POLYPROTEIN GP140 PRECURSOR	٦	T	613-710	116 617	734-141				
201176	PAYEL OPE POLYPROTEIN GP140 PRECURSOR	٦	Т							
ENV UVILON	ENVELOPE POLYPROTEIN CP160 PRECURSOR	링	7			163.635				
ENV HVINS	ENVELOPE POLYPROTEIN GP160 PRECURSOR		T	93.384	101-101	344.812				
CALVI VAS	ENVELOPE POLYPROTEIN GP140 PRECURSON	٦	٦	497-393	27.010					
ANION ANION	ENVELOPE POLYPROTEIN GPIM PRECURSOR	_	٦	610-712	707.843	134.000				
CAN INIBN	ENVELOPE POLYPROTEIN GPIGO PRECURSOR	Ε)	٦	\$07-603	27.610					
1	ENVELOPE POLYPROTEIN OPIGO PRECUISOR	HUMAN BANDAGE CITETY VIETS TYPE I (SF162 ISOCATE)	496-515	602-703	738-830					
ENV HVIAG	SANCE OF BOTH YPROTEIN GPI40 PRECURSOR	HOMAN BOAURODE ICIENCE VINCE LYCEN ISOLATE)	333-366	494-590	607.708	763-637				
PENY HVIST	THE CURSON	HOMAN BORRNODEFICIENCY VINUS 1102 1001 KTE	Γ	496-394	611-312	767-834				
ENV HVIST	ENVELORE FOLITACION DE COMISOR	HOMAN DOWNODEFICIENCY VIRUS 1 VF. 1 (SC 130CA12)	Т	198.594	611-712	767-836				
PENV HVISC	ENVELOPE POLYPROJEIA GETANITA	HABIAN BARNODEFICIENCY VIAUS TYPE I (WAI) I SULATE)	T	780 007	602.703	758-827				
FIN HVIWI	ENVELOPE POLYPROTEIN GPING PAELUNSON	LA RALA MARRINDE FICIENCY VIRUS TYPE I (WAUZ ISOLATE)	127-361		906	764.831				
BELLY HVIW?	ENVELOPE POLYPROTEIN GP160 PRECURSOR	ALEST A PARTAMONE FICIENCY VIRUS TYPE I (22/CDC-234 ISOLA)	255-296	302-301	2					
10/173	ENVELOPE POLYPROTEIN GP160 PRECURSOR	THOMAS ASSESSMENT OF VIBUS TYPE I (ZAIRE 3 ISOLATE)	251-292			970 770				
	ENVELOPE POLYTROTEIN OP 160 PRECURSOR	HUMAN IMMUNOSERICENCY VIRING TYPE I (ZAIRE 6 ISOLATE)	156-297	904.593	116.60	100-00				
PENV HVIES	CANCEL OF POR VPROTEIN GP160 PRECURSOR	HUMAN IMMUNOUTE ICHERY STATE 17-14 ISOLATE)		113-601	617-675	612-719				
EN HVIZO	CHARLES OF THE CONTRACT OF THE CURSOR	HOWAN BANCHODE ICIEM, TAIRCS THE 12 A 19 E 17 13 150	Γ	612-671	675-712	177-619				-
PENV HVIZE	ENVELOR OF THE OTHER CP160 PRECURSOR	HUNCAN DAIGNODEFICIENCY VIAUS LIVE I LEADEN	447.481	\$10.595	617-610		-			1
PERV HVIZH	ENVELOR TO THE OPEN OF 160 PRECURSOR	HUMAN BEAUNODEFICIENCY VIRUS I THE A LISOLATE CALLS	Ι	619.709						-
PENV HV288	ENVELOPE POLITICAL STATE PRECIESOR	HUMAN BOADNODEFICIENCY VIKUS TYPE 7 (150LA 15 CONTA	T	108-691						1
PENV HYZCA	ENVELOPE POLITICO ELINO ESTA PRECIENCIA	HIDMAN DORONODEFICIENCY VIRUS TYPE 2 (150LATE DIM)		403 403	A09-699					1
PENV HYZDI	ENVELOPE POLYPROTEIN GFING PACCONSON	HIDAAN DOUNODEFICIENCY VIRUS TYPE 2 (150LATE GHANA-	-	007 007						\downarrow
ENV HYZGI	ENVELOPE POLYPROTEIN GF 180 PACCORSON	IN MAN THAT MAN THOUSE FICIENCY VIRUS TYPE 2 (1SOLATE NIH-Z)		600.000		-		L		
FINY HYZNZ	ENVELOPE POLYPROTEIN GP160 PRECURSOR	LIBRAN DAMINODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	311.3%	10.10	1					
DEN HYDEO	ENVELOPS POLYPROTEIN GP160 PILECUKSUR	AND AND MANDEN PRICE NOW VIRUS TYPE 2 (150LATE \$1724.1C)	443.476	203-200			-	-		
ENV HV283	ENVELOPE POLYPROTEIN GP160 PRECURSOR	THE SHOW THE SHOUST WAS TAKE I (ISOLATE SHLISY)		914-700		-	-			
FNV HV25B	ENVELOPE POLYPROTEIN GP166 PRECURSOR	INDIAN PANINODEFICIENCY VIRUS TYPE 1 (ISOLATE ST)	-	203.50	70.71	1				
PENY HY25T	ENVELOPE POLYPROTEIN GP180 PRELUNSOR	MANIES INTRACISTERNAL A-PARTICLE	167.412			-				
ENV DALAE	ENV POLYPROTEIN PRECURSOR	CHEEP PIR MONARY ADEMONIATOSIS VIRUS	403-455	200			-			
ENV ISEV	ENV POLYPROTEIN PRECURSOR	ATTACHER FORMING NUMBE LEUKENIA VIRUS		20.00		-				
PEN MITTE			_	25.5			-			_
ELV VICES	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTE		_	267.60		-	-			
VAV AN VAV	ENV POLYPROTEIN PRECURSOR	ANY MONTH OF PRINCIPALLY VIRUS	498-550	26.58						 -
STATE AND A	ENV POLYPROTEIN PRECURSOR	CAS-BR-E MUMINE LECTRINIS (ISOLATE 57)	330-564	276-610						 -
200	SHY POLYPROTEIN PRECURSOR	FUERU BIONINE LECENTRA VIRILA (1501.ATE F029)	\$20.564	576-610			1			-
PAY MENT	FRV POL YPROTEIN PRECURSOR	FRIEND MUNINE LEUNEVILLA VIBILA (150LATE PVC-211)	\$20-564	876-610			 	-		-
A	ENV POL YPROTEIN PRECURSOR	FREND KIULING LEUKENIN VINCEL	504-551	\$63.597			-	-	-	 -
ENV MEVE	ENV POL YPROTEIN PRECURSOR	HONDAY MUNDY LEUNERING TIPLIS	40.92	104-131			1	-	1	: -
DAY MEVED	STORES VERNING	KINSTEN MULTAE LEUKENIO VINCE	502-554	266.60					-	:
PENV MEVE	THE PRECURSOR	MOLCYEY ANALYE LEUKENIA VIAUS	497.549	361.595			-			-
PEN MENNO	SAV BOL VPROTEIN PRECURSOR	RADIATION MURUE LEUKENIA VINOS	497.549	361.595				1		-
EN MAN	THE STATE OF THE PRECURSOR	RADIATION NICHWE LEGARNIC VINCE IN THE A	417.530	536-612	_		j			-
PEN MENTE	SAV POLITER	MOUSE MANDIARY TURIOR VINUS (STRAIN CR.)	417.539	156-612			1		1	; -
DAY NOTINE	Sent Sent By	MOUSE MARNIARY TUNIOR VIXUS (21 PORT)	403.474	L	L				-	
PEN MATTO	CALCON TO THE PARTY OF THE PART	SDAAN MASON-PIZER VIRUS	41.05	107.141				1		- -
PEN MON	ENVICENCE	FIBI MUNIME OSTEOSARCOMA VIRUS	23.65	18:33	664.746	310-014				
PENV MSVTB	DAY FOLTROITES	OVINE LENTIVIRUS (STRAIN SA-ONINV)	107.101	\$40.574						
PEN OHINS	DAY FOL TRACESS PROCESS	PAUSCIER MINK CELL FOCUS-INDUCING VINUS	41.61		-					:
PENY MINGY	ENV POLITICAL SECTION	RAUSCIER SPLEEN FOCUS-FORMING VIRUS		100	154-205	131.35	180.08	A\$1.69)	ž	į.
PEN ISTY	ENV POLYMOIEIN FACTOR	SDATAN FOARN VIRUS (TYPE 1)			319-357	\$60.706	161.001			-
PEN STVI	ENV POLYPROTEIN	SDAILAN FOAMY VIRUS (TYPE 37 STRAIN LK3)		1	643.693	-			_	_
EN STYL	EXV POLYTROTEIN	STATION DOMINODEFICIENCY VIAUS (AGNISS ISOLATE)	216:207							
PENV SIVAI	BAVELOPE POLYPROTEIN UPIN FALLENCE				•					

PCGENE	ALLAROTTS	All Viruses (so betterioghages)				11		Ιì	П	
THENAME	PROTEIN	YIRUS	7	7	7710	1000	2001	440	4	A.4.4.
PENY SIVAG	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SOCIAN INDICATOR (CENTRALIS (AGM) ISOLATE)	20-06	031-079	107.00	437.64	192.840	T		İ
PENV SIVAI	ENVELOPE POLYPROTEIN GP160 PAECURSOR	LONE OF	147-767	215-917	100-676					-
PENV SIVAT	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SPRIAN INDIVIDUE (ICENCY VIRUS (ITU-I ISULATE)	10	176.00	700 611	649.701	101.817			-
PENV SIVEZ	ENVELOPE POLYPROTEIN GP160 PRECURSOR	CHING ANZEE INCIDENCE VIEW (SIV(CPZ))	137-627	601-361	2000	2			Ì	
PENY SIVER	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SINITAN INDICADE PICIENCY VIRUS (1500-A) E CHILL	300-034		117 060	1	100.844			:
PENV SIVAI	ENVELOPE POLYPROTEIN GP140 PRECURSOR	SIMIAN INDICACE ICIENCY VIRUS (AMINATOR INCLAIR)	907.12	161.318	345.316					:
PENV SINAD	ENVELOPE POLYPROTEIN GP160 PRECURSOR	SIMILAN INITIAL DEFICIENCY VIALUS (AINLES) INCLAIRE	30		76.374		-		i	_
PENY SIVACK	ENVELOPE POLYPROTEIN OPION PRECURSOR	SIMILAN INDICATION TO THE STAND SON ATEN	19.19	100	611.724		 			
PENV STAR	ENVELOPE POLYPROTEIN GP160 PRECURSON	SIMILAR INVIDENCE OF VIRIS (N. 1900) 15	2 77		4.18.728	13.611				
PENV SIVSA	ENVELOPE POLYPROTEIN GP166 PRECURSOR	SIMILAN MANUMULETICIENCY VIRUS (F. 2003) INTERIOR	200	0.7	16.65					:
PENV SIVSP	ENVELOPE POLYPROTEIN GP 160 PRECURSOR	SPAIN BRIUNDEPRCIENCY VIRUS (PRIVACES ISOLATE)	200.00	070-170			+			
PENV SHOWH	ENV POLYPROTEIN PRECURSOR	SQUIRREL MONREY RETROVINGS (SNIRV-III)	99-74-7							
PEN SAVI	ENV POLYPROTEIN	SIMIAN RETROVIRUS SRV.	409-473							
PEN VILV	ENV POLYPROTEIN PRECURSOR	VISMA LENTIVIRUS (STRAIN 1514)	21.62	184.222	637.740	773-80-				
PEN VILVI	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAM IS14/CLONE LVI-IKSI)	21-62	2	977.740	780.818	+			
PENV VILV3	ENV POLYPROTEIN PRECURSOR	VISMA LENTIVIAUS (STRAIN 1514/CLONE LVI-IKS2)	21-62	<u> </u>	145.741		-		<u>;</u>	
PENBA AVTER		AVIAN ERYTIMODLASTOSIS \TRUS (STRAIN ES4)	09-1-90							
PETFI FOWPI		FOWLPOX VIRUS (STRAIN FP.1)	180.724	337.33						
METEL SPUKA	EARLY TRANSCRIPTION FACTOR TO KD SUBUNIT	SHOPE FIBROALA VIRUS (STRAÍN KASZA)	17:71	267.340	3:0.587					:
PETF1 VACCC	EALLY TRANSCRIPTION FACTOR 10 KD SUBUNIT	VACCIMIA VIRUS (STRAIN COPENTIAGEN)	23.71	307.341						:
PETFI VACCV	EARLY TRANSCRIPTION FACTOR TO KD SUBLINIT	VACCINIA VIRUS (STRAIN WR)	11.11	307-341						
PETEZ VACCO	EARLY TRANSCIUPTION FACTOR 62 KD SUBUNIT	VACCIMIA VIRUS (STRAIN COPENHAGEN)	13.01	174.208						:
PETF2 VARV	EARLY TRANSCRIPTION FACTOR 12 KD SUBUNIT	VARIOLA VIRUS	18.53	174.208						
AVACH VOX34	ALKALDIE EXONUCLEASE	MIRIAN CYTONEGALOVIAUS (STRAIN AD169)	10.114							:
PEXON HIVE	ALKALDE EXONUCLEASE	EQUINE HERPESVIRUS TYPE I (STRAIN ABAT)	19.141							:
PEXON PRVNJ	ALKALINE EXONUCLEASE	PSEUDORABIES VIRUS (STRAIN NIA-1)	03-120	-						:
PEXON VZVD	ALKALINE EXONUCLEASE	VANCELLA-ZOSTER VIRUS (STRAIN DUNAS)	109-157	143.313						:
FIB1 ADE40	41.4 KD FIBER PROTEIN	HUNIAN ADENOVIRUS TYPE 40	183-233							:
FIRE ADEA	41.4 KD FIBER PROTEIN	HUNIAN ADENOVIRUS TYPE 41	113-233				1			-
FIRE ADEOS	FIBER PROTEIN	HUMAN ADEMOVIRUS TYPE J	156-194							
PFERP ADEO?	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 7	176.210							
PFIRE ADEAD	FREAPAOTEN	HUMAN ADENOVIRUS TYPE 40	303-352							
PETRY ADEA!	FIREK PROTEIN	HUMAN ADENOVIRUS TYPE 41	320-366							:
PERP ADERS	FIDER PROTEIN	BOVINE ADENOVIAUS TYPE 3	101-215	515-626						
PFOSX MSVFR	V-FOS/FOX TRANSFORMING PROTEIN	FBR MUTUNE OSTEOSARCOMA VIRUS	131-169							-
PFOS AVDIX	PSS-V-FOS TRANSFORMING PROTEIN	AVIAN RETROVIRUS MK24	109-152				1			
PTOS MISVER	PJS-V-FOS TRANSFORMING PROTEIN	FBI MUNINE OSTEOSARCONIA VIRUS	153-193				+			-
POAGC_AVISC	PAYGAG-CAK) PROTEIN	AVIAN SARCONA VIRUS (STRAIN CT 10)	37-101				1			
POAG AVEVI	GAG POLYPROTEIN	AVIAN ENDOCEROUS VIRUS EV-I	X.							!
PGAO AVEV2	GAG POLYPROTEIN	AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0							Ì	:
POAG AYDAC	DAG POLYPROTEIN	AVIAN MYELOCYTONIA TOSIS VIRUS MC.29	***				1			-
PGAG_AVD-D	GAG POLYPROTEIN	AVIAN MTELIOL TIUMIA 10315 VIRUS 1181								İ
PGAG AVISU	COLE PROTEIN PIP	AVIAN SARCONA VIRUS (STRAIM URZ)								
POAG AVISY	GAG POLYPROTEIN	AVIAN SARCORIA VIRUS (STRAIN T.D.)	24-16							İ
POAD BIVOS	GAG POLYPROTEIN (PSS)	BOYING BAILMODEFICIENCY VIRUS (ISOLATE 106)	-				+			Ī
POAG ELAYY	GAG POLYPROTED	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL22)	811.118							
POAD FIVE	GAD POLYPROTEIN	FELINE DOMINODEFICIENCY VIRUS (ISOLATE PETALUNIA)	76-110							
POAD FTVSD	GAG POLYPROTEIN	FELINE DOMINODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	76-110							
POAD FIVE	GAG POLYPROTEIN	FELINE DOMINODEFICIENCY VIRUS (ISOLATE TAIT)	76-110							
POAG PLV	DAG POLYPROTEIN	FELINE LEUKEMIA VIRUS	496-533							
POAG FOAMY	GAG POLYPROTEIN	HUMAN SPUNIALETROVIRUS	20.00	191-425	2076	607-635	+			İ
POAO FSVAD	GAG POLYPROTEIN	FELINE SARCOMA VIRUS (STRAIN ACDONOUGH)	1499-334							

											,
OLIGINATION CHARGE CHARG		NOTIS MOTIS		П	П	Т	1414	1	Γ		
OLIO CHATTERINE GLOBAL MELLING MATERIA NATURE OLIO CHATTERINE	LAND	PROTEIN	AM CARCONA VIRUS	7.5							
OLIC PATEMENT COLOR TRANSPORT COLOR TRANSP	Valley o	GAO POLYPROTEIN	1116								
ACTIVE PROPERTY ACTIVE PROPERTY CONTRIBUTION	2173	DAD POLYPROTEIN	GIBBON ATE LEGAZONIA TOTALIS TYPE I (ARVOST 2 ISOLATE B)		34.33						_
OLIGINATION MACHINICATION MALE	1 1 1 1 1	DAG POLYPROTEIN			102:326			1			L
OLIGIONATION NUMBER NUMB	141,41	DAD POLYPROTEIN			192-326			1			<u> </u>
OLIGINATIONS	100	DAD POLYPROTEIN			193-126			-			
OLIO CATTORINE COLOR MAN COLOR MAN	200	GAG POLYPROTEIN	(10)		297-326			1	-		! ! -
October Principles Control Con	I Alley	OAD POLATEDIEDA	_		192-326						! !
COLOG STREETS COLOG STREET	2	MAIOTEN APPOIEDA	_		291-326						 -
COLORYMORINA MALAN BARNOODITEST, VILLY 171 1911 19	O HVIEL	A DECK VENTER	Γ	17.131	352-1356			-			-
GAO FOR TWOTEN MAJAN BACANOCE INTERCY VILLY TOTE 1 (NAT.) 191-191 191-	NVING NVING	CAN CAROLEIN	Т	17-131	292.336						<u>:</u>
GAD FOLTROITER HIGAN BERNOCESTICISECY VINUS TYPE I GAN TOCAS STATES 151119 1	IO HAID	UAU POLITICALISM	Т	64.113							
GAO POLYMOTER HOLAND BACHOOGENEERY VIRIS TYPE I DOR WALKS 1501 POLITICAL DAR PACKED TO A CHANDER HOLAND BACHOOGENEERY VIRIS TYPE I DOR WALKS 1501 1511 1511 1511	NO HVIJA	GAO POLYFRUILIN	Т		305,130						į
Quad Poly Principies Public Poly Public	IQ HVIMA	GAG POLYPROTEIN		21.13	200.00		-				-
GAD POLYTROTER	D HYING	GAG FOLYPROTEIN	톏	161-26	200.763						
GAO POLYMOTER HUMAN EAGMODERIERS Y VALUE TYPE POLYMOTER 90-111 191-118	IO HVINS	DAD POLYTROTEIN		17.121	289-323		-	1			_
CAG POLYMOTER HUMAN BARMORETICENT VINUS TYPE [(PV1) 1804/TE] 90-11 189-138	5	GAO POLYPROTEIN		101-06	193-116			1			<u> </u> -
CAG POLYPOTER CAG		OLO BOL VPROTEIN		161-06	192-116			1			-
CAG POLYPTOTEIN HIGANE BACINODE/ICIENCY VIALS TYPE (STACINE) (19.13)	O HAID!	CAST VEROTER	7	10.00	193.336				-		<u> </u>
CAG POLYMOTERN HIGHARD BACKNODE HICHENCY VIRLS 177E LOLUME LINEAR DESCRIPTION 191-131 191-131	ALAN O	75 Cast Sec. 6	7	17.137							-
CAG POLYPOTEN CAG POLYPOTE	E HAILE										-
CAGO POLYPROTEIN	IG HVIU	GACTOROSE	HUMAN DOATHODEFICIENCY VIRUS 177E 1 (WALL 130LATE)		301.137		L				-
GAG POLYTROTEIN HIDAAN BORINGGENCIESCY VARIATYEE 501577 135-128 130-131 141-131 141-132 141-13	DAINH DI	GAO POLYPROJESP	HAMAN DARINODEFICIENCY VIRUS TYPE I (ZICDC-ZIA ISOCA	****			-	_			-
GAO POLYTROTEN WASSTER NITLAGISTERNAL A-ARTICLE 01:101 10:1101 10:	10 HV123	GAO POLYPROTEIN	INTIMAN BARINODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIST)	292-320							_
RETROYBUL HEALTED GAG POLYPROTEIN MOUSE INTACTSTED/ALA A-PARTICLE 91-170	O HV25B	GAG POLYPROTEIN	_	17.16	100.00						4
	O PHA	RETROVINUS-RELATED GAG FOLTEROIEM		63-103		-	-	-		_	_
LETROPRUS_ARIATED CAG FRA TFOLDER** SEEP FULLAGONARY ADENOBATORS STAIN BRADE** STAIN B	O DYCA	RETROVERUS RELATED GAG FOLT FROIEIN		19.17			-				
CAG POLYPROTEIN MOUSE MANGALAY TUNIOR VIRUS (STRAIN BRA) 151-151 154-199	O IPMAR	RETROVEUS RELATED UND POLITICALES		20.00							
GAG POLYPROTEIN	O ISAV	GAG POLYPROTEIN		2 2	2		-				L
GAG POLYPROTERN SINGAN MASGN-FIZER VIRUS 172-100	NO MONTYB	GAG POLYPROTEIN			21:02:			-			-
OAG POLYPROTEIN SOUIS SAACGAA VRIUS (STRAIN PAGUE C) 17-19 171-11	AG MONTVO	GAG POLYPROTEIN	SINGAN MASON-PFIZER VIRUS	22-782							- -
OAG POLYMOTERN SACCIAJONYCES CEAEVISAE VIRUS LA (SCV.L.A) 10-174 114-414 114	AD MONV	OAG POLYPROTERY	ROUS SALCONA VIRUS (STRAIN PRAGUE C)		111	1	-				-
A MARON COAT PROTEIN STATAN FORANY VIRUS (TYPE 1) 111-171	AG RSVP	GAO POLYMOTER	CACCHARDALYCES CEREVISIAE VIRUS L-A (SCV-L-A)	107:101			-				_
CAG POLYTROTEN SHALM POLANY VIRUS (177E 3/ STAÄN LK.) 131-323	AD SCALA	MAJOR COAT PROTEIN	EDITAL FORMY VIRUS (TYPE 1)		173-416		-				
CAG POLYTROTEN STRAIN BOATMODE FICIENCY VIRUS (ACALIS) 102-316 102-3	AG SEVI	GAO POLYPROTEIN	STATES OF STATES (TYPE) / STRAIN LK.)	117-407	413-322	34:07	-				<u>-</u>
GAG POLYPROTEN STATISH BATCHOOFFICIENCY VIRUS (AGA!) ISOLATE 206-340	AC SYNL	GAO POLYPROTEIN	STRICK IN THE PROPERCIENCY VIRUS (ACAILLY ISOLATE)	102-336			1	-			-
GAG PCLYPROTEN SPACE 119-107 171-107	AO SIVAL	GAO POLYTROTEIN	STATES TO BE THE STATE OF THE S					+			<u> </u>
GAG PGL YPROTEDN STAND MANDER CLEAKY VIRUS (TYO-1 ISOLATE) 501-315	0470	DAG POLYPROTEIN	SIMILAR DE SOUCE DE VIRIS (150LATE AGA) CLONE GR		473-507						! _
GAG PGL YRROTERN SPAGAN BAGING CPETCH 101-115 10	AN SILVE	GAG POLYPROTEDY	Spaan Removericienty waite (TVO-) ISOLATE)	_				1		1	+
GAD POLYPROTEIN CHID-PANZEE INDICATE GISI) 163-156 133-156 GAG POLYPROTEIN SIRAIN PROTINCENCY VINUS (ISOLATE GISI) 194-431 GAG POLYPROTEIN SIRAIN SACROAL VINUS 172-156 195-131 GAG POLYPROTEIN HELES SIRVELEX VINUS (ITVE I / STRAIN IN) 172-156 195-131 GAG POLYPROTEIN HELES SIRVELEX VINUS (ITVE I / STRAIN IN) 172-156 195-131 PROGABLE PELLCASE VANCELLA-ZOSTER VARUS (STRAIN BUMAS) 141-149 192-131 PROGABLE PELCASE VANCELLA-ZOSTER VARUS (STRAIN EIS) 101-141 PROGABLE PELCASE BOVIDE CORONAVIRUS (STRAIN EIS) 101-141 PEDAGGLUTRON-ESTELASE PECURSOR BOVIDE CORONAVIRUS (STRAIN GEBUS) 101-141 PEDAGGLUTRON-ESTELASE PECURSOR BOVIDE CORONAVIRUS (STRAIN QUEBEC) 101-141 PEDAGGLUTRON-ESTELASE PECURSOR BOVIDE CORONAVIRUS (STRAIN AGEBUS) 101-141 PEDAGGLUTRON-ESTELASE PECURSOR HUDAAN CORONAVIRUS (STRAIN AGEBUS) 101-141 PEDAGGLUTRON PECURSOR HUDAAN CORONAVIRUS (STRAIN AGEBUS) 101-141 PEDAGGLUTRON PECURSOR HUDAAN CORONAVIRUS (STRAIN AGEBUS) 101-141 PEDAGGLUTRON PECURSOR	7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GAG POLYPROTEIN	SDALA BOMUMOURINGENCY VINES (SIVICPZ))	301-335			4	1	1	-	<u>!</u>
STATE STAT	AVE OA	OAD POLYPROTEIN	CHING ANZEE INCOMPOSTICITATE (1801)	3.3	333.267	213-317		1			<u>.</u>
13.200 15.200 1	NO NAC	CAD BOX VEROTER	SPATAN MANUNCOLF ICIENCE TO STATE ST	194-431	_				1	1	: 1
PROBABLE PELICASE PERPES SIGNELX VIRUS (1772 13 EACH 174 17 EACH	AO SIVUB	CANADA VEROTEN	SIMIAN SARCOMA VIRUS	172.706	769.820	_					+
HEBPES SIGNAL FELICASE	AV SMSVA	100 Oct 100 Oc	HERPES SOUTEX VIRUS (1 TPE 1) SINAIR 1)	468.502	676.72						+
PROBABLE PELICASE PREPENTAUS SARINI (STACIN UNAS) 113-131 PROBABLE PELICASE PROBABLE PELICASE PROBABLE PELICASE PROBABLE PELICASE PROBABLE PELICASE PROBABLE PELICASE PECURSOR POWIE CORONAVIRUS (STRAIN LY-131) 101-342 PEDAGGLUTINGN-ESTERASE PECURSOR POWIE CORONAVIRUS (STRAIN PEBUS) 101-342 PEDAGGLUTINGN-ESTERASE PECURSOR POWIE CORONAVIRUS (STRAIN QUEBEC) 101-342 PEDAGGLUTINGN-ESTERASE PECURSOR PUDAKA CORONAVIRUS (STRAIN ACEDIC) 101-343 PEDAGGLUTINGN PIECURSOR PUDAKA CORONAVIRUS (STRAIN ACEDICALIAS) 101-344 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/II) 104-440 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/II) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGLUTINGN PIECURSOR PRILIDEZA A VIRUS (STRAIN AGANGKOKI/III) 101-444 PEDAGGRUTINGN PIECURSOR PRILIDEZA A VIRUS	ELI HSVI	PRUBABLE NELVASE	HEADES SIMPLEX VIRUS (TYPE 1/ STRAIN HOSZ)	108.301	13.44	199.633				-	4
PROBABLE RELICASE PROBABLE RELICASE PROBABLE RELICASE PROBABLE RELICASE PROBABLE RELICASE PROBABLE RELICASE PROBAGGAUTINON-ESTEASE PRECINSOR PROME CORDINAVINUS (STAAIN LY-119) PROMOGAUTINON-ESTEASE PRECINSOR PROMOGAUTINON-ESTEASE PRECINSOR PROMOGAUTINON-ESTEASE PRECINSOR PROMOGAUTINON-ESTEASE PRECINSOR PROMOGAUTINON PROMOGRAPHICATION PROMOG	ELI HSV2H	PAUGABLE MELICANIE	HEAPESVIRUS SAININ (STIAIN II)	6	382.821		_				+
HOWARLE NECLASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION-ESTELASE PLECIASOR HOWACCULTION PLECIASOR HOWACCULTION PLECIASOR HOWACCULTION ACUDICATION PLECIASOR HOWACCULTION STRAIN ACUDICATION HOWACCULTION PLECIASOR HOWACCULTION PLECIASOR HOWACCULTION ACUDICATION	OELL HISVSA	PROBABLE RELIANSE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)			-		-			+
HEMACGLUTRIN-ESTEMASE PRECINSOR HEMACGLUTRIN-ESTEMASE PRECINSOR HEMACGLUTRIN-ESTEMASE PRECINSOR HEMACGLUTRIN-ESTEMASE PRECINSOR HEMACGLUTRIN-ESTEMASE PRECINSOR HEMACGLUTRIN-ESTEMASE PRECINSOR HEMACGLUTRIN FRECINSOR HEMACGLUTRIN FRECINSOR HEMACGLUTRIN FRECINSOR HEMACGLUTRIN FRECINSOR HEMACGLUTRIN STEMASE PRECINSOR ZA LIE	PROBABLE MELICASE	BOVINE CORONAVIRUS (STRAIN P18)			-					$\frac{1}{2}$	
HEMAGGLUTHAN 45 INCAR TOCATOR HEMAGGLUTHAN 45 INCAR 50 IN	HELLA CYBE		BOVINE CORONAVIRUS (STRAIN LY-131)	7	-			-			-
HEMAGGLUTOME STEATS PRECINSOR BOVINE CORONAVINUS (STRAIN QUEBEC). PEDAGGLUTOMINE-STEATS PRECINSOR HUMAN CORONAVINUS (STRAIN OCCU) PEDAGGLUTOMINE-STEATS PRECINSOR INFLUENCA A YMIUS (STRAIN MAJORICALIAN) PEDAGGLUTOMINE PRECINSOR INFLUENCA A YMIUS (STRAIN MAJORICALIAN) PEDAGGLUTOMINE PRECINSOR INFLUENCA A YMIUS (STRAIN MAGUOCIATIAN) PEDAGGLUTOMINE PRECINSOR INFLUENCA A YMIUS (STRAIN ARUDGENIGANOKAIDOLITIA)	HEALA CYBLY		BOVINE CONONAVIRUS (STRAIN MEBUS)		-	-	-	-			
HEMAGGLUTINGS STREAMS PECTASOR HOMAN CORONAVRIUS (STRAIN OCS.)) FEBAGGGLUTINGS STREAMS PECTASOR RETURNA ANALOGOUS (STRAIN ANALOGOUS) FEBAGGGLUTINGS PECTASOR RETURNA PRECEDIANS (STRAIN ANALOGOUS) FEBAGGGLUTINGS PECTASOR RETURNAM ANALOGOUS (STRAIN ANALOGOUS)	HEMA CYBM		BOVINE CORONAVIRUS (STRAIN QUEBEC).			-	-	-			-
HEMAGGLUTHIN PRECINSOR HEMAGGLUTHIN PRECINSOR HEMAGGLUTHIN PRECINSOR HEMAGGLUTHIN PRECINSOR HEMAGGLUTHIN PRECINSOR HEMAGGLUTHIN PRECINSOR HEMAGGLUTHIN ARUDGENGARHOKKAIDOUNT	HENTY CARO		HUMAN CORONAVIRUS (STRAIN OC41)	7	+	1	-				-
HEMAGGLUTHYR PRECENSOR HEMAGGLUTHYR PRECENSOR HEMILENZA A VIRUS (STRAIN ARBUDGENIGARMOKKAIDOHITH)	HEMA CVHO		INTLUENZA A VIRUS (STRAIN A/AICHUZ66)			1					+
HEDAAOGLUTININ PLECUNOR INTLUENZA A VTRUS (STRAIN ABUDGERUGARAHOKKAIDOI/II)	HEMA IMAC		INGTLIENZA A VIRUS (STRAIN ABANGKOKUM)	-+	+	1	-				
	HENCY TABAN		THE A VINITE STRAIN ABUDGENGARHOKKAIDOVIAN	_							

PCGENE	Ацмотя	uses (na bacteriophages)	IT	П	П		7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1000	1	4 1 1 1 1 1
FILERAME	PROTEIN	T	3	Tonut.	7	Т	Τ	Т	ī	
PHEMA IACKA	HEMAGGLUTININ PRECURSOR		T		100,404	+				:
PIEMA IACKO	HEMACCLUTININ PRECURSOR		T	Ţ			l			:
PHEMA INCKP	HEMAGGLUTININ PRECURSOR	INCLUENZA A VIAUS (STRAIN ACHER REWLENNST L'ARMIANT)	Τ				+			! : :
PHEMA INCKO	HEMAGGLUTININ PRECURSOR			504.520		T				:
PHEMA LACKS	HEMAGGLUTININ PRECURSOR		T	977						
PIEMA IACKY	HEMAGGLUTININ PRECURSOR	Ť	T		1					
PHEMA INDAI	HEMAGGLUTININ PRECURSOR	Ī	T	207		1				
PHENIA IADAS	HEMADOLUTIMIN PRECURSOR		T		-	Ì			Ţ	İ
PHEMA_LADAS	HENAGGLUTININ PRECURSOR .		T			T	\dagger	Ī		
PHEMA INDA	HEMADOLUTININ PRECURSOR	Т	T	, Contraction	†	+				
PHEMA LADCZ	HEMAGGLUTIMIN PRECURSOR	K (%)			1	+	1			
PHEMA IADE!	HEMAGGLUTININ PRECURSOR		٦	217-111	1	1				İ
PHENA IADRI	HEMACGLUTIMIN PRECURSOR		364.440			1				
PIESKA LADING	HEMADOLUTININ PRECURSOR		164-440							
PHEMA JADHU	HEMACOLUTININ PRECURSOR		364-440			-				
PHEMA IADIM	HEMAGGLUTININ PRECURSOR		097-140							
PHEMA IADHS	HEMAGGLUTPAN PRECURSOR	INFLUENZA A VIRUS (STRAIN ANDICKMOKKAIDOGIAZ)	054-440							
PUTCHA IA THE	MEMACAR LITTINGS PRECURSOR		164-440							
BUTENA JAPAN	MEMACCH LITHER PRECURSOR	Ĺ	364-440							
PUEVA IADIO	HEMACOLLITININ PRECURSOR		179-471	156-306						
THE PARTY	MENACO LITINA PERCHASIS		21.55		-		0			
- NO.	TOTAL CONTRACTOR CONTR		380-456		-					
PHENA MANA	MENACON HOMAN PRECIDENT		21-55							
THE STATE OF THE S	The state of the s	176)	178-454		-	-				
PHEMA IADAZ	HEMACULUI ININ FACTORSON	Τ	21.55		-		-			
PIEMA (ADU)	PEMACACULININ TRECOASOR		180-456							
PREMA IADUS	TEMACULUININ TRECONSON		180-456							
PIEMA IMENI	HEMACKEU ININ PACLURSON	TRUSAOSTOCK	177.477			I				
MEMA INT	HEMACACO INTO PRECONSOR	DEFINENT A A WAITE ATT AND ANCREY TEAL ATTENTION IN THE	1711/454							
PHENA IACRUS	HEMACIACO INTO PAECUASOR	Т	178-473		-					
PIEMA IAUG	ACCOUNTS TO THE PARTY IS COME.		377-776	1						
PIEMA IAUNA	TEMACOLULINIS PRECURSOR		179-455		-	T				
TEMA IMA	TEMPORTURAL PROCESSOR	(8)	Γ	360-4114	503-537					
MEMA IMEG	HEMAUGULININ PACCONSON	T	T	Τ	103-537					
THEMA IMPL	MENACOL ITEMS PRECIBIOS	T		T	-					
PUTELLA LAUTE	HELACT LITHIN PRECURSOR		360-484 50	503-537	-		-			
PHEMA IMPO	HEMAGOLUTININ PRECURSOR	AUM6)	379-455							
PHEMA MACA	HEMADOLUTIMIN PRECURSOR		379-455							
PHEMA LANCE?	HEMAGGLUTININ PRECURSOR		379-455							
PHEMA WALE	HEMAGGLUTININ PRECURSOR		٦		503-537		-			
PHEMA IMILO	HEMAGGLUTININ PRECUASOR	((7)	1	160.484	503-537					
PHEMA INITIO	HEMAGGLUTININ PRECURSOR	1	179-455			1				
PHEMA LANDA	HEMAGGLUTININ PRECURSOR,	1	1	1		1	1			
PHEMA (AHDON	HEMAGGLUTININ PRECURSOR.	E	7	٦	503-537		1			
PHEMA LANDR	HEMAGGLUTININ PRECURSOR			28.43	501-517					
PHENA INDIO	HEMAGGLUTININ PRECURSOR		179.455				1			
PHENA WHISA	HEMAGGLUTTININ PRECURSOR		1	٦	-					i
PHENA WHSP	HEMAGGLUTININ PRECURSOR	_		٦	501-111					
PREDALA LAHSW	HEMAGGLUTININ PRECURSOR	<u> </u>	7	2	201-337	1	1			
PHEMA WHITE	HEMAOGLUTININ PRECURSOR	75/16)	178-455			1				
PHESAL MATTO	HEMAGGLUTDAM PRECURSOR		170.455	1	+	+	+		T	-
PHENA LAHUR	HEDALOGEUTIPHIN PRECURSOR	[INTLUENZA A VIRUS (STILAIM MEQUINEMRUGUAY/IM)]	179-455	1		1				
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MAINTANDON'S ANEAL A							Т	T	Т	ABFAT	AREA
REALGGLITTON FACURED WILLINGS A VINUS (STAIN GUIDANNESS) 111-41 154		An worths	ner (ne batteriophafei)			ABGAZ	124	- FONTO	9		
REALGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-141 SELAGGLUTION PRECISED NELLIGIZA A VIRLE STRAIN ACREDIALISM DI 11-1	14.7	MIZION-	THE A VIBITE STRAIN AUAPANDONS	1	20.50						
The standout of the processor	1000	HEMACOLUTION PRECURSOR			206-541						
THE PROCESS PRICE AND PRICE AS A WILL STAN A CHARLAGE ATTAINSTAND STANDS	333	LESTANCE LITRIN PRECURSOR		376-476	506-548						
RELACCALTITION RECURSOR RILLEGA A VIRIG STAND AGRENIEUR 1014444 10144444 1014444444 10144444 10144444 101444444 10144444 10144444 10144	an A	LEVA COLLITION PLECURSOR	-	377.453							
	WA IALEN	THE LANGES LITTOWN PRECURSOR	_	383-586							L
	NA IAMAA	SECURSOR	_	310-456							
INCLUDENCE OF THE PROCESSION INCLUDED A VINUS STRAIN AGREDIALISMS 194410 194	MA MAN	TOTAL PROPERTY OF	1	310-456							 -
HEMACGLITHRIN PECUSSAN SITLURGEA A VIRILS (STAIN AARIENISTINE) 194-40	MA IAMAO	MEMACANA MANAGEMENT		110.456							
INCLUSION INCL	MA IAMEI	HEMAGGLUTININ PRECORDER									į
RELACCALITION PRECURSOR PRILIERA A VIRUS (STAIN ANINGSWEDEN) 18-14 18-	MA_IAME2	HEMAGGLUTININ PRECURSOR					-	L			
REALGGLUTION PRECURSOR PRILIERA A VINUS (STAIN APPROAID) 194-19	MA LANGE	INTRACCLUTIVIN PRECURSOR	THE SENSE A VIBIG (STRAIN AMINKS WEDENAW)	108.142	200						
REALGGLUTION PRECURSOR FINLERIA A PRINT (STAIN ANTICOT WITALECONOM 178-41) 18-411 18-414 18-446GLUTION PRECURSOR FINLERIA A PRINT (STAIN ANTICOTAL CONTONING PRECURSOR FINLERIA A PRINT (STAIN BENECOLUTION FRECURSOR FINLERIA A PRINT	VA IAMON	KEMAGGLUTININ PRECURSOR	INTLUCATION OF THE ANTI-MONEY	180-456				-			
RELACCALTIPRY PRECURSOR PRILIERA A WIND ISTANA PATONO IN NECESTRALISMS 114-14 RELACCALTIPRY PRECURSOR PRILIERA A WIND ISTANA AND AND AND AND AND AND AND AND AND	200	HEMACCH UTININ PRECURSOR	INTLUENCE A VINUE (STANIE) OF WILL FAIR NE/120/04)	111.477	476-534						ļ
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HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STEELAND) 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STEELAND) 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTION RECURSOR TOTALDERA A VIRUS (STAND AGRICANS CHOST STAND 1744 HEALGOLUTIO	1 N	TOTAL TOTAL SECTION	INTLUENZA A VIRUS (STRAIN ANDERTO NICCESS)					 -			-
REALOGLUTION RECURSOR RELUENZA A VIRUS (STAND AZSILERAN PERCURSOR) 113-141	MA IANUE	THE STATE OF THE S	INCLUENZA A VIRUS (STRAIN ARUIN)Y TURNS LINGUE								·
REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ATTRICEVORTAND) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIATA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND ASVIRCEOURDOUT) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND RECURSOR) 171-14 REALOGUTION RECURSOR RELIGIALA A VIRUS (STAND	MA IARUD	IEMACOLULINIA PRECUESOS	INGLUENZA A VIRUS (STRAIN A/SEALMIASSACHUSE) I STIJINALI		100.40			_	į		<u> </u>
REMACGLUTION RECURSOR STILLERA A VIRUS (STAND ACTORICATORS) 111-114	KA IASE2	HEMAGGLUTINGS PILLURSON	MENTA A VIRUS (STRAIN ASSIEARWATER/AUSTRALIA/72)	-	2				L		_
PERMOGLUTION RECURSOR PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ATUNKEVORIZADIANO 174-44 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-44 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-15 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-15 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI) 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUENZA A VINUS STRAIN ANDONUNOTI 174-16 PRILUEN	LA IASK?	HEMAGGLUTIMIN PRECURSOR	CONTRACTOR AND AND THE CONTRACTOR (AND AND AND AND AND AND AND AND AND AND	113.146	377.40						_
PERAGGAUTISMY PRECINGOR PRILIPERA A VINUS STRAIN ACTURKEVORITIONS 191-419	A A SA A A A A A A A A A A A A A A A A	HEMAGGLUTION PRECURSOR	INCLUENCE A VINOS (STEEL AND VIDE VAREL AND VIDE)	179.471	188-905						:
HEALGGLUTIRRY PRECINSOR PRILIERY A VINUS STRAIN ATURKEYONTALONTISSON 191-49		VENA OCE LITERAL PRECURSOR	INTLUENZA A VIACO LO INCOMENDA AND MANAGED LA AND M	378-454							:
REDACCE UTION PECUNSOR PRELIERA A VINUS STAND ACTORES ON 19 11-41	W IAIKI	TO CONTRACT OF THE PARTY OF THE	INTLUENZA A VIRUS (STRAIN A TURNE TAIRNING SOLD	0,770	\$04.548						- -
REPLACCALITION PRECINSOR PRELIERZA A VIRUS (STRAIN ATURKEVANICOREDAY) 11-41	MA IATION	HENACALOLINIA PARCES CO.	DALUENZA A VIRUS (STRAIN AMURKEYON) AND 11200		107						-
HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ATTOREVATSCONSTINA) 11-31 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ATTOREVATSCONSTINA) 11-31 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ATTOREVATSCONSTINA) 11-31 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ANDORANDOTT) 11-31 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ANDORANDOTT) 11-31 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ANDORANDOTT) 11-31 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ANDORANDOTT) 11-41 HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ASWIRETORION CONCULTION PRECINSOR HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ASWIRETORION CONCULTION PRECINSOR HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ASWIRETORION CONCULTION PRECINSOR HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ASWIRETORION CONCULTION PRECINSOR HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ASWIRETORION CONCULTION PRECINSOR HEALOGLUTHON PRECINSOR PRILIERAA A VINUS (STRAIN ASWIRETORION CONCULTION PRECINSOR HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERAA B VINUS (STRAIN BAREWATION) 110-410 HEALOGLUTHON PRECINSOR PRILIERA	MA INTRO	HEMACCLUTIMIN PRECURSOR	DATIFIER A VIRUS (STRAIN ATURKEYONTARION) 18/04)	1/1			-			_	_
HELLOGGLUTHIN PRECURSOR	AA IATE	HEMACOLUTION PRECURSOR	THE LOCK OF THE STREET AND ANTIMER WORE CONTIN	30-64	374-474			-			-
HEMACGLUTININ PRECURSOR PRILEBRA A VIRUS (STANIN AZERBALAUSTRALLAGTOCOS) 111-151 HEMACGLUTININ PRECURSOR PRILEBRA A VIRUS (STANIN AZERBALAUSTRALLAGTOCOS) 111-151 HEMACGLUTININ PRECURSOR PRILEBRA A VIRUS (STANIN AZERBALOZOS) 111-151 HEMACGLUTININ PRECURSOR PRILEBRA A VIRUS (STANIN AZERBALOZOSOS) 111-151 HEMACGLUTININ PRECURSOR PRILEBRA A VIRUS (STANIN AZERBALOZOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSO		HEMADOLUTININ PRECURSOR	INCLUENCY A LINGS (ST. A. LINGS CA. INCLUENCE VALIACIONSINI MAS)	111-111	487.539				-	-	: :-
REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ALDODRADORN) 191-438 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ALDODRADORN) 191-431 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN AND COLOLADORN) 191-431 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN AND RECURSOR) 191-431 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA A VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN ASWINERRODAND (NOVICINIA) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOR CONCARI) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOR CONCARIO) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOR CONCARIO) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOR CONCARIO) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOR CONCARIO) 194-430 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOGLUTION PRECURSOR REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOGLUTION 194-131 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOGLUTION 194-131 REALOGGLUTION PRECURSOR PRILLENZA B VIRUS (STANIN BORNOGLUTION 194-131 REALOGGLUTION PRECURSOR PRILLENZA E VIRUS (STANIN CERCALIONIN) 410-131 REALOGGLUTION PRECURSOR PRILLENZA E VIRUS (STANIN CERCALIONIN) 410-131 REALOGGLUTION PRECURSOR PRILLENZA E VIRUS (STANIN CERCALIONIN) 410-131 REALOGGLUTION PRECURS	4	SECURIOR PRECURSOR	INFLUENZA A VIRUS (STRAIN COURSE)	15:15		_					; ;
REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ALOSSANDON) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN ACHIGOLACIA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN BACRONICA) 111-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN CALIFORNIAN) 411-431 REALOGGLUTININ PRECURSOR PRILIERIZ A VIRUS (STACIN CALIFO	MA IMIXW		INFLUENZA A VIRUS (STRAIN AT ENVIAGE INVITAGE)	27.606							:
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HEMAGGLUTPRIN PRECURSOR PRILUENZA A VIRUS (STRAIN ASWINGAIGHONG KONGU1241) 194-419 HEMAGGLUTRIN PRECURSOR PRILUENZA A VIRUS (STRAIN ASWINGAIGHONG KONGU1241) 179-419 HEMAGGLUTRIN PRECURSOR PRILUENZA A VIRUS (STRAIN ASWINGAREUMA HEMAGGLUTRIN PRECURSOR PRILUENZA A VIRUS (STRAIN BAREIMOLIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMOLIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMOLIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMORIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMORIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMORIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMORIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMORIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BAREIMORIN) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BARSKIGON) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BARSKIGON) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BARSKIGON) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BARSKIGON) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA B VIRUS (STRAIN BARSKIGON) 191-419 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN) 411-519 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN) 411-519 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518 HEMAGGLUTRIN PRECURSOR PRILUENZA C VIRUS (STRAIN CORPACILIDANIN 410-518		HEMACCI UTININ PRECURSOR	INTEGRAL OF THE ANALYMENONG KONCOLING	364-440				İ		-	<u> </u> _
HEMAGGLUTRIN PRECURSOR PRELIERZA A VIRUS STRAIN ASWINSANDITZARI) 194-11 HEMAGGLUTRIN PRECURSOR PRELIERZA A VIRUS STRAIN ASWINSANDITZARI) 194-11 HEMAGGLUTRIN PRECURSOR PRELIERZA A VIRUS STRAIN ASWINSANDITZARI 110-15 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN BANDONAUS 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA B VIRUS STRAIN CORCIOULATOR 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-16 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOULATOR 111-15 HERAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOURAND 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CORCIOURAND 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CAREAT LAKES URGUNAND 111-15 HEMAGGLUTRIN PRECURSOR PRELIERZA C VIRUS STRAIN CAREAT LAKES URGUNAND 111-15 H		HENACOL UTDAN PLECUASOR	INTUENCA A VINCE (STORMAND AND KONG/12612)	164-440							:
HEMAGGLUTRIN PRECINSOR NPTLERZA A VIRUS (STRAIN ASWINEAREW RESEVILITA) 179-418 HEMAGGLUTRIN PRECINSOR NPTLERZA A VIRUS (STRAIN ASWINEAREW RESEVILITA) 130-436 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-431 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA B VIRUS (STRAIN BAREIMOUT) 131-441 HEMAGGLUTRIN PRECINSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECINSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECINSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECINSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKESI 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKES I 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKES I 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (STRAIN COREAT LAKES I 1871) 411-539 HEMAGGLUTRIN PRECUNSOR NPTLERZA C VIRUS (2	STATE OF THE PARTICIPATOR	INTLUENZA A VIRUS (STRAIM ASSAURCE)	139.478	\$00.41	L				1	-
REMACGLUTIRIN PRECINSOR RFLUENZA A VIRUS (STRAIN ASWINEDINGER) 110-136	DIA IAZHO	TENNOMINE STATE OF THE STATE OF	DELUENZA A VIRUS (STRAIN ASWINFLINDIAMA)		197.53		L				!
REMACGLUTININ PRECINSOR REPLICENZA À VIRUS (STANIN ASWINGUIA)	DAA IAZIN	HEMACCLUINING FACCORDS	INTLUENZA A VIRUS (STRAIN A/SWINENEW JERSET/11/10)								-
PERAGGLUTION PRECINSOR PRELIERZA B VIRUS (STAAIN BAREIMOCIA)	DA IAZNI	HEMAGGLUININ PRECURSOR	THE LENZA A VIRUS (STRAIN ASWINEAURKELJIMA	310-430			-			-	_
HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN GROCNAS) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BROCNAS) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BROCNAS) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALEROI) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALEROINSOR) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALEROINSOR) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN BALSSRICON) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELENZA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CORLAIN LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CARLAIL LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CARLAIL LAIS) HEMACGLUTRIN PRECINSOR HELURYA & VIRUS (STRAIN CARLAIL LAIS)	DAY WZUK	PENAGGLUTIMIN PRECURSOR	MATHENZA B VIRUS (STRAIN BIREITINGIA)	310-03	1		+		-		
HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BENGLAND?????!) HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BARONAY?!) HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BALENCH) HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BALENCHNISA!) HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BACKENPHISA') HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BACKENPHISA') HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BACKENDA') HEMAGGLUTRIN PRECINSOR INFLUENZA B VIRUS (STRAIN BACKENDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINDA') HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN) HEMAGGLUTRIN PRECINSOR INFLUENZA C VIRUS (STRAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CORLAINCAIN CO	DAY DOBE	HEMAGGLUTDIN PRECURSOR	THE PARTY OF STRAIN PROUNTS	371-463			1				-
NEDIAGGLUTPRIN PRECINSOR NETLIERZA B VIRUS (STAIN BARONG KONGPIN) NEDIAGGLUTPRIN PRECINSOR NETLIERZA B VIRUS (STAIN BARENO) NEDIAGGLUTRIN PRECINSOR NETLIERZA B VIRUS (STAIN BARENOHISMAS) NEDIAGGLUTRIN PRECINSOR NETLIERZA B VIRUS (STAIN BARENOHISMAS) NEDIAGGLUTRIN PRECINSOR NETLIERZA B VIRUS (STAIN BASINGAPORTIZIS) NEDIAGGLUTRIN PRECINSOR NETLIERZA B VIRUS (STAIN BASINGAPORTIZIS) NEDIAGGLUTRIN PRECINSOR NETLIERZA B VIRUS (STAIN BASINGAPORTIZIS) NEDIAGGLUTRIN PRECINSOR NETLIERZA B VIRUS (STAIN BAYCTORIAZIS) NETLIERZA CURININ PRECINSOR NETLIERZA C VIRUS (STAIN CORIGANIPAL) NETLIERZA C VIRUS (STAIN CORIGANIPAL) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETLIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALIERZA C VIRUS (STAIN CALET LAKESI 1471/4) NETALI	DOING VAN	HEMAGGLUTININ PRECURSOR	INTOCALLA SUBLIS (STRAIN INFINGLAND/22/02)	386-471					+	-	-
IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BALERUS) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BALERUS) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BALERUHISARIS) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BAUSSKIOON) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BAUSSKIOON) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BAUSSKIOON) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BAUSSKIOON) IEDALGGLUTRIN PRECURSOR INFLUENZA B VIRUS (STRAIN BAUSSKIOON) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCALIFORNIATI) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCOLUM) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCOLUM) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCOLUM) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCOLUM) IEDALGGLUTRIN PRECURSOR INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C VIRUS (STRAIN COCOLUM) INFLUENZA C		WENT OF UT DOTH PRECUTSOR	INTLUENCE TINGS (STEER STEERING FONDER)	181-463	_					-	-
NEMACGLUTRIN PLECURSOR DIFLURIZA B VIRUS (STACIN BALENTANDES)	S IN IN	HENANGE LITTER PRECURSOR	INTLUENZA B VIRUS (STRAIN GROUPS	317.472		L					+
NEALOGALUTION PRECURSOR NETLUENZA B VINUS (STAN BARATANIAN)	News Mark	TOTAL STATE OF STATE	ONTLUENZA B VIRUS (STRAIN BACEDAY)	137.463	-						+
HEMACGULTIMIN PLECINGON HEMACG	DA MILE	POSCOLUTION CALCULATION	DATLUENZA B VIRUS (STRAIN BALARYLANDOSV)			-		_			1
HEMAGGLUTININ PRECURSOR INFLUENZA B VINUS (STIAN BOOLEGONYAD) HEMAGGLUTININ PRECURSOR INFLUENZA B VINUS (STIAN BANCORLITATI) HEMAGGLUTININ PRECURSOR INFLUENZA B VINUS (STIAN BANCTORLAZI) HEMAGGLUTININ PRECURSOR INFLUENZA B VINUS (STIAN BANCTORLAZI) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN BANCTORLAZI) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLATORNIZI) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLATORNIZI) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLAMPESBURGUM) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLAMPESBURGUM) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLAMPESBURGUM) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLAMPESBURGUM) HEMAGGLUTININ PRECURSOR INFLUENZA C VINUS (STIAN CORLAMPESBURGUM)	DAY DONO	NEWACCEUTINA PACCONSON	INFLUENZA B VIRUS (STRAIN BACENDHISATIO)			-					-
HEMAGGLUTRIN PRECURSOR PRELIERZA B VRUS (STAIN BASINGANORE/122/19) HEMAGGLUTRIN PRECURSOR PRELIERZA B VRUS (STAIN BASINGARIA) HEMAGGLUTRIN PRECURSOR PRELIERZA B VRUS (STAIN BAYCTORIA/21) HEMAGGLUTRIN PRECURSOR PRELIERZA B VRUS (STAIN BAYCTORIA/21) HEMAGGLUTRIN PRECURSOR PRELIERZA C VRUS (STAIN CARLANDARIA) HEMAGGLUTRIN PRECURSOR PRELIERZA C VRUS (STAIN CARLANDARIA) HEMAGGLUTRIN PRECURSOR PRELIERZA C VRUS (STAIN CARLA LAKESI 147/14) HEMAGGLUTRIN PRECURSOR PRELUERZA C VRUS (STAIN CARLA LAKESI 147/14) HEMAGGLUTRIN PRECURSOR PRELUERZA C VRUS (STAIN CARLA LAKESI 147/14) HEMAGGLUTRIN PRECURSOR PRELUERZA C VRUS (STAIN CARCOLAIN PRECURSOR C VRU	ENA DOBME	HENADOL UTININ PRELUASON	INTI UENZA B VIRUS (STRAIN BYOREGONYNO)	780-6		-					
FELAGGLUTININ PRECINSOR PRELIERZA B VIRUS (STRÁIN BAUSSANIODAI) FELAGGLUTININ PRECINSOR PRELIERZA B VIRUS (STRÁIN BAUSSANIODAIA) FELAGGLUTININ PRECINSOR PRELIERZA B VIRUS (STRÁIN BAUCTORIAZATA) FELAGGLUTININ PRECINSOR PRELIERZA C VIRUS (STRÁIN CENGLAIDAPATA) FELAGGLUTININ PRECINSOR PRELIERZA C VIRUS (STRÁIN CENGLAIDAPATA) FELAGGLUTININ PRECINSOR PRELIERZA C VIRUS (STRÁIN CINCIANDAPATA) FELAGGLUTININ PRECINSOR PRELIERZA C VIRUS (STRÁIN CINCIANTESINGUMS) FELAGGLUTININ PRECINSOR PRELIERZA C VIRUS (STRÁIN CINCIANTESINGUMS) FELAGGLUTININ PRECINSOR PRELIERZA C VIRUS (STRÁIN CINCIANTESINGUMS) FELAGGLUTININ PLECURSOR PRELIERZA C VIRUS (STRÁIN CINCIANTESINGUMS)	EMA MBOR	HEMAGGLUTININ PRECURSOR	THE LIENZA B VIRUS (STRAIN BISINGAPORE/12/79)	386-471		1	-				
HEDAGGLUTRIN PRECINSOR NOT LIERZA B VILUS (STAIN BAYICTORIANA)	EMA DOSS	HEMAGGLUTININ PRECURSOR,	INCLUSION A VILLIS (STRAIN BAUSSAVICARI)	379-464				+	-		L
IEDAGGLUTRIN PRECINSOR INTLUENZA B VILLON STRAIN BYLICTONIANATH IEDAGGLUTRIN PRECINSOR INTLUENZA C VILLON STRAIN CICALIFORNIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VILLON STRAIN CICALIFORNIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VILLON STRAIN CICALIFORNIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VILLON STRAIN CICALIFORNIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VILLON STRAIN CICALIFORNIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CICALIFORNIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANTORVINIANTI IEDAGGLUTRIN PRECINSOR INTLUENZA C VIRLOS (STRAIN CANT	ALA DOUGH	HEMADOLUTININ PRECUNSOR.	THE STATE OF THE STATE BANCHON AGES	311-466				1			-
HEMAGGLUTININ PRECINSOR RELURAZA C VIRUS (STALIN CCALIFORNIA/11) o INTLURAZA C VIRUS (STALIN CCALIFORNIA/11) o INTLURAZA C VIRUS (STALIN CCREAT LATES/11/11/11) O INTLURAZA C VIRUS (STALIN CCREAT LATES/11/11/11) O INTLURAZA C VIRUS (STALIN CCREAT LATES/11/11/11) O INTLURAZA C VIRUS (STALIN CCREAT LATES/11/11/11) O INTLURAZA C VIRUS (STALIN CCREAT LATES/11/11/11) O INTLURAZA C VIRUS (STALIN CCREAT LATES/11/11/11) O INTLURAZA C VIRUS (STALIN CORLANDES/11/11/11) O INTLURAZA C VIRUS (STALIN CORLANDES/11/11/11/11) O INTLURAZA C VIRUS (STALIN CORLANDES/11/11/11)	Value 1	HENAGOLUTINAN PRECURSOR	INCLUENCE STREET OF BANCTORIANA?	316-473					-	-	<u> </u>
HEMAGGLUTININ PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGGLUTIN PRECURSOR HEMAGG	ARVE	HEMAGGLUTININ PRECURSOR		413-571			4	-	+	1	T
HEMAGGLUTION PRECURSOR NATURENES CYRUS (STACH CGREAT LAKES) 18734) HEMAGGLUTION PRECURSOR NATURENES CYRUS (STACH COPOGOVIA) HEMAGGLUTION PRECURSOR NATURENES CYRUS (STACH COPOGOVIA) HEMAGGLUTION PRECURSOR NATURENES CYRUS (STACH CAYOTOVIAN) HEMAGGLUTION		HEMAGGLUTTIMIN PRECURSOR	INTEGRAL VIEWS (CTB A DATE AND A DATE)	471-559				1	1		+
HEMAGGLUTINTH PRECURSOR INTLURIA C VILUS (STAAN CONTANT) HEMAGGLUTINTH PRECURSOR INTLURIA C VIRUS (STAAN CHYGOCUIA)) HEMAGGLUTINTH PRECURSOR INTLURIA C VIRUS (STAAN CAYOTOMIA) HEMAGGLUTINTH	1	HEMAGGLUTININ PRECUNSOR	INPLUENCE CUINOS (SI POLICIO EN LAKES/1167/34)	471-359							
HEMAGGLUTINGN RECURSOR RETURNER CYRUS (STACH CHOLANESBURGUM) HEMAGGLUTINGN PRECURSOR RETURNER CYRUS (STACH CHOLANESBURGUM) HEMAGGLUTINGN	1	HELMA COST LITTINGS PRECURSOR	INFLUENZA C VIXOS (STRAIN CONTOURS)	470-558					-		-
HEMAGGLUTININ PLECURSOR PRILIENZA C VINUS (STRAIN CAYOTONIAS) HEMAGGLUTININ	DAY DATE	SEVANCE LITTION	INFLUENZA C VIRUS (STRAIN CHILLOSOMES)	484.572	_				-	1	1
HENALOGUUTININ	HENA DICH	STATE OF STREET PRECIUESOR	INTLUENZA C VIRUS (STRAIN CHANNELSBURG)	470-558						$\left \right $	4
HEMACGLUININ	ADA PICH	PENALURIN INC.	INFLUENZA C VIRUS (STRAIN CATOTOMINA)								
	HENA INCKT	HEMAUGEUTIPH	(
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PCGENE	ALLMOTIS	All Virgers (as bacteriophages)	П	IT	П	П		П		10.10
FILE MANIE	PROTEIN		J	14.44	7010	2000	7	2000	7	A STATE OF
PHENA INCA	HEMADOLUTININ PRECINSOR	PV(0)	4/0-228							
MEMA INOM	HEMAGGLUTININ		10-57							
HEMA DICTI	HEMAGGLUTININ PRECURSOR		471-559							İ
PHEMA INCPI	HEMAGGLUTIMIN PRECURSOR		66.							
MENA INCES	MEASLES VIRUS (STRAIN HALLE)	(2)	411-359	Ī		•				
PHEMA INCTA	HEMAGGLUTININ PRECURSOR		ACC-1/2							
PHEMA INCYA	HEMAGGLUTININ PRECURSOR	ATAIOSIJ	****							
PHEMA MEASE	HEMAGGLUTININ-NEURAMINIDASE	TOM)	R.							
PHEMA MEASH	HEMAGGLUTIMIN-NEURAMINIDASB		46-90							
PIEMA MEASI	HEMACCLUTININ-NEURAMINIDASS		46-87				Ī			
PHEMA MEASY	HEMAGGLUT DAM: NEURAMINDASE	MEASLES VIRUS (STRAIN YAMAGATA-I)	46-87							-
PHEMA MUNO!	HEMAGGLUTININ-NEURAMINIDASE		14.99							
PHEMA MUROW	HEMAGGLUTININ-NEURANIMIDASE	WARA VACCINE)	14.99							
PHENA MAROR	HEMAGGLUTDAM-NEURANDMIDASE		8.5							
MEMA MUMOS	HEMADOL UTRAIN-NEURANIMIDASE		14.99							İ
MEMA NOVA	HEMAGGLUTININ-NEURAMINIDASE	いしんりょう	1.52	477-529						
PHEMA NOVE	HEMAGGLUTIMIN-NEUKAKINIDASE	ETTE C/45)	\$							
PHENA NOVO	HEMADOLUTININ-NEURANIMIDASE		<u>:</u>							
PHENA NOVA	HEMAGGLUTIMIN-NEUNAMINIDASE		<u>:</u>							İ
PHEMA NDVO	HEMAGGLUTININ-NEURAMINIDASÉ	(9)	-52							
MEMA NOVTO	HEMAGGLUTINDI-WEUTCAMMIDASE	49)	67							
MENA NOVU	HEMAGGLUTIMIN NEURANIMIDASE	(STRAIN ULSTER/67)	1.52							
PHEMA PHODY	HEMAGGLUTTIMEN NEURANDMIDASE	_	19.73							
PIEMA PIEM	HEMAGGLUTING HEURAMINIDASE	(STRAIN WASHINGTON/1957)	66-110							1
PATENA PASH	HEMACOL UTDOWNEURANDMIDASE		247-281							
PHEMA PIZHT	HEMAGG UTDAN-HEURAMINIDASE	(STRAIN TOSHIBA)	247-281							
PIENA PID	HEMAGOLUTININ-NEURAMINIDASE		18-93							
PIEMA PIJH	HEMAGGLUTDWINEURANDMDASE		I	27.73						
PHEMA_PIJHA	HEMAGGLUTININ-YEUTAMINIDASE	ē	T	2						
PHEMA PISHT	HEMAGGLUTININ-NEURAMINIDASE	Ī	1	120-146						
MEMA MINU	HEMAGGLUTININ-NEURAMINIDAS&		T	24.428						
PREMA_PUHV	HEMAGGLUTININ-MEURAMINIDASE									
PHEMA MINW	HEMAGGLUTININ-WEURAMINIDASE	HUMAN PAKAIN LUENZA 3 VIRUS (SIRKIN WASHINI)	T	277-147						
PHENA, PUHX	HEMAGGLUTBMIN-NEUTAMMINDASE	Ī	T							
PHEMA PIAHA	HEMAGGLUT INTH-MEURAMINITASE		1	256-390						
PHENA MACY	ASSESSMENT OF THE CONTRACTOR AND A CONTR	TRAIN KABETE O)	Γ							
PHENA MACH	HEMACCI LITIMIN NEUTRAMINIDASE		1	191-225						
PUENA CENTRA	HEMACCE LITININ-NEUTAMINIDASE	T MUTANTS)	57.110							
PIEMA SENDE	HEMAGGLUTIMIN-NEURAMINIDASE	SENDAI VIRUS (STRAIN FUSHINII)	53.110							
PIEMA SENDH	HEMAGGLUTIMIN-NEURANTHIDASE	US)	2.110							
PHEMA SENDA	FEMAGGLUTININ-NEURANIINIDASE	ć,	91:							
PHEMA KENDZ	HEMAGGLUTININ-NEURAMINIDASE	TRAIN 2)								
PHEMA SV41	HEMAGGLUTINGN-NEURAMINIDASE			27.5						
PHEMA SVS	HEMAOCI UTININ-NEUTANONIDASE		=							
PHEMA SVS! N	HEMAOGLUTIMM-NEURANGNIDASE	(ISOLATE INMAMAN)	17:62							
PIEMA VARV	HEMAGGLUTININ PRECURSOR		133.11							
PHE XI ADEDI			8.54							
PHE YO A DE DS	PERIFERTONAL HEXON-ASSOCIATED PROTEIN		8.54							
PHEXI ADEM	HEXON-ASSOCIATED PROTEIN		15-134							
PHEXY ADEDS	HEXON-ASSOCIATED PROTEIN		2							
PIEXT ADEO?	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 1, AND IRUMAN ADENOVIRUS TYPE	3:3							
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	A11 MOT18	weer (as batterlopheget)		ABEA1 A	7737	ABEA1	7	9	П	
T		MRUS	11:13		T					
T			67.126							
1724			53-103	+						
TEXT APEN			٦	T						
THE AN ADENT		TUPAIA AMERICANES	341.316	41)-467	7.07					
MEAN ADEM		KUNIAN ADENOVINGS	7	٦						
A Amend		HUMAN ADEROVINGS	٦	Т	357-387					
AND ADEAD		HUMAN ADENOVING TYPE 41	7	7		304.310	-			
ACE A ANEA!		HUNIAN ADENOVINOS TYPE 1	Ī	٦	344-378					
THEY WEST		JOVINE ADENOVIROS LITES	330-395	455-489						L
EX AUCED	DIED	COWPOX VIRUS	110-131							
PIGG COWPA		AFUCAN SWINE FEVER VIRUS (SIRVING BATTY)	Γ	378-419						
PILLS ASTBY	THE PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN 124)	379.470							
CANA		CAULIFLOWER MOSAIC VIRUS (STRAIN BARLI)	T	178-419						
PIBMP_CAMM		CALLIFLOWER MOSAIC VIRUS (STRAIN CAL-1141)	T	134.419						
PIBLO CAMVC		CALLIFLOWER MOSAIC VIRUS (STRAIN DAI)	T							
ALP CAMYD	INCLUSION BOOY MATRUX PRUIELIN	CALL IFLOWER MOSAIC VIRUS (STRAIN PAC)	1				-			
PIBNIP CAMVE	INCLUSION BODY MATRIX PROTEIN	CAILLIFE OWER MOSAIC VIRUS (STRAIN S-JAPAN)								
PIBNO CAMVS	INCLUSION BOOY MATRIX PROTEIN	CAUTIFLOWER MOSAIC VIRUS (STRAIN NYBISS)								
IND CANTA	INCLUSION BODY MATRIX PROTEIN	CALE THE OWER MOSAIC VIRUS (STRAIN PVIAT)								
PEND CAMP	DACLUSION BODY MATRIX PROTEIN	CAIR TEL DWER MOSAIC VIRUS (STRAIN STRASBOURG)								
STATE CANVS	INCLUSION BODY MATRIX PROTEIN	CARNATION ETCHED KING VIRUS	2							
WO CENV	INCLUSION BOOY MATRIX PROTEIN	SIGNORT MOSAIC VIRUS (STRAIN DXS)	=======================================	372-400			-			
PEND DAYD				22:179						
VO02 041	INCLUSION BODY MATRIX PROTEIN	STEP IS BANK CYTOMEGAL DVIRUS (STRAIN AD169)	٦	290-324	777		-			L
HC11 HCMVA	2	TOTAL STATE OF THE CASE I STRAIN IN	331,365				-	-		
MOLE WAY!!	PROCESSING AND TRANSPORT PROTEIN	THE TEST STATES OF THE TYPE I / STRAIN ANGELOTTI)	331-369							
ALVA!	PROCESSING AND TRANSPORT PROTEIN	ACCOUNT OF VIRIAL CANADA P.	124.362				-	-		L
PICIO POVIE			466-500				1	-		
ICH HEVRY			341-375				\downarrow			
TOTAL HISVER			58-99	361-395				-		
AND WENCE	PROBABLE PROCESSING AND TRANSPORT PROTEIN	PERCENTINGS SALES (STEATH SAUTH)	60-112	290-140	647-691					
\$000m	PROBABLE PROCESSING AND TRANSPORT PROTEIN			303-337				-	-	
PRVD	PROBABLE PROCESSING AND TRANSPORT PROJECT	SOUTH HER PECVIRUS TYPE I (STRAIN JUTA)					-			
ICHO HSVBJ	TRANS-ACTING TRANSCRUPTIONAL PROTEIN ICES		190-224			1	-	-	_	
PICTO HSVBK	THAMS ACTING TRANSCRIPTIONAL PROJECT ISSUED		1023-1056				-			
DAY HSVARD	TRANS.ACTING TRANS. PLOUVE ACTION IN PROTECT IN ICPA		920-934							
CAZA ASAD		-	207-241			-	L			
PIE63 HOMYA		HERPES SOULEX VIXUS (TYPE I / STRAIN 17)	24:02			-				4
TEAS HISVII	TRANSCIU IIONAL RECOLMANDI IEST HOMOLOG	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	015.707	308.306			_			-
EGS HSVEB	TRANSCULTIONAL ACCURATOR HES HOMOLOG	VANCELLA-ZOSTER VIRUS (STRAIN DURÍAS)	13.64							1
TEAL VZVD	TRANSCIA PER A PROTEIN ESS	EQUINE HEAPESVIRUS TYPE 4 (STRAIN 1942)	88.133							-
PIE64 HSVE4	DO SENATE BARLY PROTEIN TESS	EQUINE HERPESVIRUS TYPE I (3 INAIN ABAT)	41.15						1	+
PIE68 HSVEB	DAMEDIATE PARLY PROTEIN	HELPESVIKUS SABGRU (STRAIN III)	17(1						+	+
TEAU HSVSA	INNOTITETAL PROTEIN DLS .	HUNGAN CYTCHEGALOVINUS (STANIN AD10)	74.162						+	1
TOO HOWA		HUMAN CYTONEGALOVIRUS (STRAIN AD19)	250-314						1	+
WIN HOUSE	NSFORMER	T FELINE SARCOMA VIRUS (STRAIN INCIDENTIAL	131.15				-		-	1
KABL FSWHT	TYROCHE PROTEIN KINASE TRANSFORMING PROT		112-227	263-304					1	+
TOTAL MENA	ANT KINASE TRANSFORMENO PROTEIN	AKTO MUNICIPEDIA VINUS	3.5	104-178					-	+
PLAKE MEVAL	톗	TELINE SARCOMA VINOS (STAMIN CARDNER, RASHEED)	218-252			1		1	+	1
TOAS STATE	TYROSINE PROTEIN KINASE TRANSFORMING PROT	TIFELINE SALCOMA VINUS (STRAIN MCDONOUGH)	113-362	638-679	913-69	1	-	1	+	-
	PACS TYROSING KINASE TRANSFORMING PROTEIN	OTEIN FELINB SANCOPA, VIOLE COTA AN PACIT	68-69				1	1		
TANKS TANKS	TYROSINE PROTEIN KINASE TRANSFORMING PROT	TAVIAN SARCOMA VINOS (STRAME ROM)								
PKJPS AVIST		. 7								

PCCEME	ALLMOIN							7 - 14 -		
		YRUS	_	25.0	SETA	OBLA!	10000	9	1	:
CHERAPH	THOUSENE PROTEIN KINASE TRANSFORMING PROT	FUTINAMI SARCONIA YIRUS		Т	341.34	Ţ				;
PKP75 FUISV	I TROSINE-FROIENT NATIONAL INC.	AMSACTA MOOREI ENTOMOPOXVIRUS	47.81							:
AMEN	THYMIDINE RIMASE	CAPRIDOXVIRIIS (STRAIN KS-1	31.83							-
XIII CAN	THYMIDINE KINASE	PPOTEDLINAR VIRUS (STRAIN B95-6)	116-262	431-472						1
PKITH EBV	THYMDINE KINASE	PERPES SECTION EX VIRUS CTYPE 1 / STRAIN 17)	90-124							:
PKTTH HSVII	THYMDIME KINASE	PERPER CRAFT EX VIRIN (TYPE I / STRAIN CLIDI)	20-134							
KITH HSVIC	THYNDINE KINASE	TERREC CACE EX CIRCL (TYPE I / STRAIN HERA)	90-124							!
PKITH HSVIE	THYNODINE KITASE	LEBBER CILE EX CIRIS (TYPE I / STILAIN KOS)	90-124							-
PKITH HSVIK	THYMDINE KINASE	PROPERTY OF VIRIALITY OF A STRAIN SCIE)	30-134							
PKITH HSVIS	THYMDINE KINASE	LEADER SILMI EX CIPITO (1795 2/ STRAIN 111)	91.125							
PRITH HSV23	THYMDINE KINASE	MENCES SIMPLEA VIACALITY E 17 STRONG 12 STRONG	616-665							-
РКІТН НЅУВМ	THYMIDINE KINASE	BOVING PERFECT VIALS I LEG / STEAM AND SECOND	19.51	138.219						:
PKITH HSVE4	THYMIDINE KINASE	EQUINE HEIGHTS (175 - 131AAH)	19.51	11.230						
PKITH HSVED	THYMIDME KINASE	EQUINE MERFESVIRUS TYPE I (STRAIM ADMI)	716							_
PKITH HSV	THYMIOME KINASE	PELINE MERPESVIRUS (PELID HERFESVIRUS I)					-	-		
PKTH HSVAR	THY ALD DREKEN ASE	NIARAOSET ITERPESVIRUS	32.40					<u> </u>	-	:
PETTY MEVEA	THYMIDINE KINASE	HERPESVIRUS SAINIIM (STRAIN 11)	337-389							-
DAVE TITLE	THYMIDINE KINASE	PSEUDORABIES VIRUS (STRAIN NIA-3)	161-202							:
2000	NA CCENTACTION ON THE PROTEIN KINASE TRANSF	AVIAN RETROVIRUS AIII2	69.10)							
PKMIL AVIMI	MAL SCHOOL STATE OF S	ICTALLIAID SERVESVIRUS I	190.224							
PKKIS HSVII	CENE IS PROTEIN ANY ASSE	HERPES STATE EX VIRUS (TYTE I / STRAFA 17)	19.65	\$16.125						1
PKRZ HSVII	TAUBABLE SERVICE INVESTIGATION	ACTALLIZATION DE RESIGNATION	417.528	169.605						
PKR74 HSVII	GENE 74 PROTEIN AINASE		\$7:1							
PICLAS MSV36	Z L		133.168			 -				i -
PKRBI VACCC	30 KD PROTEIN KINASE HOMOLLAN	TACTION AND STREET OF THE PROPERTY OF THE PROP	133.168							
PKRB1 VACCV	10 KD PROTEIN KINASE HOMOLOG	VACCINIA VIRUS (31 KAIN WR)								
PICES VARV	39 KD PROTEIN KINASE HOMOLOG	VARIOLA VIRUS				-				:
PKRB1 VACCC	POSSIBLE PROTEIN KINASE BIZ	VACCINIA VIRUS (STRAÍN COPENTAGEN)								! !_
PKRB2 VACCV	POSSIBLE PROTEIN KINASE BIZ	VACCINIA VIRUS (STRAIN WR)	147.181						-	<u>:</u>
PKIET VACCO	POSSIBLE PROTEIN KINASE 7 10	VACCINIA VIRUS (STRAIN COFEMIAGEN)	104-20)							-
PKAE VACO	POSSIBLE PROTEIN KINASE FIO	VACCIMIA VIRUS (STRAIN L-IVP)	130-170							
PERF VARV	POSSIBLE PROTEIN KINASE F10	VARIOLA VIRUS	169-703				-			İ
PK BOK AVISU	IROS TYROSINE KINASE TRANSFORMING PROTEIN		111-145						-	
CELON ASSESSED	TYROSINE PROTEIN KINASE TRANSFORMING PROT		15-66							
	TOWNS ATT KINASE		135-169							j
PAYER AVIEW	TYROSINE PROTEIN KINASE TRANSFORMING PROT		174-333							
ADE02	LATE 100 KD PROTEIN	HUMAN ADEMOVIRUS TYPE 2	441-475						-	
TO ADEOL	LATE 100 KD PROTEIN	HURLAN ADEMOVIRUS TYPE S	223-264			-				: -
TEIN ANEW	I ATE 100 KD PROTEIN	HUMAN ADENOVIRUS TYPE 40	191-332	~ 						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LATE 100 KD PROTEIN	HUMAN ADENOVIRUS TYPE 41	199-213							
1 ADEA	I ATE 1.1 52 KD PROTEIN	HUMAN ADENOVIRUS TYPE 2	238-214	301.349						
M CS ADEOL	LATEL 1 52 KD PROTEIN	HUMAN ADENOVIRUS TYPE S	138-214	301.349						
MAN ENV	GENE TERMINAL PROTEIN	EPSTEIN-BARK VIRUS (STRAIN B95-8)	144.179	34.33						1
1	LOW CAPONG DAY VACE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	54-153	623-656						
WELL SPVIA	CONTRACTOR OF THE	VACCINIA VIRUS (STRAIN COPENHAGEN)	171	623-657						
MCEL VACCE	MUNA CATTING ENE I FILE	VACCINIA VIRUS (STRAIN WR.)	14-1	623-657						
PHOEL VACEV	MUNA CATTUN ENGINE	VARIOLA VIRUS	1.39	623-657						
PHOEL VARY	MUNA CAPTURA EACTIFICE	VACCINIA VIRUS (STRAIN COPENHAGEN)	72.137	345-286						
PACES VACCO	MUCA CAPTING ENGINEER	VACCINIA VIRUS (STRAIN WR)	12-137	345-286						
PHOES VACEV	MANA CAMPAN ENGINE	VARIOLA VIRUS	111-111	243-216						
PMCES VARV	MANA CAPTING EACH PAIR	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	116-157	179.313	118-712					
PMCE ASPEC	MUNA CASTINO ENE I PER	ODONTOGLOSSUM RINGSPOT VIRUS	51.90							
PAOVE ORSY	Т	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	26-66							
Frans	7	TOBACCO MILD GREEN MOSAIC VIRUS (TAIV STRAIN U.)	39-62							
PHOVE THICHLY	MOVEMENT PROTEIN									

AMALI ON LAID AMALI AMAL	÷		AB Virasra (ne batterdopha pri)	П			П	Т	71301		781.78
	PCCEME	ALLMOTIS		1	151	CELAL	T	Ī	ī	Ī	!
	THAME TO SERVICE	PROTEIN	TOBACCO MOSAIC VIRUS (STRAIN TOMATOAL)	23-46				†			
	PHOVE THATO	MOVEMENT PROJECT	TOWATO MOSAIC VIRUS (STRAIN LIIA)	33.10							
	PHOVE TOMOVA	MOVEMENT PROTEIN	TOWNS TO MOSAIC VIRUS (STRAIN LII)	33-40				1			
	PMOVE TOWN.	MOVEMENT PROTEIN	CHOOLELLA VIRUS MC.1A	111.156							
PAGE PAGE	איזכן טעאן	MODIFICATION METHTLASE CVIDE	PARALGEGIST BIRSABIA CICLORELLA VIRUS I	115-164							
	PATCI CHWI	MODIFICATION METHTLASE CVIAIL	AND MAYEL OCYTOMATOSIS VIRUS CALI	339.266	175-419						
	PATC AVBG	MYC TLANSFORMANO PROTEIN	ANAMANTEL OCYTOMIA TOSIS VIRUS INCIG	130-263	176-470						
NET EAGUS BANKER 1751-151 1	PATYC, AVDAC	MYC TRANSFORMING PROTEIN	AVIAN MYEL OCYTONATOSIS VIRUS IMI	130-267	176-420						
VALUE LONG STATEMENT VALUE VAL	PATYC AVIDED	MYC TRANSFORMING PROJECT	AVIAN BETROVIAUS MISES!	337-421							
VACTO CARRENT FOLIARY TABLE STEERING MAY 1941	PARC AVIDGE	MYC TICASFOLMING PROTEIN	AVAN BETROVIEWS OK 10	191-111	370-414						
MACE COLVED PROTEST MACE COLVED PROTEST	PAINC AVIOR	MYC TRANSFORMING PROTEIN	COLUMN DELINE LATER VIOLES	193.417							
MACE COATE DETECTED	PMYC FLV	MYC TRANSFORMING PROTEIN	PELINE LEUNCHIN VINUS	193.417							Ì
MCLECASID DOILEN MUNICICAMINION SHILLS SHILLS SHILLS STATE STATE	MAYC FLYTT	MYC TRANSFORMING PROTEIN	FELINE LEUKEMIA PROVINCIA I I	12.46							
	PNCA2 CYMAS	MUCLEOCAPSID PROTEIN	MURSINE COMONAVINUS MILLY (STRAIN ATT)	115.76							
	PHCAP AINOV	MUCLEOCAPSID PROTEIN	AINO VIRUS		133.156						
MACE ECOLUTION FOR THE STATE AND STREAM TO STATE THAT WERS STATE AND STREAM TO STATE	PNCAP BEV	NUCL EOCAPSID PROTEIN	BEANE VIRUS		12.00	241.303	10:00				
NECTORATION NATIONAL NATION	ANCAR BREVA	MICL EDCAPSID PROTEDY	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN ASING)	201.70	3						
	SUCA BIDGE	MACH EOCAPSID PROTEIN	BUNYAVTRUS CERMISTON	877-0/1							
	PAICAS BEING C	MINI EOCAPSID PROTEIN	BUNYAVIRUS LA CROSSE	499-011							
	TOWN BUTTON	MICH FOCAPSID PROTEIN	BUNYAVIRUS SHOWSHOE HARE	477-97							
COUNTY NICESCO-VIOLED COUNTY CO	THE POST	Mary GOCAPSON PROTEIN	BUNY AVAWERA VIRUS	175.221							
	PRCAL BURIN	MAIN ECCAPED PROTEIN	CALICEAN CONGO HEMORRHAGIC FEVER VIRUS (1SOLATE C610)	233-306	27.48						-
	אכירה היים	LANCE COCARGO PROTEDA	CANTHE DISTRAIPER VIRUS (STRAIN ONDERSTEPOORT)	117.174	3.27	154-402					-
MCLECASIO FIGURE BIOTHE COROLAWING STRANK 131 149.313 149.	WCAP CDVO	NACTOR OF THE PROPERTY	CHANDIPURA VIRUS (STRAIN 1611514)	40.44	22.36						i
MCLEGCAPIO FOTEN	PICA CHAV	MOLECUATION PROTEIN	BOVINE CORONAVIRUS (STRAIN F15)	149.313							
MCLEGCASID FOTEN	PICAP CVIII	ROLLECCA 310 FACTER	BOVINE COROMAVIRUS (STRAIN ACEDUS)	149.333							
NOTICECAPSIS PROTEIN	PNCAP CVBN	ACCAPITO PROTEIN	CANTHE ENTERIC CORONAVIRUS (STRAIN K 178)	165-227							
MICLEGARD PROTECT MICREGARD PROTECT MICREGARD PROTECT MICREGARD PROTECT MICREGARD PROTECT MICREGARD PROTECT MICREGARD PROTECT MICR	TO CACA	ANGESCAPEDIEM	HUMAN CORONAVIRUS (STRAIN OC41)	149.383							!
MUCLEGCASID FROTEN	THE CANOL	MICH FOCAPSID PROTEIN	AUJUNE CORONAVIRUS AIIIV (STRAIM IIIXI)							-	
MUCLECCASID FACIEN	THE AV CVICIN	MIC SOCAPED PROTEIN									-
MUCLECCASID PROTEIN	PRODUCTION OF THE PROPERTY OF	Mary Encapember (IN)									-
MUCLECCAPID PROTERN	PHCAP CVPFO	MAIN ENCAPED PODEIN	PORCINE RESPIRATORY CORONAVIRUS (STRAIN 66/1) YOO / BRIT	149-321							:
NUCLECCASID PROTEIN	PRCAP CVTRB	New COCAPUDITION	POACINE RESPIRATORY CORONAVIRUS (STRAIN RAI)	149-128							-
NUCLEOCASID FROTEN	PNCAP CVPIOR	MAIN SOCKASIO PROTEIN	RAT CORONAVIRUS (STRAIN 441)	97							
MUCLECCASID PROTEIN LASTAN VIRUS (STRAIN TR-1144) 131-300 131-314	THE CARSE	MICE FOCAPSID PROTEIN	TURKEY ENTERIC CORONAVIRUS	34.10							-
MUCLECCASID PROTEIN FELINE RATECTIOUS PERTONTIS VIRUS (STAN) 79-1140 131-300 141-301 141-300 141-301 141-300 141-301 141-300 141-301 1	200.00	MAICH FOCAPSID PROTEIN		230-306				Ť	-		!
MUCLEGCAPID PROTEIN	ALVE ERV	MICLEOCAPSID PROTEIN	T	8	72. 0	100,100		T			
MCC.ECCAPID PROTEIN	PACAB HANTV	MUCH EOCAPSID PROTEIN									
MCLEGCAPED FROTEN	PACAP HAZVI	MUCLEOCAPSID PROTEIN		Ī	300	101.101	141.180				
MACLEGGAPIO PROTEIN	IN UT OF THE	NAICE COLAS TO PROTEIN		T		101 171	141.110				! !
MUCLEOCASID PROTEIN	AND THE PARTY	MAIC EDCAPSID PROTEIN			37:0	101-107					
MUCLECCASID PROTEIN AVIAN EMECTIOUS BRONCHITIS VIRUS 13 FACES AREA (1912) 155-174	DACAP DVG	MJCI EOCAPSID PROTEIN		12.01							:
NUCLECCASID PROTEIN TARIA VALUA STRAIN GASIS 154-174 NUCLECCASID PROTEIN LASSA VIUUS STRAIN DSIARI) 154-174 NUCLECCASID PROTEIN LASTA VIUUS STRAIN DSIARI) 154-174 NUCLECCASID PROTEIN LASTA VIUUS STRAIN DSIARIS VIRUS STRAIN WES 1-40 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-17 NUCLECCASID PROTEIN LACUALAN VIRUS 154-11 NUCLECCASID PROTEIN LACUALAN	PACAP BAYK	NUCLEOCAPSID PROTEIN		200							
MUCLECCASID PROTEIN LASSA VILUS (STRAIN GANT) MUCLECCASID PROTEIN LASSA VILUS (STRAIN GANT) MUCLECCASID PROTEIN LASSA VILUS (STRAIN GANT) MUCLECCASID PROTEIN LAGRANGE MARKELEVATING VIRUS (STRAIN WE) 1-40 MUCLECCASID PROTEIN LYPPHOCYTIC CHORIONENNIGTIS VIRUS (STRAIN WE) 15-17 MUCLECCASID PROTEIN LYPPHOCYTIC CHORIONENNIGTIS VIRUS (STRAIN WE) 15-17 MUCLECCASID PROTEIN LAGRANGE VIRUS (STRAIN GASTON) LIS-231 MUCLECCASID PROTEIN LAGRANGE VIRUS (STRAIN MALLE) LIS-231	THEAT REPORT	MUCLEOCAPSID PROTEIN			15.1%			<u> </u>			
MACLEGGASTO PROTEIN	PNCAP LASSO	MUCL EOCAPSID PROTEIN		T	27.174	467.504					
MCC. EDCAPS OF MOTERN LACTATE DESTONAGENATE CATEGORY 100-497	PHCAP LASSI	MUCLEOCAPSID PROTEIN		T							
MCCLEGCASTO PROTEIN LYAPIDCYTIC CHORIONENINGHIS VIRUS (STALIN WE) 45.79 15.11	PACA LDV	MUCL EOCAPSID PROTEIN	LACTATE DELIYDROGEMASE FLEEVALING VIAUS	Ī	160.497						
MACE COCASTO PROTEIN LYAPHOCYTIC CHDRIOMENNALISS VIROS 121 151-221 MACE COCASTO PROTEIN MACE SECULATION 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLE) 111-224 151-211 MACE COCASTO PROTEIN MEASURES VIROS (STRAMM MALLES VIROS (STRAMM MALLES VIROS VIROS (STRAMM MALLES VIROS VIROS (STRAMM MALLES VIROS VIROS VIROS (STRAMM MALLES VIROS VIR	PACAP LYCVA	MUCLEOCAPSID PROTEIN	LYAMIOCYTIC CHOMORIENING HIS VIKUS (STRAIN ARKISTEN)	T		440.433			i		
MJCLEOCASIO PROTEIN	MCAP LYCVW	MUCL EOCAPSTO PROTEIN	HORIOMEMINGITIS VIRUS (STRAIN WE)							-	!
MACLECCASID FROTEIN AGASLES VRUS (STAIN ECHICAS I UNIT STAIN INCLESCASION) MACLECCASID FROTEIN AGASLES VRUS (STAIN IN-1-CA) MACLECCASID FROTEIN AGASLES VRUS (STAIN IN-1-CA)	PAT AP MADY	NUCL ECCAPSID PROTEIN		T							!
NACLEGGASTO PROTEIN AGASLES VIRUS (STRAN IN-1-CA) NACLEGGASTO PROTEIN AGASLES VIRUS (STRAN IN-1-CA)	PACAP MEASE	MUCLEOCAPSID PROTEIN	1001	Τ							
NICLE COCAPSID PROTEIN (ATASLES VINUS (STRAIN IP-1-CA)	PACAP LEASH	NUCLEOCAPSID PROTEIN		T				-			i
	1345	MAICH EOCAPSID PROTEIN	MEASLES VIRUS (STRAIN IP-J-CA)	7							

Profess	INTERIORIS.	All Virues (se bacteriophages)	П	П	lΤ	П	П	IT	П	
THE WAME	PROTEIN	MAN	J	brack	ARTA!	ABIA	FORGE	70798	2000	
PHCAP LGASY	MUCL EOCAPSID PROTEIN	MEASLES VIRUS (STRAIN YANIAGATA-1)		100						
PACAP MOPEL	MAICH FOCAPSID PROTEIN	MOPELA VIRUS	٦	25.50						
PACAP LALED!	MUCH EDCAPSID PROTEIN	LACADS VIRUS (STRAIN SAL-I)	114-155	28.53				1		-
PNCAP MARPH	MUCLEOCAPSID PROTEIN	INDERS VIRUS (STRAIN ANY ALIARA VACCINE)	214-255							1
PICAP PIC	MACLEOCAPSID PROTEIN	PROSPECT JINL VIRUS	-	5.74	78.					::
PHCA PIEC	MUCL ECCAPSID PROTEIN	INDIAN PARAINFLUENZA I VIRUS (STRAIN CJ9)	212-213	3.30					İ	;
PHCAP PINT	MICL EOCAPSID PROTEDY	IRBIAN PARAINTLIENZA I VIRIIS (STRATN WASHLNGTON/1957)	217.717	01:10						!
PHCAP PIZHT	MUCL EOCAPSID PROTEIN	HERIAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	20 10.				-			:
PHCAP MIB	MUCLEOCAPSID PROTEIN	BOVINE PARAINTLUENZA J VIRUS	100-403	6.0					İ	
PHCAP PIDHA	MUCL EOCAPSID PROTEIN	HUNIAN PARAINFI.UENZA J VIRUS (STRAIK NIII 47845)	25.03	30.00	344-403	460.491				
PNCAP PIARA	MUCL EOCAPSID PROTEIN	HURIAN PARADY LUENZA 4A VIRUS (STRAIN TOSHINA)	20.00	91-167					1	
PHCAP PISSE	MUCL EOCAPSID PROTEIN	HUNIAN PARAINFLUENZA 4B (TRUS (STRAM 48-333)	2	191.267						_
PHCAP PIARY	MICLEOCAPSID PROTEIN	PICHINDE ARENAVIRUS	65-113							
PNCAD PIRTY	MUCLEOCAPSID PROTEIN	PIRY VIRUS	•	125.339					_	_
PHCAP PUSABI	MUCLEOCAPSID PROTEIN	PUDIALA VIRUS (STRAIN HALLMAS RI)			111.79:			i		
PACAP PUCAG	MUCL EOCAPSID PROTEIN	PUTMALA VIRUS (STRAIN SOTKANO)	1.33	٦	317-115				-	_
PNCAP PWH	MUCL EOCAPSIO PROTEIN	PNEUAIONIA VIRUS OF MICE	93.141	141.303	144.304					:
PACAP BARVA	MICH ECCAPITO PROTEIN	RANIES VIRUS (STRAIN AVOI)	113-167							
200	MINI BOCAPCO PROTEON	SENDAL WRUS (STRAIN Z / 110ST ARUTANTS)	217.272	145.404					į	
	SACT FOCAPSID PROTEIN	SENDAI VIRUS (STRAIN ENDERS)	213:273	145.404					7	
2000	Marci Focabito Provide	SENDAI VIRUS (STRAIN 2)	111.111	303.408						
200	THE POLYPEN PROTEIN	SEOUL VIRUS (STRAIN SR-11)	5:-	40.74	137.381					
1000	Marci Cocketto Panten	SPADAN VIRUS 41	215.267	337-406	419.466		İ			
2	The section and the section of the s	CONCINIC VELLOW AFT VARIES	112.366					_		
PACAZ STRV	MUCLEUCATION FROIDING	7-2-2 PE C-2-7	Γ	210.264						!
PHCAP TACV	MULEUCASIUTROILIN	SULTAN VILLE	Ī.							<u>:</u>
PNCAL TOSV	MUCLEOCAPSID PROTEIN	CONTRACTOR CONTRACTOR AND AND AND AND AND AND AND AND AND AND	39.130				İ			
PHCAD TSWVI	NUCLEOCAPSID PRUIEIN		90.130							-
PCA TSWH	MUCLEOCAVSIO PROTEIN		91				+			. !
PHCAP ISWAL	MUCLEOCAPSID PROTEIN		201	İ		T	+			
PHCAP UUR	MUCLEOCAVSID PROJEIN	CIC SERVICES MAINE SETS AND 03 233			†		T			-
PHCAP VISW	MUCLEOCAPSID PROTEIN	٤	T	311.011						
PNCA VHSVM	NUCLEOCAPSID PROTEIN	Īž	T		Ī					
PHCAP VSVID	MUCLEOCAPSID PROTEIN			T			İ			
PICAL VSVID	NICLEUC APRIL PROTEIN		5113							
74CA 1313	NOCLECTOR STORES	TE BEN	7							
PNEJ HV2BE	AECALIVE FACTOR	HARAN BARNODEFICIENCY VIRUS TYPE 2 (ISOLATE DIP)	7							
200	NECKLIVE FACTOR	Γ	113-165							
THE HAVE	VECATIVE BACTOR	۶	09-150							
בועבי שייים	LANCO AND RACTOR	INDIAN PARINDDEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	01-10							
PAGE CIVAL	MEDATIVE FACTOR	IE GR	96.140							
73013	WEGATIVE FACTOR	SULIAN BRITHODEFICIENCY VIRUS (F236/SARI4 ISOLATE)	7	233-267						
AND LABOR	NET TRANSMIND SE	תופע	47.81							
TATAL TATAL	MEIRANDEDASE		11.74							
PART INCH	MELITAMONIDASE	_	16-05							
PARAM IACTO	NEURAMONIDASE	INTLUENZA A VIRUS (STRATN ANCHICKENMENNSYLVANIAN) 10	349.383							
PARAM IACTOR	NEURAMPHDASE		149-181							
PARAM IADGE	NEURANDASE		141							
PARALI IAFPW	MEURANDMIDASE	USWEYBUD		194-329						
MOUNT WHEO	HEURANDHIDASE			13:23						
PHRAM WARI	NEURAARMDASE	MTUCKY/IAI)		161-402			†	1		
PHRAM IAKE	NEURAMMIDASE	INTLUENZA A VIRUS (STRAIN AKIEVISMS)	50.01		1		1	1	1	1
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	ALL MOTES	1942 (no bacieriofinife)	4	10330	2628	10100	Ţ	ī	1	1
1000	PROTEIN	THUS A VIBILE STRAIN ALENINGADYSWID	- ×			Ī				
V3 141 VV	WEURAMINIDASE	MATERIAL STATES AND A STENDING INTHE ABELLANIYATH	20.11							
TANK IALVE	NEURAMBYIDASE	INTLUENCE A MAIN ARUDOY TURNSTONEMEN EAST	10.01							
SAN ALLE	MEURAMPHDASE		10-44							
573 77 27	NEURAMPHIDASE	INTELLEGIA OF THE AND ACTURE YOREGOND!	7							
THE PARTY OF THE P	WEITH AMINIDASE	ŝ	9.0							
LINCOLD IN COLUMN	MEI IN A LENGTH DASE	Γ	16-05							
THE IN IN	METRAMONDASE	DOLUENZA A VIRUS (3) RAIM ANVIAL PAIA PRIATOR	19.61							
PRICAL IAUSS	VACIONA AUDIEDASE	INTLUENZA A VIRUS (STRAIN ASSIDED FORMS)	27.	146-383						i i
PINAH WIN	A SAMPLE OF THE PROPERTY OF TH	INTEREST BYRUS (STRAIN PRETITO STATE		149-111						!
PARAM PABE	NEUKOWANIA	INTLUENZA B VIRUS (STRAIN BIRONG ROTORIS)	Ī	110.311						:
PRAM PRICE	NEURAMINIDASE		Ī							
PARAM PARLE	NEUTANIMIDASE	(18 CANANA	2							
N I WAY	NEURANIMDASE	INTOCACA STATES CONTRACTOR AND SOLUTION OF STATES OF STA		36.31						
	WELL A LONG TO A	DALUENZA B VINOS (STANIS PART MILECIAN)	97-5	148-312						
MONTH INDIVIDUAL	1000000	PALUENZA O VIRUS (STRAIN OF THE STREET	97.	149-313						
PARAM DABA	Trong and the second se	INTLUENZA B VIRUS (STRAIN BONE OU AND A	5	16.313						
PRILAM INBOR	WELECOMING ASS	INFLUENZA B VIRUS (STRAIN BASINGAPORE/22019)		101.07						
MANA INDS	NEURANGHIDASE	MALLIENZA B VIRUS (STRATH BAUSSIVIONIS)	T							
WOLAN DIBUS	NEURAMINIDASE	DATIFIED A WIRLS ISTRATO BYTCTORIA 3/18	Т							: : :
NEW COMME		SUBSTITUTE BOSIC VIRUS	790-121						L	
200	PROMETER STRUCTURAL PROTEIN PRECURSOR	BONETA DETACTION OF VIEW ATTENDANCED	95-129	204.338						
200	ACCES OF THE ALL PROTEIN	INCATIONS MELADINE SECTION AND AND AND COMMINGE	1.33							
PHSS INSVI	TOTAL PROPERTY OF THE PROPERTY	TONIATO SPOTTED WILT VINUS (BACKLES)	13.							İ
PNSS TSWVB	NOW STRUCTURED TO SEE OF	TOWATO SPOTTED WILT VIRUS (STRAIN LI)		110.164						
PHSS TSWAL	NON-STRUCTURAL PROTEIN	AMSACTA MICOREI ENTOMIOPOXVIRUS	١,	877.317	116.555					
PATPI AMEPY	NUCLEOSIDE TUTHOSTINA I ASE	CHARISTONEURA BIENNIS ENTOMOPOXVIAUS	T		100.000					
PACTP1 CBEPV	NUCL EOSIDE TRIPHOSPHATASE	VACCING VIRUS ISTRAIN COPEMIAGEM)	1							
WITH VACCO	MUCLEOSIDE TRUPHOSPHATASE	CACCESA VIBIS (STRAIN WR)	1	101-101						
2047	MUCLEOSIDE TRUPHOSPHATASE!			155.503						
AND THE PERSON NAMED IN	MUCLEOSIDE TRIPIOSPITATASE I	VARIOUS STRAIN EX VIBILE TYPE & STRAIN UGAMDA-1102)	189-123	22						
1100011	MAJOR ANTIGENIC STRUCTURAL PROTEIN	THE CASE STATE AND COPENIAGEN	131-110							
	POR YIAN POLYPIERASE CATALYTIC SUBLINIT	VACCIMIA VINCE SCIENCE WITH	111-110							<u> </u>
	POR YAN POLYMERASE CATALYTIC SUBLINIT	VACCINIA VINUS (3 INC.)	131.180							!
WAFE VALLE	WAY BOY YNE RASE CATALYTIC SUBUNIT	VARIOLA VIRUS	113:106							
PAPIVARY	STATE OF THE REGULATORY SUBURIT	CAPRIBOXVIRUS (STRAIM A 2 · ·)	93.134							
PAN CAM	THE THE STATE STATE ATOMY SUBUNIT	row Pox VIRUS	201.268		L					:
PPAPE FOWPV	POLY(A) PUL IMENASE TECH A TORY SUBLINIT	VACCIDIA VIRUS (STRAIN COPEMINGEM)								!:
PAPP VACCC	POLY(A) FOLT PREMASE RECUR A TORY SUBJUNIT	VACCINIA VIRUS (STRAIN WR)	301.340							1
PPAPT VACCV	POLY(A) POLYMERASE RECORD ATORY SIMILARIT	VARIOLA VIRUS		101.04						į
PPAP1 VARV	POLY(A) POLYMENASE ALCONOM	AUTOGRAPHA CALIFORNICA MUCLEAR FOLVIEDRUSIS VIAUS								i
PPEI3 NOVAC	12.1 KD PROTECH IN TE JACK	ORGYIA PSEUDOI SUGATA AND TICAPSID POLYIEDROSIS VIANI							į	1
PPELL NOVOP	11.5 KD PROTEIN IN PAR STAUGH	ATTOGRAPHA CALIFORNICA MUCLEAR FOLYIEDROSIS VIRUS	2							!
PPETE NOVAC	MAJOR BORDIATE EARLY PROJECT	CAPACIAL PERIODISLIGATA MULTICAPSID POLYTEDAOSIS VIRUS							L	
PRESE NOVOP	MAJOR BAIEDIATE EARLY PROTEIN	LITTOCE APILA CALIFORNICA NUCLEAR FOLYIEDROSIS VIAUS	4.42							
SPEAS LPVAC	AC RE	SECULO PER PROPERTY AND TICAPSID POLYTEDROSIS VIRUS	-	2						
2000	49 3 KD PROTEIN IN PE.P36 INTERCENTO REGION	UKUTA PERUNISIK TVAR 7	414-448							
200	MATURATION PROTEIN	HURAN ADERO TITO TO THE TOTAL	11.11							
NA PAR	SOUTH OF PRECUBSOR	HUNDAN ADENOVIRUS 1176 4	17:11						4	
PPIV6 ADE01	TAULEN TIPE TO THE TOP TO THE TOT	HUMLAN ADENOVIRUS 177E 3	113.161	3.3	957-991	1365-1299	1339-3266	100.50	Page 1	.01.
PPIVE ADEOS	TROISIN WINDOWS	BALLEY YELLOW MOSAIC VIRUS (ULICANIA)	136.161	5	111.111	957.994	1265-1299	227.2164	2101-1130	1
PPOLI BAYMO	GENOME FOLLTROILES	BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN 11:1)		90	230-273	111-415				
PPOLI BATHU	GENOME POLITICISM	HUNDADIAN GRAPEVINE CHRONE MOSAIC VIRUS	1		416.677	681-128	1157-1196	1378-1412	1906-1943	
PPOLI CON	NAMI POLYPROTER	GRAPEVINE FANCEAF VIRUS	10.215							
אינים מדי	ANAI POLYPROTEIN	TOMATO BLACK RING VIRUS (STRAIN S)	227.210			-				
PPOLI TBRVS	NAM POLYPROTEIN	TOWATO RINGSPOT VIAUS (ISULATE RASPOERRY)	807-10		111.011	117.030				
AVSIT 13049	RMAI POLYPROTEIN	BASE EN VELLOW MOSAIC VIRUS (DEPAIAN ISOCATE)	240:311							
	GENOME POLYPROTEIN 3	BANCEL ICHE								
22.4										

		All Variation Laboration								
TICHE.	PROTEIN	YIRUS	ABEA1	AREAL	AREA?	AREAd	AREAS	AREA 6	AREA?	AFFA
PPOL3 BATHU	GENOME FOLYPROTEIN 2	BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1)		134.773	117-111					
אטרז כיונע	RNAJ POLYPROTEDI	GRAPEVINE PANLEAF VINUS	365-406	242-602						
PPOL2 TBAVS	RNA2 POLYPROTEIN	TOMATO BLACK RING VIRUS (STRAIN S)								
PPOLJ TRSVR	RNAJ POLYPROTEIN	TOWATO MNOSPOT VIRUS (ISOLATE RASPBERRY)		134.368						
PPOLG BOVEV	GENOME POLYPROTEIN	BOVINE ENTEROVIRUS (STRAIN VG-5-27)	149.116	1008-1064	1382-1416	1459-1507	1376-1617			
PPOLO BYDYN	GENOME POLYPROTEIN	BOVINE VIRAL DIARRIEA VIRUS (ISOLATE NADL)	244-219	16795	629-663	1033-1074	1303-134	1392-1443	1069-1910	2226-2260
PPOLG BYDYS	GENOME POLYPROTEIN	BOVINE VIRAL DIAMMEA VIRUS (STRAIN SD-1)	245-389	167-91	629-663	1017-1074	1303-1344	1393-1443	1779-1820	2136-2170
PPOLG BYNV	GENOME POLYPROTEIN	BEAN YELLOW MOSAIC VIRUS	96-130							
PPOLG COXA2	GENOME POLYPROTEIN	COXSACKIEVIRUS A21 (STRAÎN COE)	9-43	362-396	664-698	1045-1100	1491-1346	1607-1648	1205-1839	1901-1946
PPOLG COXA9	GENOME POLYPROTEIN	COXSACKIEVIRUS AP (STRAIN GAIGGS)	15-49	1040-1016	1395-1940					
POLO COXBI	GENOME POLYPROTEIN	COXSACKIEVIAUS BI	15-49	1031-1067	1876-1921					
PPOLG COXB3	GENOME POLYPROTEIN	COXSACKIEVIRUS BI	15.49	1024-1030	1879-1924					
POLG COXBA	GENOME POLYPROTEIN	COXSACKIEVIRUS B4	15-49	1997	1033-1068	1877-1922				
PPOLG COXBS	GENOME POLYPROTEIN	COXSACKIEVIAUS BS	15-49	1034-1070	1879-1924					
PPOLO CYVV	GENOME POLYPROTEIN	CLOVER YELLOW VIEW VIRUS	120-154							
PPOLG DENIS	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN 816-1)	74-108							
PPOLO DENIA	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN AIG 03-10)	14.108							
PPOLO DENIC	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN CVI63677)	34-108							
PPOLG DENIS	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STILAIN SINGAPORE S275/90)	74-108	632-873	P66-096	1143-1179	1386-1420	1614-1648	2518.2554	2946-3016
PPOLO DENIW	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN WESTERN PACIFIC)	74-108	133.874	\$64-196	1143-1180				
PPOLG DENZI	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA MI)	148-492							
PPOLO DENT	GENORGE POLYPROTEDN	DENGUR VIRUS TYPE 1 (ISOLATE MALAYSIA M1)								
PPOLO DENZA	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 1661)	74-108	776-357	566-196	1146-1180	1246-1210	1418-1452	1615-1649	2517-2551
PPOLO DENO?	GENOME POLYPROTEIN	DENGUE VINUS TYPE 2 (STRAIN 1661)-PDK53)		728-777		1146-1180	1246-1210	1418-1452	1615-1649	2485-2551
PPOLO DENZO	GENOME POLYPROTEDM	DENGUE VIRUS TYPE 2 (STRAIN D2-04)	728-777							
PPOLO DEDCH	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN TH-16)	497-546						П	
PPOLO DENTI	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN JAMAJCA)	74-108	728-777	961-995	146-1180	1246-1280	1418-1452	1615-1649	2517-2551
PPOLG DENZH	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1 (STRAIN NEW GUINEA C)	1	398-432					Т	
PPOLO DENTP	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PRISMSI)	Т	728-777	832-675	2	144-110	1246-1280	100	1615-1649
PPOLO_DEDUT	GENOME POLYTROTEIN	DENGUE VIRUS TYPE 2 (STRAIN TONGA 1974)	I	552-595	601-715	00-991	966-1000	1205-1239		
PPOLO DENDU	GENCINE POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN PUO-218)	(99-719				H		T	
PPCCOLDENS	GENOME POLYPROTEIN	DENGUE VIRUS TYPE)	130-872	959.993	1	1224-2258	- 1	2704-2738	2940-2978	2980-3014
PPOLG, DENA	GENOME POLYTROTEIN	DENGLE VIRUS TYPE 4	27.99	1380-1414	2514-2555	2701-273	2941-2975	1977-3011		
POLO ECI IG	GENOME POLYPROTEIN	ECHOVEROS II (STRAIN UNECORT)		10.3	0000	746. 377	1700.1033			
POLG EMCV	GENOME FOLTPROTEIN	ENCETHALOM TO AUTO STATE	10/4-1113	11(1-7/11	0/21-275	201	(701-40/)			
PPOLO EMCVB	GENOME FOLVENOIEIN	ENCENIAL ON OCABITIES VIRUS (STRAIN ENC.D DIABETOCK	200	1076-117	474.1570	1534.1573	1647-1708			
Proto EMCVD	GENOME FOR VEROTEIN	MENGO ENCEPHALOMY OCARDITIS VIRUS (STRAIN 17A)								
CONCO CONCO	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS	21.5							
INDIO ENDA	GENOME POLYPROTEDN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A10-61)	231-255	294-328	578-612	1103-1153	1493-1528	2165-2200		
POLO FADVA	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12)	220-254	293-327	119-115	1103-1164	1493-1528	2164-2199		
Prot.a TABVO	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIBFS)	231-255	1103-1153	1493-1528	2164-2199				
PPOLG FADVS	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI-SANTA PAU (C-S		127.669						
PPOLG FADVT	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI)	221-255	203-317	577-611					•
PPOLO HCVI	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE I)	364-398							
POLG HCVA	GENOME POLYPROTEIN	HOG CHOLERA VTRUS (STILATA ALFORT)	440-493	616-660	652-359	1033-1070	1190-1235	1307-1343	1779.1820	2136-2170
			2466-2500	2525-255	2667-2708	3057-3098	3152-3193	3406-3440		
PPOLO HCVB	GENOME FOLYPROTEIN	HOG CHOLERA VIRUS (STRAM BRESCIA)	440493	626-660	655-729	1033-1070	1173-1235	1779-1820	2136-2170	2388-3436
PPOLO HCVBK			1466-1500	2525-2559	2667-2708	3057-3098	3152-3195	3406-3440	3521-3562	
PPOLO HCVEO	GENOME POLYPROTEIN	IEPATITIS C VIRUS (ISOLATE DK)	157.398	2328-2365						
PPOLO HCVH	GENOME FOLYPROTEIN	HEPATITIS C VIRUS (ISOLATE ECIO)	8:8				brack			7

ANADO	A113A0T18	All Viruses (no bacteriaphuges)	T		100	ABFA A	AREA S	AREA	AREA?	AREA 8
TO BE MA LATE	MINIOR	VIRUS	9	10100	1		Γ	Γ		
THE PARTY	CENTRAL POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE H)	104-37							
POLO HCVR	CENTRAL POLITICAL	HEPATITIS C VIXUS (ISOLATE HCV-476)	364-398						\[\]	
POLO HCVH7	GENOME TOURS OF THE	HEPATITIS C VIRUS (ISOLATE HCT27)	236-270							
PPOLG HCVRI	GENOME FOLTEN	LEPATITIS C VIRUS (ISOLATE HCT18)	248-282							
PPOLO HCVRX	GENOME FOLTFRUIE IN	LINEDATITIES CARRIES (ISOLATE HCV-KF)	157.398							
PPOLO HCV12	GENOME FOLTPROTEIN	UNE A TITLE OF VIRUS (ISOLATE HC-12)	387-388							
PPOLG HCVIS	GENOME POLYPROTEIN	LICEA TITLE C VIEWS (ISOLATE HC-15)	364-398							
PPOCO HCVM	GENOME POLYPRUTLIN	KEPATTIS C VIRUS (ISOLATE HC-16)	364-401	1716-1750	2062-2116					
POLG HCVI7	GENOME FOLTPROTEIN	MERATTIC MRIS (ISOLATE HC.IT)	364-398							
PPOLO HCV/I	GENOME FOLTMUTEIN	INFRATITIS C VIRUS (ISOCATE HC-19)	364-398	1716-1750	2082-2116	2461-2502	2531-2572			
POLO HCVIA	GENOMA POLYPROTEIN	INTERACTION CORTS (ISOLATE JAPANESE)	357-405	2331-1368						
PPOLO HCVIT	GENOME POLYPROTEIN	WERN THE CHARLE GOLD AT BUCH	357.391	2331-2365						
PPOLID HCVTW	GENOME FOLYPROTEIN	LEBATTER COURT HOLE ATE TAIWAN	357.398	3328-3365	1444-1503					
PPOLO_HPAY1	GENOLG POLYPROTEIN	ACCALLIST VINOS (SOCKAL)	3.53	101-135	203-237	170-904	1021-1055	1117-1151		
PPOLG HPAV4	GENOME POLYPROTEIN	TECALITIES A VINOS (STREAM STILL)	3.43	101-135	203.237	100-001	1021-1055	1117-1151		
PPOLO HOAVS	GENOME POLYTROTEIN	TOTAL TITLE A CORE (STEP AND 100)	143	101-135	701-237	170-904	1021-1055	1117-1151		
PPOLO HPAVC	GENOME POLYTROTEIN	LEGATINE A MELIE (STRAIN CR.)26)	17.	101-135	203-237					
PPOLO HPAVG	GENOMO FOLYPROTEIN	HEBATITIS A VIRUS (STRAIN GA76)	\$0-114	183-316						
PPOLO HPAVH	GENOME POLYPROTEIN	GENTLES A VIETE (STRAIN IN. 175)	7	101-135	203-233	870-904	1021-1055	1103-1151		
POLO HOAVL	GENONG POLYPROTEIN	LECATION A VARIATION AND AND AND AND AND AND AND AND AND AN	7	101-135	761-137	870-904	1021-1095	1103-1151		
PPOLO HPAYN	GENOME POLYPROTEIN	THE ACTION A STREET A PARTY AND A STREET AND	17.	20:00	203-233	170.904	1021-1055	1103-1159		
PPOLO HOAVS	GENOME POLYPROTEDY	ALCALISTA VIACO (STACK) FIRST	Ĵ	105-139	207.241	849.908	1623-1059	1115-1155	1158-1198	
PPOLO HPAYT	GENOME POLYPROTEIN	SPRIAN INCATING A VIBIR (STRAIN CY-143)	143	101-135	101-131					
PPOLO HAVIA	GENOME POLYPROTEIN	SINIAN IECKINIS A VINOS (SINOS CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA D	1020-1054	1393-1437	1479-1513	1877-1920				
PPOLO KRVIA	GENONG POLYPROTEIN	HUMAN MINOVINES IN CONT.	362.396							
PPOLO HOLVIB	GENOME POLYPROTEIN	MONTH OF THE CONTRACT OF THE C	117-111	26. 163.	1133-1160					
PPOLO HOVO	GENOME POLYPROTEIN	IN PLAN BURDOVELIS 2 OCI V.3)	156-197	1126-1169	1352-1593					
PPOLO HOWIP	GENOME POLYFIOTEIN	IN DALAN BHINOVIRUS B9 CCR V-89)	1366-1607							
PPOLO HUEVI	GENOME POLYPROTEIN	MALAN ENTEROVINIS 20 (STRAIN 167071)	159.397	116-911	1033-1088	1403-1441	1196-1934			
PPOLG BOVO	GENOME POLYPROTEIN	AND PRECIOUS BIRCAL DISEASE VIRUS (STRAIN ON	134-168	150-291	475-524					
PPOLO JAEVI	STRUCTURAL POLYPROTEIN	A VIAN IN ECTIODS BOKSAL CITED AND AND AND AND AND AND AND AND AND AN	14.133	211.256	539-576	910-1014	1409-1450	2463-2497	2719-2777	2762-2623
PPOLG JAEVS	GENOME POLYPROTEIN	IAPANESE ENCEPHALITIS VIAUS (STRAIN SATIS)	200	3317-3428						
		CONTRACTOR STATE AND CACO.	24.13	311.236	519.576	980-1014	1409-1450	2463-2497	2739-2777	2782-2823
PPOLO JAEVI	GENOME POLYPROTEIN	JAPANESE EMEETIVELIIS VIKUS (SINXIII SALVI)	333-3359	1387-3428						
		SACRET CONTRACTOR CONTRACTOR AND SACRES	74-128	311-256	539-576	101-016	1409-1430	2463-2497	1119-2777	2182-2823
PPOLO_IAEVN	GENOME POLYPROTEIN	A Anese encembering trace (strong property)	1322-3359	1317.3428						
		LIAPANESE ENCEPHALITIS VIRUS (STRAIN NAKAYAMA)	7	131-103	467-504	908-943	133-133			
PPOLO KUNDA	GENOME POLYPROTEIN	KINIM VIRUS (STRAIN MEMBIC)	74-108	207-351	\$21-151	2464-2498	1518-1579	1740-1778	200	38.343
POLO LANY	GENOME FOLVTRUTEIN	I ANGAT VIRUS (STRAIN TP2))	66-103	431-463	963.996	101-1472	1933-1966	1536-2591	3967-3001	200.703
POLO LAWY	GENOME FOLTPRUIEIN		3102-3145							
	NEW YORK THE PARTY OF THE PARTY	LANGAT VIRUS (STRAIN YELANTSEV)	68-103	597-10						
Polo Liv	CENONG POLYPROTEIN	Louping fll virus (LJ)	55-13	11:12	2 46					
and not	CENOME POLYPROTEDI	LOUPING ILL VIRUS (STRAIN SB 326)	21:12				100	1760		
A COLOR	CENOAG POLYPROTEIN	MOSQUITO CELL FUSING AGENT (CFA FLAVIVIRUS)	ž.	908.93	2049-2087	2630-2647	500 - 1000	1490-134		1
300	GENOVE POLYMOTER	MUNICAY VALLEY ENCEPHALITIS VIRUS	67-115	200.23	133.00	1	22.000			
1000	CENTAGE POLYPROTEIN	DRAITHOGALUM MOSAIC VIRUS	S : 32	26-92	10/2:100				1961	182.131
	CENTRALE POLYPROTEON	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	25-180	207.70	117	10.00	700-/70	0146 3046	101.101	
1000			1488-1339		2001-1005	202-202	106-120	1607.1947		
21 704 0 7044	GENOME POLYPROTEIN	POLIOVIAUS TYPE I (STRAIN MAHONEY)	3		201		971.151	1610-1631	1008-1442	1904-1949
1000	GENOME POLYPROTEIN	POLIOVIRUS TYPE I (STRAIN SABIN)	3		701.100	1412.147	12	1608.1640	106-1845	1902-1947
* 104 C	GENOME POLYPROTEIN	POLYOVIRUS TYPE 1 (STRAIN LANSING)	3	18./48	345	121				
1										

2555										
FILENAME	PROTEIN	VIRUS	4054		1000	1000				
אסגם אסרוז	GENOME POLYPROTEIN	POLIOVIRUS TYPE 2 (STRAIN W-2)	17.		1045.1100		5	077	OTHER PROPERTY.	9
וווסרס שטור	GENOME POLYPROTEIN	POLIDVIAUS TYPE 3 (STIAIN 23127)	2	96-930	1044-1091	14.2.1446	1494-1546	1607.1648	1104.1818	1901-1946
PPOLO, PPVD	GENOME POLYPROTEIN	EDN'T AND PIALEON (2A(1)B)		000-96	104-1099	1412-1446	1491-1546	1607.1648	1805.1810	1001
PPOLO PPVEA	GENOME POLYPROTEIN	M.UM POX POTYVIRUS (STRAIN D)	164-308	441-503	128-769	913-967	921.955	1741-1782		
PPOLO PPVNA	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN EL ANIAR)	116-157	784.818	1146-1197		L			
PPOLO PPVIA	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (ISOLATE NAT)	164-208	403-437	440-502	23.768	14.873	930-954	1740-1781	
PPOLG PLSVH	GENONG POLYPROTEIN	PLUM POX POTYVIKUS (STRAIN RANKOVIC)	164-201	403-437	440-502	727.768	914-866	920-954	1340-131	
ויטום וויטום	GENONG POLYPROTEIN	PAPAYA RINGSPOT VIRUS (STRAIN P/MUTANT HA)	61-102	134-461			L			
PPOLO PRSVVV	GENOME POLYPROTEIN	PAPAYA RINGSPOT VIRUS (STRAIN P / MUTANT HA 5-1)	325-359							
Proco PSBNV	GENOME POLYPROTEIN		125-359							
PPOLO_PVYC	GENOME POLYPROTEIN	PEA SEED-BORNE MOSALC, TERR (STRAIN DPD!)	23.33	355.319	28.50	935.976	944-1011	180-117	1588.1677	1808.1860
			1971-2015	2379-2413	2712-2746	2870-2907				
PPOLG PYYHU	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN C)	28.156	201-135	102-854					
PPOLO_PVYN	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN HUNGARIAN)	<u>14-18</u>	201-735	103-863	676-106	1401-1441	1492.1526	1711.1772	1777.1818
			2272-2306							
PPOLO_PVYO	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN M)	149-196	£.12	701-735	803-863	1401-1461	1492-1536	1738.1773	1332.0018
			1929-1970							
PPOLG_PWYSE	GENOMB POLYPROTEIN	POTATO VIRUS Y (STRAIN O)	140-196	\$11.26	701-735	103.856				
PPOLO PWYTB	GENOME POLYPROTEIN	PASSIONFRUIT WOODINESS VIRUS (STRAIN SEVERE)	203-237							
PIOLO PYTVI	GENOME POLYPROTEIN	PASSIONFRUIT WOODINESS VIRUS (STRAIN TIP BRIGHT)	101-131							
PPOLO STEVM	GENOME POLYPROTEIN		194-328	1111-1112	1379-1413	1858-1899	1950-1991	103.2737		
PPOLO SVDVH	GENOME POLYPROTEIN		106-143	673.707	739.773	975-1009	1404-1438			
MOLO SVOVO	GENOME POLYPROTEIN		15-49	1024-1070	1339-1613	1390-1924				
PPOLO TREVS	GENOME POLYPROTEIN	(2.2	15-49	1024-1070	1890-1924					
PPOLO TREVW	GENOME POLYPROTEIN	TICK-BORNE ENCEPHALITIS VIRUS (STRAIN SOFIN)	61-140	231-272	431-465	1158-1192	1431-1473	1929-1966	2182-2216	2535-2590
			\$	1051-3092	1100-1141					
V31, 0.1047	GENOME FOL YPROTEIN	TICK-BONNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	П	211-272	59710	1154-1192	1431-1492	1912-1966	2936-2591	2967-3001
	- 1 -		3003-3057	3053-3094	3102-3143					
POC DEVE	THEILER'S MURINE ENCEPHALOMYELTHS VIRUS	(S)TOBACCO ETCH VIRUS	2:2	166-222	540-584	720-782	121-925	1148-1192	1416-1460	1494-1535
0.00	200000000000000000000000000000000000000	_	T	1747-1761	1792-1826	2395-2434	1282-2821			
TOTO INCADO	CONCRET VOLTROLEIN	THE LEAN & MURINE ENCENACIONALELITIS VIKUS (STRAIN BEAN)	Т	40.510	1601-1635					
STATE OF THE PARTY	CONOME DOLVED TEN	7	200	1216	1599-1663					
Proto TVAV	GENOME POLYPROTEIN	TURNE MOSAIC VIRIS	7		1601-1633	960 056				
PPOLG WAY	GENOME POLYPROTEIN	NG VIBUS	Τ	Τ	146.542				╅	
			â	ŀ	2701.2740	3814.3848		10148	7/01:101	101
PPOLO WNV	GENOME POLYPROTEIN	WATERMELON MOSAIC VIRUS II	Т	203-336						
POLO_YEFVI	GENOME POLYPROTEIN	WEST NILE VIRUS	26.101	207-351	847-881	973-1007	1413-1447	2461-2495	2525.2576	222.223
			Ē					Т	Т	
POLG YEFY	GENOME POLYPROTEDY		418-452		728-768	1	1	_	2958-2996	3097-3143
PPOLO YEFVE	GENOME POLYPROTEIN	R 17D-204)	418-452	125-563	728.768	I - I	2231-2276	Г	Т	3097-3143
POLH POLIM	GENOME POLYTROTEIN		9		П	728-768		_		
PPOCH EEVYT	GENOME FOLYPROTEIN	POLIDIVIRUS TYPE I (STRAIN MAHONEY)		_	1415-1449	1501-1549	1610-1651	\$>81-\$0\$1	1904-1949	
FOUN FOVE	MONSTRUCTURAL POLYPROTEIN	US (STRAIN TRINIDAD		198-912	1945-1979					
POCH FCVF9	NON-STRUCTURAL POLYPROTEIN	/68 FIV)	544							
POLY REVBU	NON-STRUCTURAL POLYPROTEIN		Ì		986-1020	1023-1061				
PPOLY HEWAG	NON-STRUCTURAL POLYPROTEIN			1139-1177						
PPOLY HEWAY	NON-STRUCTURAL POLYPROTERN		338-379							
PPOLY HEVPA	NON-STRUCTURAL POLYPROTEIN		Г	11361114						
PPOLN MIDDV	NON-STRUCTURAL POLYPROTEIN	STRAIN PAKISTAN)	117-116	1136-1176						
PPOLN ONNVG	MONSTRUCTURAL POLYPROTEIN		116-114						T	

PROTEIN NOWSTRUCTURAL POLYROTEN NOWSTRUCTURAL POLYROTEN NOWSTRUCTURAL POLYROTEN NOWSTRUCTURAL POLYROTEN NOWSTRUCTURAL POLYROTEN NOWSTRUCTURAL POLYROTEN FOL POLYROTEN FOL POLYROT		ILAIN EDSBYN 82-1) (STRAIN VAUITEN BRA RUS (STRAIN TG-11) RUS (STRAIN STRAIN TG-11) RUS (STRAIN STRAIN THE THE THE THE THE THE THE THE THE THE		9 3 2 2 2	(444-2502 109-457 1414-2467	1637-1716				
PRINCE P		ALIN EDSBYN 83-1) 1 ALIN EDSBYN 83-1) 1 1 1 1 1 1 1 1 1 1 1 1		1111	1414-2467	1637-1716				
The contribution of the		TAIN EDSBYN 81-1) 1 1 TAIN EDSBYN 81-1) 1 2 STAANN VALIJIEN BRO THUS (STRAIN TC-1) THUS (STRAIN TC-1) THUS (STRAIN TC-1) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO) THUS (STRAIN STO)			1414-3467	1863-1896				
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		PAULE RALE		1	1001	3444.3478				L
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		IIS VIRUS TITIS VIRUS TITIS VIRUS STALIN STRAIN VAJIJIEN BRA TALITIS VIRUS (STRAIN TACAT) SEASE VIRUS (STRAIN AUTO) SEASE VIRUS (STRAIN AUTO) SEASE VIRUS (STRAIN CL-1) SEASE VIRUS (STRAIN ED-9) SEASE VIRUS (STRAIN ED-9) SEASE VIRUS (STRAIN ED-9) SEASE VIRUS (STRAIN ED-9) SEASE VIRUS (STRAIN ED-9) SEASE VIRUS (STRAIN STO) TOSIS VIRUS (STRAIN NI) TOSIS VIRUS (STRAIN NI) TOSIS VIRUS (STRAIN NI) TOSIS VIRUS (STRAIN NI)		20-100	242:2416					
INTECTIONAL OFFICIALS LATER EQUIPE DECEMBALIS WING STRANT VALIFIES 114-251		ISTRAIN VAJITEN BRO RUS (STRAIN 1279) RUS (STRAIN 1270) RUS (STRAIN 5270) RUS (STRAIN CU-1) RUS (STRAIN PBG-91) RUS (STRAIN PBG-91) RUS (STRAIN STG) RUS (STRAIN STG)	77	2						
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THUCTURAL POLYMOTER	***			20.52						
THUCTURAL POLYMOITES	124		116-1250							
THUCTULAL FOR YMOTED	***		116-1250							\downarrow
TRUCTIOLAL POLYMOTER AVIAN PRECIDOUS BUGAL DISASS VALUE (TRANS CAP) 11-141 11-151 1	774	PER (I)	Γ		470-523					
TRUCTIOLAL POLYMOTERN AVIAN PRECITIOS BUSALD DISLASS WOUL (STAND GLA) 11-144 11-134 11-144	7	VILLAN INTECTIOUS BURSAL DISEASE VRUIS (STRAIN CU.!) VILLAN INTECTIOUS BURSAL DISEASE VRUIS (STRAIN E) VALAN INTECTIOUS BURSAL DISEASE VRUIS (STRAIN PBG-99) VALAN INTECTIOUS BURSAL DISEASE VRUIS (STRAIN PBG-99) VALAN INTECTIOUS BURSAL DISEASE VRUIS (STRAIN STG) INTECTIOUS PANCHEATIC NECLOSIS VRUIS (SEXOTYPE JASPER) INTECTIOUS PANCHEATIC NECROSIS VRUIS (STRAIN NI) THORUS STRAIN STRAIN STRAIN STRAIN NI) THE STRAIN STRAIN STRAIN STRAIN NI) THE STRAIN STRAIN STRAIN STRAIN STRAIN NI) THE STRAIN STRAIN STRAIN STRAIN STRAIN NI)	Γ		470-513					
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TRACTIOLAL POLYMOTER AVAIN PRECIDED SUBSAL DESACE VING (TRACHEGON) 11:141 10:151		2		31-286	304-340					\downarrow
STRUCTURAL FOLYMOITEN			Г	12-267	451-504					
STRUCTUAL FOUR TROOTES ACCRETION FANCEL RIC REGIGISTORY (\$1500 PRE 116-15) 110-151		E		49-283	470-523					\downarrow
STRUCTIONAL POLYMOTERN PARTICULOS PARCEATIC RECOGNS YOUR (STRANK NIL) 116-1116			Γ	23-785						1
STRUCTIOLAL POLYMOTERN OFFICIAL STATES 199-71 199			16-716							1
TILUCTUALA POLYMOTER MOSS EVER VULS (STRAM RESPOS) 194-01 194-91			104-1238							1
STRUCTUAL POLYMOTER KOSS SIVER VIRUS (STRACH PSSSS) 198-913 198-913 STRUCTUAL POLYMOTER STRUCTUAL			569					1		1
STRUCTUAL POLYMOTER KOSS EVICEA VIRUS (STIACAN F44) 919-871				39.973						1
STRUCTUAL POLYMOTER NUMELLY VOUS (YACCINE STRAIN BAYN) 999-1016 999-1			19-973							1
STANCTIONAL POLYMOTERN AUDELLA VIRGI (YACCING STRAIN RAJIN) 999-1014			9601-666							1
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STRUCTURAL POLYMOTERN WESTERN EQUING ENCEPTALITIS VALUE 616-74) 794-133 1001-1041		_	4-68					+		1
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POLYMOTER CAUGITOWER MOSAUC VRUIS (STRAIN DAY) 177.311 131.347 447-99 191.106 195.900 177.311 131.347 447-99 191.106 195.900 177.311 131.347 447-99 191.106 192.10		S)	72-934			-		1		ļ
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FOL POLYMOTEIN EQUIME INVECTIOUS AND ALAY WILLS (CLONE 1189) 11-369 11-1018	VPROTED		1	137-307	467/2					L
FOL POLYTROTEIN EQUINE INFECTIOUS AND ALVING (GLONE CL11) 111-369 1011-1015 10	DIEN		8	Bro1-7701						L
FOL. POLYTROTEIN EQUINE INFECTIOUS AIRMAN VIRUS (ISOLATE WYONGRU) 313-809	DIEN	T	8	1077-1030		-	-			-
POL POLYPROTED PELNE BADGRINOUS VRUS ECE 191-713 191-645	DIEN	T	T	631.450	161.100		L			L
POL POLYMOTEN FELINE DAGINODEFICENCY VILUS (SOLATE EAT ALLIANA) 121-213 100-0442 100-0474	OTEN	T	T	404.44)		-				
POL POLYPROTEIN FELING BAACHNODEFICENCY VILLS (SOLATE SAN DIEAV) 11-17 191-402	OTED	T	T	(04.44)		-		_		L
POL POLYRATIC POLYRATICH FELDA BAACHNODEFICIENCY VIRUS (SOLATE ING.) 113-134	DIED	T	T	101			-			-
BGZNATIC POLYPROTEIN FIGWORT MOSALC VILUS (STRAIN DXS) 101-334 111-3	OTEN	DLATE TAB)	7/2	333-000		+	-	-	L	
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POL POLYTROTEIN HUMAN BAACHODEFICIENCY VIRUS TYPE I (ALVZS) Z ISOLATE SSI 237 237 237 237 237 237 237 237 237 237	OTEN	HUMAN T-CELL LEUKENDA VIRUS TYPE I (CALIBBEAN ISOLATE)	T	777		-		-		L
HUMAN BOATHOOFFICIENCY VIRUS TYPE I (BHIO ISOLATE) 1313-349	OTEN	#1	T	200			-		-	
	Name of the last o	1		979-679						
PPOL HVIBS POL POLYPROTEIN	OTEN STEP		HIDAAN SPUAADETIOYRUS (POANY YRUS) GBBON AFE LEUKEMA, YRUS HIDAAN T-CELL LEUKEMA YRUS TYPE I (STIAM ATK) HIDAAN T-CELL LEUKEMA YRUS TYPE I (ANDSEN ISOLATE HUMAN DAAINODEFICENCY YRUS TYPE I (ANZASFI ISOLATE HUMAN DAAINODEFICENCY YRUS TYPE I (BHIO ISOLATE)	HUMAN SPURALETROYRUS (FOARY YRUS) 1921	HUMAN SPUNALETROYRUS (FOARY YRUS) 1921	HUMAN SPUNALETROYRUS (FOAMY YRUS) 192174 1517.20 GEBSON ALE LEUKENGA YRUS 1517.00 15211 1517.00 15211 1517.00 15211 1517.00 15211 1517.00 15211 1517.00 15211 1517.00 15211 1517.00 15211 1521.00 15211 1521.00	HUMAN SPUNALETROYRUS (FOAMY YRUS) 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 19217	HUMAN SPUNALETROYRUS (FOAMY YRUS) 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 1921744 192174 192174 192174 192174 192174 192174 19217	HUMAN SPUMALETROYRUS (FOAKY YRUS) 192174 151274 1	HUMAN SPUMALETROYRUS (FOAKY YRUS) 11-217 1

PCGENE	ALLMOTIS	All Viruses (no bacteriophages)					_			
THE PARTY	CKODIK	YARUS	AREAI	AREA?	AREAZ	AREA	AREA S	AREAG	AREA 7	AREA
TOL HVIBIL	POL POLYPROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (BHS ISOLATE)	\$13-549	618-676						
TOL HVIEL	POC. POLYPROTEIN	INDIAN DOWNODEFICIENCY VIRUS TYPE I (BRU ISOLATE)	\$13.549	919-819			_			
POL PVIRO	POL POLYPROTEIN	HUMAN DAMUNODEFICIENCY VIRUS TYPE I (ELJ ISOLATE)	500-536	636-663						
POL HVIR	POL POLYPROTEIN	HUMAN INDMUNODEFICIENCY VIRUS TYPE I (HXB2 ISOLATE)	XI:537	20,00						
POL HVIKA	POL POLYPROTEIN	HUMAN DANUNODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	505-541	930.66			_			
TOL HVINO	POL POLYPROTEIN	HUMAN DAMUNODEFICIENCY VIRUS TYPE I (NIAL ISOLATE)	476-536	(99-109	L		L			
FOLL HVINS	POL POLYPROTEIN	HUMAN BAMUNODEFICIENCY VIRUS TYPE I (MIN ISOLATE)	504-540	199-609		L				
PIOC HVIND	POL POLYPROTEIN	HUMAN DAMUNODEFICIENCY VIRUS TYPE I (NEW YORK-S ISOL	501-537	627-664		L				
PPOL HVIOY	POL POLYPROTEIN	HUMAN BARANODEFICIENCY VIRUS TYPE I (NDK 150LATE)		626-463						
TOTAL HAIFY	FOL FOLTPROTEIN	HUMAN DIRITHODEFICIENCY VIRUS TYPE I (OYI ISOLATE)	501-517	299-909		L				
POC RVIDA	POL POLYPROTEIN	HUMAN INDIGMODEFICIENCY VIRUS TYPE I (PV22 ISOLATE)	513-549	693-676						
FIG. HVICE	FOL FOLYPROTEIN	HUMAN INDANNODEFICIENCY VIRUS TYPE I (REMAT ISOLATE)	300-536	(99-509)		L				
TOL HVIZZ	POL POLYPROTEIN	HUMAN INGRUNODEFICIENCY VIRUS TYPE I (STRAIN UGANDAN	\$00-536	699-109			L			
FOL HYZBE	POL POLYPROTEIN	OLA OLA	\$00-536	(99-929						
TOL HYZCA	FOL FOLYTROTEIN	HUMAN BOMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)	49-83	484-582	653-487	13.51				
HYZDI	POL POLYMO I EIN		156-390	464-562	632-466	L				
TOT HVZD1	FOL FOLTFROTEIN	HUMAN DAMUNODEFICIENCY VIRUS TYPE 1 (ISOLATE DI94)	203-600	671-705					-	
TOTAL MASON	TOUR TOUR THE STATE OF	HUMAN INDIUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D205,7)	376-410	414.526	\$29.577	653-687				
TOUR DAYEN	TOL TOLITHOLEIN	HUMAN INDIANOBERCIENCY VIRUS TYPE 2 (150CATE GHANA-)	164-562	(9)-((9			_			
TOUR BYAND	TOLINITE IN)	44-78	956-390	464-529	633-667				
TOTAL PASSE	TOL TOLITAGE IN	ı	157-391	195-599	634-668	L				
POC BUA	TOUR TOUR TOUR TOUR	23	46-80	413.562	633-667					
Very Por	PICTATION BOX WAS DEED	1 (ISOLATE ST)	484.516	523-577	653-687					
777 07 200	POLICY VIEW TOLITICAL		462-503							
POL MLVAV	POL POLYPROTEIN	AXB LATINGTANT ADENDAM TOSIS VIRUS	20.21							
PPOL MEVES	POL POL YPROTEIN		165-526							
POL MENTE	POL POLYPROTEIN	IN STE US	7.75							
PPOL MEVIF	POL POLYPROTEIN	100	, , , , ,							
PPOL MENMO	POL POLYPROTEIN	1	27.748							
OL MEVID	POL POLYPROTEIN		693.744							
PPOL MEVIE	POL POLYPROTEIN	Γ	677.744							
PPOL MONIV	POL POLYPROTEIN	STRAIN KAPLAM	62-129							
PPOL_COATVVS	POL POLYPROTEIN		L	578-413						
OL RSVP	POL POLYPROTEIN		470.505	155.910					T	
POL RTBV	POL POLYPROTEIN	IGUE C)								
MI SEVI	POLITICIEIN	1		29.96	101-135	176-236	125-362	03-474	1005-1039	405-1439
100	POLITICALISM	RUS (ISOLATE PHILIPPINES)		39.96	101-135	176-236	125-362	1770	Т	1405-1439
PER SIVAS	POLITICAL DE VINCENTE			427-464	494-535				1	
POL SIVAT	POL POLYPROTEIN	CIMIAN TOWN T VINUS (1TPE J/STRAIN LRJ)	T	479-467						
POC SIVAG	MA POLYBOILE		_	617.678	111-111	938-979				
POL SIVAL	POL POLYPROTEIN		T							
POL SIVAT	POL POLYPROTEIN	2000	Т	42.603	I					
POL SIVCZ	POL POLYPROTEIN		Т	676-515	£:78	83.983	1020-1054			
POL SIVGD	POL POLYPROTEIN		T	137-79						
POL SIVAI	POL POLYPROTEIN		100,77	110-070	T					
POL STANK	POL POLYPROTEIN	1			629-673	793-827	912-946			
POL SIVSA	POL POLYPROTEIN	T	Т	910-000						
POL SIVSP	POL POLYPROTEIN	É	J	634-611			•			
PPOL SOCAV	POL POLYPROTEIN		797-97	630 655						
PPOL SRVI	ENZYMATIC POLYPROTEIN	T	1	1000						
				3416						i

				9	7990	0.010			
	PROTEIN		130,504	Γ	Γ				
VIIV ION	POL POLYPROTEIN		T	174.070					
10 10	POL POLYPROTEIN				T				
3 2	POL VPROTEDN		T						
	BOY BOX VEROTEDA	-IKS2)	T	474	T				
EVEN TO SERVE	LARGE STRUCTURAL PHOSPHOPROTEIN PP 150		2 2						
PRETT MONTHS	PROTEIN PR73		37.76						
TO TOOL	PROTEIN PR73			100.00					
PPR TL NOVITVO	MOTEIN PAT		145.364	170.111					
PPRTR BOATVO	PROTEIN PATS		\$ E	366.303					
PEND COVEM	PROTEIN PA.13								
PPIND NOVAC	POLYMEDAIN PRECURSOR	_							
PYHD MPVAS	POLYAGDRIN	ALTIOGRAPHA CALIFORNICA MULLEAR POLITICEDROSIS VIRGO	1						
PEYTO NEVBK	POLYHEDRIN		2.54						
PEYND NOVES	POLYHEDRIN	ISVIRUS	97						
PEND WALD	POLYMEDIUM	V SIS	14-48						
PYYED MPVAGE	POLYNEDILIN	MANAGERA BRASSICAE NUCLEAR POLYNEDROSIS VIRUS	14.48						
PYND NEVOP	POLYMEDIUM	VIRUS	13-47						
PYO MYOS	POLYBEDIUM	DROYIA PSEUDOTSUGATA SINGLE CAPSID NUCLEAR POLYHED	7						
PYND NOVIE	POLYMEDIUM		14-48						
PYND MYSE	FOLTHERMAN	SPODOPTERA EXIGUA NUCLEAR POLYNEDROSIS VIRUS (STRAIN	171						
NO NAVE	POLTREDALIN SOUTH THE PARTY OF	SPODOPTEJA FRUGIPEADA MUCLEAR POLYHEDROSIS VIRUS	=						
PYTO NEVST	TOT THE SALE	SPODOPTERA LITTORALIS MUCLEAR POLYNEDROSIS VIRUS	5						
PIASK MOVA	TO WELL PROTEIN 21	KIRSTEN MUNDNE SARCOMA VIRUS	25						
PARY BIVE	Mation van	BOVINE INDAINODEFICIENCY VIKUS (ISOLATE 127)	2						
MEN ELAVS	NOTE NOTE NOTE NOTE NOTE NOTE NOTE NOTE	EQUINE INTECTIOUS ANEMIA VIRUS (CLONE 1369)	21-12						
PEN EINY	REV PROTEDY	EQUINE INFECTIOUS ANEAGA VIRUS (CLONE CL12)	4						
MEV HVII2	REV PROTEIN	EQUINE INFECTIOUS ANEXIS VIRUS (ISOLATE W TOPING)							
PREV HVIA3	AEV PROTEIN	HUMAN BARUMODER LIERLY VIROS 117E 1 (LEGISE 15)							
PREV HVIBI	REV PROTEIN	HUMAN INMUNOCETICENCY CHIEF TYPE I MILLI ISOLATE							
REV HVIBI	REV PROTEIN	HUMAN INDICATOR COLOR VINOS VITE (COLOR CO	2						
PREV HVIBN	REV PROTEIN	HOMAN BANDADE FILENCY VIRUS TYPE I (BILAIN ISOLATE)	22.59						
PREV HVIBR	REV PROTEIN	INDIAN INCREMENTAL PROPERTY VIRUS TYPE I (BRU ISOLATE)	13-69						
TEV HVIEL	REV PROTEIN	HAMAN DAGINODEFICIENCY VINUS TYPE I (ELI ISOLATE)	33-66						
PREV HVIRD	REV PROTEIN	HIDMAN DAMINODEFICIENCY VIAUS TYPE I (HXD) ISOLATE)	69-51						\downarrow
PREV HVID	REV PROTEIN	HUMAN IDANIMODEFICIENCY VIRUS TYPE I (IN) ISOLATE)	19-61						1
REV HVIM	ACT PROPERTY	HUMAN INDIGNOPFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	\$ 1						
שני שניים	PEV PROTEIN	HUMAN INDIUNODEFICIENCY VIRUS TYPE I (NIAL ISOLATE)	\$	1					
MEN HAIDY	REV PROTEIN	HUMAN INDRINODEFICIENCY VIRUS TYPE I AM ISOLATE)	\$			1			
MEV HVIPV	REV PROTECH	INDIAN BORNODEFICIENCY VIRUS TYPE I (UTI ISOLATE)							
PREV HVIST	NEV PROTEIN	HORAN INMONOEFICIENCY VIROS LIVE I (FVIZIBOLATE)							
PREV HVISC	AEV PROTEIN	HUMAN INDIOMODE FICIENCY VARIS 1 VE 1 (57.3) 1000 11.	592						
PREV SIVAI	REV PROTEIN	HUMAN INCOMODERIC FOLK OF THE STATE OF THE S	×6.31						
PREV SIVAD	AEV PROTEIN	SIMILAN INCOME CONTROL AND SACRED SOLATE)	16-71						
PREV_SIVAL	REV PROTED	FINAL BARMONEFICIENCY VIRUS (ISOLATE AGM / CLONE GR	29:33						
PREV SIVAT	REV PROTEIN	SIMILA DAMNODEFICIENCY VIRUS (TYO-1 ISOLATE)	18.73						
PREV SIVEZ	REV PROTEIN	CHIND ANZEE DOMINODEFICIENCY VIAUS	13-61						
MEV VILV	REV PROTEIN	VISNA LENTIVIRUS (STRAIN 1514)	11-62	П					1
MINI ASPIG	REV PROTEIN		141		65.463				1
PLRI EBV	IN THE PROPERTY OF THE PROPERT						-	-	

ana Jose	**************************************	All Virgon (so beciginals peri)								
בור בי איינים	ALLWOID PROTEIN	VIETS	AREAI	AREA?	ARFA 3	AREA	AREAS	ARFAG	ARFA 7	ARFAI
PETRI HEVER	BIRCHARIC FOSIDE DIPHOSPHATE REDUCTASE LAR	HUMAN CYTONEGAL OVIRUS (STRAIN ADIA)	6)2-668			Г	Γ	Т	Γ	
PRIRI HSVSA			96-110							
אתו אינכנ		HERPESYTRUS SAIMIN (STRAIN II)	324-365							
PRIKI VACEV	ABONUCLEOSIDE-DPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPENHAGEN)	367-402							
PRIRI VARV		VACCINIA VIRUS (STRAIN WR)	167-402							
PRIRI VZVD	RIBORUCI EOSIDE-DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	367-402							
PAIRS EBV	AIDONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VANCELLA-20STER VIRUS (STRAIN DUNIAS)	223.257							
PALDIO_HIS VIBS			19-137							
TEASH COOL	ALBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SNA	BOVINE HERPESVIAUS TYPE I (STRAIN 14)	101-135							
PRIRZ HSVSA	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMA	EQUINE HENZESVIRUS TYPE I (STRAIN ABAP)	106-140							
PRIN SFYKA	AUBONUCLE COSIDE DIPHOSPHATE REDUCTASE SMA	HERVES VIRUS SAININ (STRAIN 11)	135-159							
PULL VACCC	REDONUCLE OSIDE. DIPHOSPHATE REDUCTASE SMA	SHOPE FIBROMA VIRUS (STRAIN KASZA)	98-133							
PRINT VACCE	RUBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SAIA	VACCINIA VIRUS (STRAIN COPENHAGEN)	98-132							
PUR VACCV	REDOMICLE OSIDE-DIPHOSPHATE REDUCTASE SALA	VACCINIA VIRUS (STRAIN L-IVP)	98-132							
PUR VARV	NIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMA	VACCINIA VIRUS (STRAIN WR)	51.13							
PILL HSV3H	REGONACLE OSIDE DIPHOSPILATE REDUCTASE SALA	VARIOLA VIRUS	98-132							
PRIMA VACCV		HERPES SINDLEX VIRUS (TYPE 2 / STRAIN HGS2)	171-212							
PRPM_VARV	INA-POLYMERASE-ASSOCIATED TRANSCRIPTION S	PTION SVACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN	116-150	465.540	187.791					
DOO'N AVECE	HOLL	VARIOLA VIRUS		116-150	465-540	187.791				
ADDYA IONA	DNA-DIRECTED RNA POLYMERASE 147 KD POLYTE	VACCINIA VIRUS (STRAIN COPEMIAGEN)	243-291	622-656	754-791	934-988	1006-1057			
ANYA IONIA	DNA-DIRECTED RNA POLYAGRASE 147 KD POLYPE	VACCINIA VIRUS (STRAIN WR)		622-656			1024-1058			
PLPO1 CAPVIC	POL YPE	VARIOLA VIRUS	143-291	627-656	154-791	954-988	1006-1057			
NAMOS CONTA	DNA-DIRECTED RNA POLYNERASE 133 KD POLYPE	CAPRIPOXYIRUS (STRAIN KS-1)	09-61	114-155	589-630					
PILOZ VACCV	DNA-DRECTED INA POLYNGRASE (13 KD POLYPE	COWPOX VRUS		159-400	133-874					
PRPOJ VARV	POLYPE	VACCONIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)	П	П	133-674					
PRIMA VACCC	DNA-DDRCTED RNA POLYNERASB 132 KD POLYPE	VARIOLA VIRUS		159-400	133.674					
PRIOR VACCY	DNA-DIRECTED ANA POLYMERASE 15 KD POLYPEP	VACCINIA VIRUS (STRAIN COPENHAGEN)	62-116							
PRIPOR VARV	DNA-DIRECTED RNA POLYACEASE 15 KD POLYPEP	VACCINIA VIRUS (STRAIN WR)	911-19							
PAPOS VACCC	DNA-DIRECTED RNA POLYACRASE 35 KD POLYTEP	VAUOLA VIRUS	62-116							
MACCY	DNA-DIRECTED NA POLYMERASE 39 KD POLYFED	VACCINIA VIAUS (STRAIN COPENHAGEM)	<u>.</u>							
PLOS VARV	UNA-DUEL I ED INA POL TREACSE JU AD POL TER	VACURIA VIAUS (STRAIN WK)	1/-1							
TAYON WALLY		COTTAIN WELL AND COTTAIN COPENHAGEN	95.50						Ī	
VACCA	DNA-DIRECTED RNA POLYAGRASE 22 KD POLYPEP	Τ	25.52							
PRPO? VARV		(STRAIN WR), AND (STRAIN COPENHAGEN)	0.93							
FRION LELY	19 KD POLYPEP		(9:0)							
PRPOL EAV			1533-1567	1721-1750	1958-1992	2109-2157				
PIULPI IAANN		EQUINE ARTENTIS VIRUS	1013-1117	1477-1511	1633-1673					
PRIVITABEL	=		1	279-313						
PRUD LADUM	RNA-DIRECTED RNA POLYMERASE SUBURIT PI			29.113	36.38					
PRAPI IAGUZ	RNA-DIRECTED RNA POLYMERASE SUBUNIT FI		7	279-313						
PRINT IMEO	ANA-DIRECTED RNA POLYMERASE SUBURIT PI	T	T							
P.W.I. WHITE	RNA-DIRECTED RNA POLYMORASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN A/EQUINE/CONDON/14/B/7)	101-202	236.213						
PAUL WATE	MA-DIRECTED MA POLIMERASE SUBURIL FI	Ī								
PULL WKOR	ANA-DIRECTED ANA POLYMERASE SUBURIT PI	INFLUENCA A VIALIS (STRAIN ARREVISAR)		277.313			1			
MU INTE		406.33	T	016-475						
PIUL INE	ANA-DIRECTED INA POLYMERASE SUBURIT FI		T	27.71			1			
MU ME	RNA-DIRECTED RNA POLYNGRASSE SUBURIT PI	┰	T	279-211			†			
PIUDI WAN	RNA-DIRECTED RNA POLYMORASE SUBURIT PI	INFUENCY A VIALUE (STRAIN ALENINGIADO) (SANTOS)	T	277-313						
PRID! IAMES	ANA-DIRECTED ANA PULTMENASE SUBURILLY	_	37.37	110.000						T
PLUP! IAMI	ANA-DUCCIED MAY TOLI MEAASE SUBJECT FI		T				+	T		
MAN INVE	MA-DURELLED MA TOLIMEASE SOBORILTI		1				1	1		

	NOTIS	Aff Virgos (no batterioping to)	AREAL	AREA!	AREAL	7	ABEA S	A PARA	
PCCENT	ALLANDIN		14.25	Γ					
TLEADE	ANY PREFITED BNA POLYNGRASE SUBURIT PI	NZA A VIRUS (STRAIN APUERTO IUCOVIA)	100	111.111					
PRIVI LASIN	CAN DUE CITED BUY BOY WATERACK SUBIDATI PI	T		111.00					
IN INTEN	KAA-DIKELIED ANA COLUMNASSE CIRCLARIE	OTA133/40	707-171						
PRIDI IANI	THA-DIRECTED ANA PULTMENASE SUBSISTED	٦	171-242	7/2-7/1	1	Ī			
PRRPI IAWIL	ANA-DIRECTED ANA PULTMENASE SUBCHISTS	((()	161.242	(16.9/2					
PRIDI LAWIS	NA DIRECTED ANA POLYMENANE SUBURILLY	,	161.242	279-313					
PRINT INZHO	ANA-DESCRED ANA POLYMENASIS SUBURITY	(126/82)	13.30	278-313					
PILLE IAZON	MANDRECTED ANA POLTMERASE SUBLIMITY		13.20	279-313					
PRUPI WZTF	ANA-DERECTED RNA FOLTMENASE SUBLINII FI	ננט	171-242	179-313					
PRUPI INDAC	RNA-DIRECTED INA POLYMELASE SUBURILLY		201-249						
PILLE INSAD	RNA-DIRECTED RNA POLYMERASE SUBLIMIT PI	WILD-TYPE)	206-249						
PLUPI DABLE	RNA-DOLECTED RNA POLYMERASE SUBUNIT PI	Г	201-249						
PERT INC.	NIA-DIRECTED RNA POLYNERASE SUBURIT ?!		28.28	919-119	707.752				
PRES LANON	ANA DIRECTED RNA POLYMERASE SUBUMT PI		100	177.216					
Ţ	BHA-DIRECTED RNA POLYMERASE SUBUNIT P2	INTLUENZA A VIRUS (STRAIM MARIA ARGUMENS)	1914	177.218					
1	ALLA CASECTED BNA POLYMERASE SUBUNIT PI	_		33.31					
١	AND THE PROPERTY OF THE SUBUNIT P.	INFLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSAUS) IUCH							
١	KAN-DISCUED BAN PAN VAFRASE SUBLINIT PA	-							
	KNA-DIKE LIED NA POLYNORASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AREQUINEACONDONI (1977))							
1	MANDURE IN THE STATE OF STRIBUTE PA	INFLUENZA A VIRUS (STRAIN AEQUINE/TENNESSEE/SAG)	2						
ا۔	NA-DUECTED ANA POLITICASE SUBSECT PE	INFLUENZA A VIRUS (STRAIN A/KOREA/416/61)	10.14	12:41					
PREP INTEL	RNA-DOLECTED KNA POLITICAASE SUBSICI		¥ =	137-3118					
PRUT INTER	ANA DIRECTED ANA POLTMEAASE SUBURIT	3)	5	177-218					
PREPT TANAN	NA DECTED RAY POLYMERASE SUBURILLY	(8750718)	110-144	177-216					
ULT INTE	RMA-DIRECTED RWA POLYMERASS SUBURIL PA		110-144	177-318					
PRATE LAPID	INA-DIRECTED RNA POLYMENASE SUBURILLY	LBERTAII 1979)	110-144	177.218					
PLUT WATE	RNA-DOLECTED RNA POLYMENASE SUBURIL 72		110-144	177-218					
	RNA-DIRECTED RNA POLYMONASE SUBURILL	NET JENZA A VIRUS (STRAIN ARUDDY TURNSTONEMENS	110-144	117-218					
Н	MAN. DOLECTED RNA POLYMELASE SUBURILLY	MAT LENZA A VIRUS (STRAIN A/SINGAPORE/1/97)	10-144	=======================================					
٠l	RNA-DIRECTED KNA POL I PRESSUR SOCIETO PO	INFLUENCE A VIRUS (STRAIN ATURKEYMINNESOTAR)3/10)	3	77:718					L
-	RNA-DIRECTED RNA POL IMENASE SCIENTIFI	INTLUENZA A VIRUS (STRAIN AVICTORIANAS)	1014	117:218					
	RNA-DIRECTED INVA POLITICANSE SOCIETA	INDITIENZA A VIRUS (STRAIN AVVILSON-SAUTHO))	200	177-216					
	RNA-DIRECTED MAY FOLT MENASE SUBJECT PS	DIFTURNZA A VIRUS (STRAIN A/SWINE/HONG KONG/BI/MB	10-14	177-2118					
	RNA-DOLECTED RNA POLTMENASE SUBSINITION	THE LENZA A VIRUS (STRAIN A/SWINE/HONG KONCHISMIS)	10.14	177.218					
1	NA-DOLECTED RNA POLYMENASIE SUBGRAFE	MET LENZA A VIRUS (STRAIN A/SWINE/10WA/15/30	₹ -	177-218					
PRUTA LAZTE	RNA-DIRECTED RNA POLTMENASE SUBURITION	INTELLIENZA A VIRUS (STRAIN ASWINE/TENNESSEE/16/77)	10-14	177.218					
PRUPT DABAC	MAN DOLECTED ANA POLTMENASA SUBDIVITY	ш	<u>*</u>	349.390					
PRUT DIRAD	MAN DIRECTED RAY POLYMERANG SUBJECT BY	MET LIFNZA B VIXIUS (STIALIN BAANN ARBONING (WILD-TIPE!)		249.380					
PRUPT DYBSI	NAN-DOLECTED RIVA POLYMENASE SUBORTES	_	<u>×</u>	345.313					
PRUPY IAANON	TUA DOLECTED THA POLYMENANE SUBJECT BY	MET HENZA A VIRUS (STRAIN WANN AUBORIGES)	3	363-402	43:314	201-101	100		
PRREJ LABORD	NA DOLECTED RNA POLTMENASE SUBORDE PO	THE ITENZA A VIRUS (STRAIN ABUDGERIGAR/10KK AIDOVINT)	?	363-402	473-514	216-30			L
PRAPI LACHI	ANA-DIRECTED MA FOLTMEMASE SUBURITY	NATIONAL A VIRUS (STRAIN ACHOLE/M)	7	163-402	473-514	787-733			ļ
PRUP INFR		THE LIESTA A VIRUS (STRAIN AFOWL PLAGUE VIRUSAOSTOCK		363-403	473-514	20.13			
PRILET LASTW	ANA-DIRECTED ANA POLYMERASE SUBURILLY	DET TENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSAWEYBRID		263-402	473-514				\downarrow
PIUP) IAGUZ		DATE TENZA A VIELIS (STEATH AGULLAMANLAND/104/17	141	363-402	473-514	107-135			
LUD INCUM		PACE (TENZY A VIRILS (STRAIN AGUL LASTRAKHAND2)//4)	7	363-403	53.51	207-735			
PLLED IAITE		COUNTY A VIETE (CTEATH ANIOUNITA ENTUCKY (2009)	1	363-403	473-514	ğ. 5			1
PERFI IAIGO		THE COUNTY OF THE CET AIM AFOR INFA ONDON (41673)	7	363-402	473-514	707-755			1
14 TO TO THE BEAT		٦	3	363-402	413-514	721-755			\downarrow
14.00		٦	3	363-402	473-514	101-155			
TAKE TAKE		٦	7	363-403	473-514	707-755			
SOUD INTE	INA-DOLECTED INA POLYMODASA SUBUNTI PI	INTLUENZA A VIKUS (3 IKAIN AKUMZANIEW)	7	363-402	413-514	227-101			
2010	RNA DRECTED RNA POLYMERASE SUBUNIT PJ		1	161-402	43-514	207-155	L		
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PCGENE	АЦМОПЗ	All Virses (no bacterisphages)								
THEMANE	PROTEIN	YIRUS	AREA I	77387	VELA 3	AREA	AREA S	AREAS	AREA?	AREA
אאינאן נאוא	ANA-DIRECTED RNA POLYMERASE SUBUMIT P)	INTLUENZA A VIRUS (STRAIN ALENINGRADVI)441/57)	7	363-402	473-514	707-755				
PRUD LANES	ANA-DIRECTED INA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AMIALLANDMEW YORK675071)	363-402	433-514	701-755					
PRUP LANTS	INVA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AMERIPHISANS)	1-1	363-402	113-514	707.755				
PILLY INFUE	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI	INTLUENZA A VIRUS (STRAIN ANTHONES)	27-1	201-191	115-661	207.755				
מואאו נישמי	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	DIFLUENZA A VIRUS (STRAIN APUERTO RICORDA)	1-13	107-(9(115-663	\$51-100				
PAUT INSEZ	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A YIRUS (STRAIN ARUDDY TURNSTONENEW IERSE I 42	~~I	361-402	113.67)	201-155				
PROD IASIN	NNA-ODRECTED RNA POLYMERASE SUBUNIT PJ	MFLUENZA A VIRUS (STRAIN ASEALMASSACHUSETTS/133/23)	77	363-402	473-514	707.755				
PULD LATKA	RNA-DIRECTED RNA POLYMERASE SUBUMIT PI	INTLUENZA A VIRUS (STRAIN ASINGAPORE/1/57)	1-42	363-402	473-514	707.755				
PRES IAVE		INFLUENZA A VIRUS (STRAIN A/TURKEYAIINNESOTA/133/110)	27-1	363-402	118-641	225-707				
PULL IAWA.	ANA-DIRECTED INVA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AVICTORIANA)	~	363-402	473-514	207.755				
PRUP [AZII	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	INTLUENZA A VIRUS (STRAIN ANYLLSON-SMITHU)	173	363-402	473-514	707-755				
PRUP)_LAZTE	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	INTLUENZA A VIRUS (STRAIN ASWINEAOWA/1500)	7	363-402	413-514	707.755				
PIND, DYBAC	RNA-DOLECTED RNA POLYMERASE SUBUNIT PJ	INFLUENZA A VIXUS (STRAIN A/SWINE/TENNESSEE/74/7)	17.	363-402	473-514	707-755				
PULL DIRAD	RNA-DOLECTED RNA POLYMERASE SUBUNIT P3	DIFLUENZA B VIAUS (STRAIN BVANN ARBONING (COLD-ADAPTE	458-533							T
PAUL DACEE	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA B VIRUS (STRAIN B/ANN ARBONI/66 [WILD-TYPE])	450-533							
PAUP INCI	NNA-DOLECTED NNA POLYMEMASE SUBUNIT PI	INTLUENZA C VIRUS (STRAIN CREALINUMS)	135-269	275-309						
PRUP THOCK	RNA-DIRECTED RNA POLYMERASE SUBLINIT PJ	MFLUENZA C VIRUS (STRAIN C/11/30)	235.269	175.316						
PRUPA CYRIZZ	M565	THOCOTO VIRUS	143-401							
PRIEZ CYMUH	RNA-DIRECTED RNA POLYNGAASE		354-392	495-571	1742-1776	1971-2008	3664-3724	3912.3946		
PRATE BEV	KNA-DIRECTED KNA POCYNGRASE	NAVOUS MAY (STRAIN NOA)	617-651	13641398	2769-2803	3566-3620	Т	Т	4319-4353	
PRIVE CYMAS	RNA-DDIECTED RNA POLYMERASB		20-65	617-651	943-1009		Τ	Т		
PRUP CYMON	INVA-DIRECTED RNA POLYNGRASE	MURINE CORONAVIRUS AGIY (STRAIN AS9)	1129-1170	1303-1337	1453-1494	1692-1726	2629-2670			
PRUTB_BATB	ANA-DIRECTED RNA POLYMERASE	MURINE CORONAVIRUS MAY (STRAIN JIDA)	1129-1170	1101-1317	1433-1494	1690-1724	2627-2668			
PARPE BYX	RNA-DIRECTED RNA POLYMERASE	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	Г	650-693	1466-1494	1509-1548	2346-2287			
PUUL BIVID	ANA-DIRECTED RNA POLYNGRASE	\$523)	115-156							
PRUT, BUNYW	RNA-DDLECTED RNA POLYMERASE	SEROTYPE 10 / ISOLATE USA)	308-342	703-748	125.903	1021-1076	1114-1201			
אמו שאי	RNA POLYMERASE	BUNYAMWERA VIRUS		10-114	308-363	371-412	1704-1741	1802-1861	1889-1935	
PRUT, HANT	RNA POLYMERASE BETA SUBUNIT	CANINE DISTEMPER VIRUS (STRAIN ONDERSTEPOORT)	10-54							
PREPL_HUSVA	RNA POLYMERASE	HANTAAN VIRUS (STRAIN 76-119)	98-139	134-208	172-431	162-258	969-559	731-783	905.949	1276-1310
			1419-1453	1742-1776	1993-2027					
PAUL MABYA	RNA POLYMERASE BETA SUBUMIT	VIRUS (STRAIN A3	П	127-161	1131-1179	1185-1220	1465-1517			
PREPL MABVE	RNA-DIRECTED RNA POLYNERASE	KE)	169-631	1046-1092	1490-1552	1804-1838	2029-2063	3194-3266		
PRUT, MEASE	MA-DIRECTED MA POLYMENASE		٦	_	1490-1553					
PIUL MUMOM	MAN FOLYMERASE BETA SUBURIT		197-231	790-824	869-903		_	2121-2155		
PRUM, NOVE	RNA POLYMERASE DETA SUDUNIT	MUNIPS VIRUS (STRAIN MIYAHARA VACCINE)	7	T	167-304	376-627	152.807	1331-1286	1447-1481	1417-1531
PRIN PINET	BNA BO! VARBACE BETA CIRCINGT	NEWCASTI P. DISEASE VIRIS (STRAIN BEALDETTE CAS)	2	222.1011		Т				
77.14	SALA BOLLONDE OF A CHILDITA	Ī	Τ	T	(107-404)	Т	7	7		
TOTAL STREET	NOW TO LIMENSE DELY SOROWI	TOWART CHANGE LOCKER & VINOS (STRAIN TOSTIBLE)	200	273-628	730-765	1226-1214	26.13	117.143	1564.1630	1617-1221
PRUT. PUCAGE	RNA POLYMERASE BETA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47885)	1	107.161	140.074	347.781	9617.99	7761 1061	,,,,	
PRIPE RABVE	RNA-DIRECTED RNA POLYNGRASE			Τ	Τ	Τ	+	Т	200 000	0007-24
			200	Ţ	Ę	Τ	Т	Τ	976-77	
PRUL RABVS	RNA POLYNERASE BETA SUBUNIT	RABIES VIRUS (STRAIN PV)	Т	Ť	T	1134-1222	1522.1580	1884.1610	2068.3131	
PRUL RDV	ANA POLYMERASE BETA SUBUNIT	AIN SAD B19)	Γ	Τ	1	7	Т	Т	186.313	Ī
PRUM, RVFVZ	ANA-DIRECTED INA POLYMERASE		Γ	Γ		T	1-	Т		T
PLUT, SENDS	ANA-DIRECTED RNA POLYMERASE	RET VALLEY FEVER VIRUS (STRAIN 2H-548 H12)	٠	Γ	Ī	=	L	1819-1870		
MUL SENDE	RNA POLYMERASE BETA SUBUNIT	SENDAJ VIRUS (STRAIN Z / HOST MUTANTS)	309-343	340-600		1	1	T	1499-1536	2000-2014
			2146-2216	Г	Γ		1	1	1-	
MUL SENDS	RNA POLYMERASE BETA SUBUNIT	SENDAJ VIRUS (STRAIN ENDERS)	129-163	360-420	4)1-476	109-195	114-939	1039-1100	1319-1356	1820-1854
			1966-2036		Г		Γ	П	7	
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TADTELIN THA POLYMEDASE BETA SUBUNIT THAN DOLYMEDASE BETA SUBUNIT THAN DRECTED NAN POLYMEDASE	SENDAI VIRUS (STRAIN Z)	П	340-600	613-656	147-711	1064-1119	1239-1280	1499-1536	2000-2034
AA POLYAGRASE BETA SUBUNIT AA DRECTED NA POLYAGRASE		7		2			1	Т	
NA-DOZECTED BUA POLYNŒPASE			Ī					•	
NA-DORECTED BNA POLYNGRASE		2146-2216	1				+		1001
HA-DOLECTED THA POLYNERASE	2 CO 10 CO 1	98-139	174-208	187-591	┑	╗	Т	100	707-661
		347-627	147-781	1225-1280	1319-1353	1592-1626	╗	1024-3058	
RNA POCYMETASE BETA SUBUNIT	WE	Γ	224.050	977-1014	1019-1137	1978-2032	1059-2107		
BNA PCK YNGTLASE BETA SUBUNIT					Т	1110-1153	Г	1321-1379	1531-1572
THE COLUMN BUT WASHASE	(BRAZILIAN ISOLATE CPNHIBIR	101	399-433	278-373			Т	Т	7809-2843
MA-DUCELIED MAY FOR IMPOSE		1684-1723	1837-1198	2017-7121	2136-7200	177-9077	8067-6167		
		127-183	112-111	196134	1030-1071	2	407-6107	1007-1007	
HA POLYMERASE	ANTICAL SECTION OF THE ASSECTION OF THE STRA		674-715	120-763	1522-1567	1002-1836			
KA POLYNŒRASE BETA SUBUNIT	VESICULAR STUMPTING VICES (STRONGE VICES V	Γ	674.715	720-763	1602-1836				
NA POLYNŒJASE BETA SUBUNIT	VESICULAR STOMATITIS VIRUS (SENOTITE NEW JEAST	Γ	136.761	1019-1074	1742-1799	2066-2107			
MA BOX YAFBASE BETA SUBURIT		Ţ			3				
		116-262	357-596	916-930	1733-1784				
AA-DOZCIED MAY IOCI MASON DATE OF	BEET WESTERN YELLOWS VIRUS (ISOLATE FL-1)	304-341							
UTATIVE MAN-DIRECTED MAN FOR IMERAND		234-215							
UTATIVE RNA-DIRECTED KNA POL I MENASE	A SECTION OWARE WRITE (SOLATE PAY)	234-265							
UTATIVE RNA-DIRECTED RNA POLITMENASE		236.365							
UTATIVE RNA-DIRECTED RNA FOLTMENASE		111.16							
ROBABLE RNA-DIRECTED RNA POLYNERASE	CAUNATION PIOTICE VINOS	7.41	327-28	446-480	726-767	1445-1479			
UTATIVE RNA-DIRECTED RNA POLYNŒILASE	CUCUMBER GREEN MOTILE MUSAIL VIAUS ("ALEXALESTICAL		166.634		-				
UTATIVE RNA-DIRECTED RNA POLYMERASE	AVIAN INTECTIOUS BURSAL DISEASE VIRUS (SI RAIR 32/10)		141.391	100.313	771-809				
HE ATTYPE RIAL DIRECTED RIVA POL YMERASE	AVIAN INTECTIOUS BUTSAL DISEASE VIRUS (STRAIN AUSTRALI		2007		100				L
ATTACHMENT OF THE BINA POLYMERASE	INTECTIOUS PANCAEATIC NECROSIS VIRUS (SEROTYPE JASPER)	167:181	707-807	301-322	2				
UIALIVE MANDIMENTED BAN BOT YAFRASE	INTECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE SP)	107-101	166-407	3	753-802				
UIAIIVE MANDIMENTED MINISTER	LYMPHOCYTIC CHONOMENTNGITIS VIRUS (STRAIN ARMISTRON	301-346	105-216	936-960	1309-1343	20502			
UNA POLTMERASSE	I YARPHOCYTIC CHONONENTINGITIS YIRUS (STRAIN WE)	301.345							
INA POLTMELASSE	MAIZE CHLOROTIC MOTTLE VIRUS	181-215	111.11						
ROBABLE RNA-DIRECTED RNA FOLT MENASE	SEA ENATION MOCALS	121-358							
WA-DOECTED RWA POLYMERASE	SOCIAL SALES OF CORES (CTRAIN)	136.373	13712						
UTATIVE RHA-DIRECTED RNA POLYMERASE	POINT LEARNING TO SERVINGEN	36.3	43.457						
MITATIVE RNA-DOLECTED RNA POLYMERASE	POLATO LEAR FOLL VIANO (31 PM) COLOR	131.163	402-454	627-661	162-196				
MITATIVE RNA-DIRECTED RNA POLYMERASE	PEPPER MILD MOTTLE VIRUS (3) MAIN STAIN	444.700							
NUTATIVE RNA-DIRECTED RNA POLYMERASE	RED CLOVER NECROTIC MOSAIC VIKUS								
NA-DIRECTED RNA POLYMERASE	REOVENUS (TYPE 3 / STRAIN DEALING)	107-015							
ANA DORECTED RNA POLYMERASE	REDYBUS (TYPE 2 / STRAIN DY/ONES)					L			
	П	200	59. 66	304.346	115.569	579-631	639-616	690-724	771-405
THE COLOR		8		2	415.560	1985	539-616	690-724	771-405
RNA-DIRECTED RNA POLYMERASE SUBURIT VPI		8 :			476.910	218-620	7001-996		
HAA-DOLECTED RWA POLYMERASE SUBUNIT VP!			27.72	1	1918	919-919	690-724	771-842	L
NA THE FITTE BYA POLYMERASE SUBUNIT VP1		87:20				40.60	690.724	771.605	_
ANA DIRECTED BNA POLYMERASE SUBUNIT VPI	Г	8	19:10	200	1000				
AND THE BUY DIRECTED BNA POLYMERASE	SOUTHERN BEAN MOSAIC VIRUS	628-663			-	\downarrow			
TROUNDER MAN DIMENSI OF A COMPACT	SACCHAROMYCES CEREVISIAE VIRUS L-A	- 18 - 13 - 13	<u>2</u>						100.
WA-DIRECTED WAS TOLD THE	TACARTE VILIS	155-204	120-178	375-416	416-518	191-929	1000		
ANA POLYMENASE	TOBACCO MED GREEN MOSAIC VIRUS (TAV STRAIN UZ)	401-449	682-720	765-818					
PUTATIVE RNA-DIRECTED RNA POLTMERASE	TOBACCO MINE OF WATER OF CARE	5	401-453	669-599					
PUTATIVE RNA-DIRECTED RNA POLYMERASE	TOBACCO MUSAIC VINOS (VINOS AND MOREAN)	2	401-453	649-599					_
MUTATIVE RUA-DIRECTED RUA POLYMENASE	TOBACCO MOSAIC VINOS (SIRXIN NOVEM)	=	157-109	166.53	-	L			
PUTATIVE RNA-DIRECTED RNA POLYMERASE	TOBACCO MOSAIC VIRUS (STRAIN TOWATOTE)								
	NAM POLYMERASIS NAM POLYMERASIS BETA SUBUNIT NAM POLYMERASIS BETA SUBUNIT NAM POLYMERASIS BETA SUBUNIT NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS FUTATIVE NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS SUBUNIT VYI NAM-DUBECTED NAM POLYMERASIS PUTATIVE NAM-DUBECTED NAM POLYMERASIS PUTATIVE NAM-DUBECTED NAM POLYMERASIS PUTATIVE NAM-DUBECTED NAM POLYMERASIS PUTATIVE NAM-DUBECTED NAM-DUBECTED NAM POLYMERASIS PUTATIVE NAM-DUBECTED NAM-DUBECTED NAM POLYMERASIS PUTATIVE NAM-DUBECTED	L'INERASE L'INER	UNKUNIEM! VINUS	UNKUMERALYMUS VASICULAS STORATITIS VARUS (SEROTYPE NEW FEREY / STRA 11-319 10	UNKURIEMI VINUS	VERTICAL AS TOWATHEN WINDS VERTICAL AS TOWATHEN WINDS (SEROTTRE NEW FEAREY 15TA, 118-319 101-107-107-107-107-107-107-107-107-107-	VESTICALAR STORANTIST VILLO GENOTYE NEW ERREY (STAA 116-13) 116-131 11	VERUMENI YRUS VERUMENI YRUS VERUCLAA STOCKTITIS YRUS SELDOTTE RWE RESEY STR. 18138 181318	VIGICIAL STOCKMEN VIRIGE VIGICIAL STOCKMENT VIRID VIGICIAL PAYON VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL STOCKMENT VIRION VIGICIAL VIRION VIRION

FILENAME	PROTEIN	VIRUS	AREAI	AREA J AREA 2	AREA	AREAS	AREA	AREA 7	AREA 8
PRATP BRSVA	ANA-DIRECTED RNA POLYMERASE	TOBACCO NECROSIS VIRUS (STRAIN D)	Г	Г				Γ	
PRATP COVO	ANA POLYMERASE ALPHA SUBUNIT	US (STRAIN AS 1901)	99-158	160-216					
PREST HOLSV	RNA POLYMERASE ALPHA SUBUNIT	CANTAE DISTEMPER VIRUS (STRAIN ONDERSTEPOORT)	112-373						
PROPE HOSVI	INA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL YIRUS	95-158	160-216					
PRUP HISYA	RMA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAI) 99-158	99-158	160-216					
PRATP HASVL	ANA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	99-158	160-216					
PRUPP_MEASE	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAI 99-158	99-158	160-216					
PREP MEASI	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN EDMONSTON)	115-374	460-495					
PRUP MEASY	RNA POLYMERASE ALPHA SUBURIT	MEASLES VIRUS (STRAIN IP-3-CA)	115-374	460-495					
PREPERTURE	ANA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN YAMAGATA-I)	115-374	460-495					
PRUP, MUNGE	RNA POLYMERASE ALPHA SUBUNIT	MUNGS VIRUS (STRAIN SBL-1)	149.183	213-275					
PRINT MUMPH	ANA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDERS)	314-276						
PRRP_NDVA	ANA POLYMERASE ALPHA SUBUNIT	MUNGS VIRUS (STRAIN MIYAHARA VACCINE)	214-276						
PULL NOVE	INNA POLYMERASE ALPHA SUBUNIT	KEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA71) 100-134	100-134						
PREST PLING	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)	100-138						
PRUP, PHINC	RNA POLYMEKASE ALPHA SUBUNIT	HUMAN PANAINFLUENZA I VIRUS (STRAIN C15)	10-114	113-364 175-437					
PROPP PIERO	RNA POLYNGRASE ALPHA SUBURIT	HUMAN PARADITLUENZA I VIRUS (STRAIN C19)	10-114	313-366 375-437					
PRULP THE	RNA POLYMERASE ALPHA SUBUNT	HUMAN PANANFLUENZA I VIRUS (STRAIN CI-5/7)	10-114	113-364 375-437					
PRAPP POH	RNA POLYNŒRASE ALPHA SUBUNT	HUMAN PARAINTLUENZA I VIRUS (STRAIN CT.14/830)	66-114	117-271 113-364	175-437				
PRRPP_PIZHT	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	218-281						
PROUP PDB	INA POLYMERASB ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	218-281						
PRRP PINH	INIA POLYMERASE ALPHA SUBUNIT	BOVING PARAINFLUENZA 1 VIRUS	31-130	414-470					
MULT THEM	RNA POLYMERASE ALPHA SUBUNT		410-499						
PRINT PIGE	INVA POLYMERASE ALPHA SUBURIT	(V		222-215					
PRRIPE PIRTY	INNA POLYMERASE ALPHA SUBUNIT	LAINFLUENZA 4B VIRUS (STILAIN 61-133)	211-215						
PRRPP_RABVA	RNA POLYMERASE ALPHA SUBINIT		177-174						
PLUT ILABVC	INVA POLYMERASB ALPHA SUBUNIT		93-127						
PRUP BABVE	RNA POLYNŒRASE ALPHA SUBUNIT		23-127						
PREP PABY	RNA POLYNGRASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN EIA), AND (STRAIN PM)	93-127		\downarrow				
PKUP KABVS	NAVA POC TRICKASE ALL'HA SUBURILI	910	01.137						
PRINT KENDS	RNA POLYMERASE ALPHA SUBUNIT	MUTANTS)	L	375-447	-				
PRATP SENDS	NA POLYNGRASE ALPHA SUBUNT		Γ	175-447					
PRUVP_SENDH	RNA POLYMERASE ALPHA SUBUNIT		П	175-447					
PARTY SENDZ	KWA POLYMERASE ALPHA SUBURIT	(RRUS)		375-447					
PRUPESVS	RNA POLYMERASE ALPHA SUBUNT		П	375-447					
PREP SYNV	INA POLYMERASE ALPHA SUBUMIT	SINGAN VIKUS 3 (STRAIN W.)	T						
PROP VSMO	KNA POLTMEKANE ALPRA SUBURILI	SCENOTYPE DUDIANA (STRAIN C		102-663					
PRICE VSVDA	ANA POLYMERASE ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYFII INDIANA / STRAIN M	7 7		-				
OLVOV GERRA	BNA POLYMURASH ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA)	=		_				
PREP VSVSJ	INA POLYMERASE ALPHA SUBUMT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JEISEY / STRA)	133						
PSPHIR AMERY	RNA POLYMENASE ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS (STRAIN SAN IUAN)	?						
PSPIL VACCY	SPIERODDA	XVIRUS	223-264	\$61-191					
PSP12_VARV	SEATHE PROTEINASE INHIBITOR	(STRAIN WR)	21-04						
rsmi vaccc	SCAING PROTEINASE IMINDITOR 2								
PSPI) VACCV	SERDIE PROTECNASE DIFFIBITION 3	ENHAGEN)		225-266					
ISPU VARV	SEAING PROTEDNASE INTEBITOR 3	VACCINIA VIXUS (STRAIN WR)	19-167	225-266	-				

90000	I MOTIS	All Virance (no bacteriophages)	T	Т		7 7 1 8 1	ABFA 5	AREA	AREA?	AREA
A LUEVE			J	3	I	Т	Γ		Γ	
1000 TO	REPORTEDIASE INCIBITOR 3			200						
ואע אערר	HOMOLOG FIRST		29-1							
117CL CHILL		RUSI	41.15				1			
MAAL VACEV	TYPE II RESING INCOMENT INCOME	AND VALUOLA VI	95-133	13.20					1	Ī
PTAGE FOWEY		-	1.51							T
PTAGI VACCV		(STRAIN W.R.), (STRAIN COPENHAGEN)	151						T	
PTAGE VARV			٦							
MALA BIOV		EDGLING DISEASE VIRUS	٦	164.498			-		T	
TALA POVED			101-101	495-537						
PTALA POVIA	LAKE I ANTOEN	S	464-501	587-621						
PTALA POVE	LAKE I ANIMEN	POR YOMAVIRUS JC	153-187	\$19-623					1	
TALA PONLY	LAIGE T ANTICEN	YAMPHOTROPIC POLYGAIAVIRUS	141	206-258	437478					
PTALA POWE	LAKGE T ANTIGEN	MOLISE POLYOMAVIRUS (STRAIN 3)	\$09-544							
PTALA POWA	LARGE T ANTIGEN	NOISE BOLYDMAVIBLIS (STRAIN A2)	507-542							
PTALA POVAC	LANGE T ANTIGEN	WFORD SHALL-PLAQUE)	504-539							
PTAME POWIA	LAIGE T ANTIOEN	MANCETER POLYOMAVIRUS	139-378							
PTAME POWA	MEDICE T ANTIGEN	CONTRACTOR OF COMMENT OF THE PARTY	211-245	311-433						
PTAME POVICE	MEDICLE T ANTIGEN	NICOSE TOLI CONTAINED (STRAIN A)	192-226	169-403		-				
PTAME POVMC	MIDDLE T ANTIGEN	WEGGE CHAIL PLAGIE	192.226	369-403						
PTASM POVBO	MIDDLE T ANTIGEN	7	41-85							
PTASM POVLY	SHALL T ANTIGEN	BOVINE POLYUMANUS	17.							
PTATE NPVAC	SWALL T ANTIGEN	LYAPHOTROPIC POLITOMANIAS	408.443	46.480	419-523					
PTATE NPVBM	IN TRANSCRIPTIONAL RI	AUTOGRAPHA CALIFORNICA NUCLEAR POLTMEDROSIS VIRUS		17.5	404-528					
STATE MOVOP	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	BONGLYX MONI NUCLEAR POLITHEDRUSIS VIANS								
PTAT CIVAL	TRANS.ACTIVATING TRANSCRIPTIONAL REGULAT	S VINO	391-433							
STATE STATE	TAT PROTEIN	SPACAN BOADNODEFICIENCY VIRUS (AGMISS ISOLATE)	/3-100							
V 10.	TAT PROTEIN	SDAAN DOWNNODEFICIENCY VIRUS (ISOLATE AGM / CLONB UN								
FIAL VILV	THANK ACTIVATING TRANSCRIPTIONAL REGULAT	VISNA LEYTIVIRUS (STRAIN 1814)	28.74							
NIA VIEW	TRANSACTIVATING TRANSCUPTIONAL REGULAT	VISNA LEMTIVIRUS (STRAIN 1914/CLONE LVI-1KSI)	2.4							
24 57	TRANS-ACTIVATING THANSCHIPTIONAL REGULAT		7.4							
	TOTAL BECTFTOR BETA CHAIN PRECURSOR		178-321							
TEC TOTAL	SEC. PARTY PROCESSED TED US9	HERPES SIMPLEX VIRUS (TYPE I / STRAIN 17)	27-61							
TECH HISPEA	I ECONEMI TROST TO THE TOTAL T									
PTEC HISVE	MUNICIPAGE									
PTEG HSVEX	MUNDENSE									
מונים שלים	MONGENCE						200	2101.0071	1700-1753	1809-1867
300	1 APOS TECHNOMY PROTEIN	EPSTEIN-BAAR VIRUS (STRAIN 895-8)	768-802	2	27.11		7071-8071			
Valle Ball			870-1910	661			3	916.031	Itor-John	1161-1200
10000	PROPARI E LARGE TEGINOMY PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	14:31				2			
			842 -/ 62	1			961361	2117111	1530,1511	1609.1669
Cavata transfer	LARGE TEGUMENT PROTEIN	HENDES SINDLEX VIRUS (TYPE I / STRAIN I7)	731-765	101-101	1022-1029	3470-1704				
200					201-001		081.1000	1001-1101	1192-1233	133.1400
BEACH DONE	I ARGE TEGUMENT PROTEIN	HEAVES SINOLEX VIRUS (TYPE 6 / STRAIN GS)	70.7	707-177	30,00		110011	77.1	1309.1451	1607.1540
ALEGO NO.	A SOCIETY PROTEIN	EQUINE HERPESVIRUS TYPE I (STILAIN ABAP)	260-397	63,663	74-148	200		271.6		
PTEGU HSVSA	LANGE LEGOMENT PROTEST		1616.1637	18 18 18 18	1703-1736					
	Charles and a second	HERPESVIRUS SADMIN (STRAIN II)	520-558	360-391	615-633	37.50	17.0	26-178	848-916	761-137
PTECU, VZVD	MOBABLE LANGE TENDARMI PROTEIN		1434-1503							
		VARICELLA. FOSTER VIRUS (STRAIN DUNAS)	969-659	713.747	104-841	113.673	13.13	202	1528-1562	272-1620
PTENN ADEM	LANGE TECUMENT PROTECT		1633-1705	1719-1756	1945-1986	137.761	·			
	202000	HUMAN ADENOVIRUS TYPE 2	490-572							
PTERM ADEOS	DNA TEMANAL PROTEIN	KINGAN ADDROVIBUS TYPE S	490-592							
PTERM ADEO?	DNA TEMONAL PROTEIN	MANAN ADEMOVINIS TYPE 3	491-559							1
PTERM ADEIZ	DNA TEMMAL PROTEIN									

PCGENE	ALLMOTIS	All Viruses (na bacteriophages)				I	٦			
THE RAPIL	PAULTIN DECTED	MANA	A SECTION	ARTA	ABEA	4854	ABEAS	AREAS	AREA?	ABEA !
PTMAF AVIS	TRANSCORMING PROTEIN BIN	AVAN SARCOMA VIBIR (STRAIN 13)	210,284	115.74						
PTOPI SFVICA	TRANSFORMING PROTEIN MAF	AVIAN NEUSCULOAPONEUROTIC FIBROSARCOMA VIRUS AS41	147.200	195-340					Ī	
PTOP2_ASFB?	DNA TOPOISOMERASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	127-163	269.310						
PTOP2 ASPACE	DNA TOPOISONERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	144-180	481-515	501-643	945-979	_	1133-1162		
PTSIS SMSAV	DNA TOPOISONERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 2011)	146-180	410-514	179-009	903-936	944.978	1038-1091	1122-1169	
CATA HELL		SIMILAN SAKLUMA VIKUS	2							
PULDI HOYVA	INTRIDITATE STRIPTS	ORGYIA PSEIDOTSIKATA AGI TICAPSID POR VJEDIOSIS VIRIGATAD	215-260							
MADS HSVII	KYPOTHETICAL PROTEIN (A.)	HIMAN CYTOMECAI OWNERS (TEAM ADIAS)	100 301							
PULOS HSV2H	MOTERAL	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128							
PULO HSVED	PROTEIN UL)	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HOSS)	92:126							
PULON HSVII	GENE 60 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	20.02						Ī	
PULOS EBV	PROTEIN ULA	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	102-136							
PULOS HCHYA	VILLON PROTEIN BBAFI	EPSTEIN-BAUR VIRUS (STRAIN B95-1)	104-145	113.347	376-410					
PULOS HSVII	HYPOTHETICAL PROTEIN UL6	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	216-250							
PULOS HSVED	VINON PROTEIN ULA	HERPES SINDLEX VIRUS (TYPE I / STRAIN 17)	16.94	103-141	294-329	111.111	416-479			
PLE OF HSVSA	VICON CENE 36 PROTEIN	EQUINE HEINESVIRUS TYPE I (STRAIN AB4P)	62.170	157-413	449.503					
CAZA SON	VILLON CENE 4) FROIEST	HEAVES VINUS SAINIIRI (STRAIN 11)	90	-5	302-336	18.40°				
PULON MCMVA	VIZUON GEME SA PROTEIN	VANCELLA.ZOSTER VIRUS (STRAIN DUNIAS)	13.13	250.409	704.738					
JOLOP HSVEB	HYPOTHETICAL PROTEIN ULS	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-50			-				
CAZA GOTA	ONIGIN OF MEN. ICATION BINDING PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	174.208							
יייייייייייייייייייייייייייייייייייייי	ONGON OF REPORTED BINDING PROTEIN	ANGELLA-COSTER VIRUS (STRAIN DUNGS)	127-163							
FULLY HOMAN	WOOTHETICAL PROTECULAL	SALAN CATANATA STREET								
PIR IA HOVER	HYPOTHETICAL PROTEIN (B.14	MAKAN CYTOMEGALOVIETS (STRAIN AD189)	100	77.61			1			
PULLE PRIVID	HYPOTHETICAL GENE 48 PROTEIN	EOUNE MERPESVIRUS TYPE I (STRAIN ABAP)	12.06	246.283			1	1		
ות וא עצעם	ULIA PROTEIN HOMOLOG	PSEUDORABIES VIRUS (STRAIN MIA-1)	2.93			T	T			
PULIS HSVEB	HYPOTHETICAL GENE 46 PROTEIN	UMAS)	61-103							
PULIT HS VOU	GENE 44 PROTEIN		366-300							
PG21 HSVEB	PROTEIN IOR	ANDA-1102	319-280							
ML23 HChVA	CENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	44-78	431-474						
MILZS HONYA	INTROPPETICAL PROTEIN ULZI	HUMAN CYTOMEGALOVINUS (STRAIN AD169)	20.23			1				
MILLS HOWA	PROTEIN UT 14 HOMOLOG	INTECTIOUS LARYNGOTA CHEMIS VIRUS (STRAIN THORNE VI	161-191		T		1			
PUL25 HSV11	HYPOTHETICAL PROTEIN UL25	HUMAN CYTOMEGALOVINUS (STRAIN ADIA)	33.34	35.38		T	1			Ī
PUL25_HSVEB	VIDUON PROTEIN UL25		370-411					T	T	
PULJS HSVSA	VINJON PROTEIN UL25			П						
P.M.15 R.TVT	VIRION GENE 19 PROTEIN		٦	П	165-406					
POLITS VZVO	WIND VILLON PROTEIN	RAIN THORNE VI	31.54	163-306						
PULJI_HSVEB	HYPOTHETICAL PROTEIN UL31		244-285				T	T		İ
PULJI VZVD	CENE 19 PROTEIN		183-187							
PULJ2 HSVEB	GENE 17 PROTEIN	П	163.197							
ZVZV ZLIDY	MAJOR ENVELOPE GLYCOPROTEIN 300	(STRAIN ABI)								
PULLU HCKVA	PROBABLE MAJOR ENVELOPE CA YOU'RDIEIN IS	VANCELLA-ZOSTER VIRUS (STRAIN DUMAS)	T	3%-344						
10.23 VE 9.0	GENE 34 PROTEIN		T	109-132		1	1			
FULLS EBV	DENE LA FROIEIR		9							
PULLA HCMVA	BARTI FROILIN	PARAM COOKERS (STRAIN 895-4)	28-30			1	1			
PIG 16 HOUSE	VEION PLOTED IN 14						1	1		
PLA 17 EBV	HYPOTHETICAL PROTEIN UT 15	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	31.36		1	1	\dagger		1	
					1	1				

		All Virgan fee bacterienhages						1	T	
PCCEME	2		AREAL	ABEAJ	AREA 2	10554	AREA S	ABEAS	AREAZ	485
CILEMANE		ALBABE CIBIT (STRAIN BOS.1)	708.742							
POL37 HSVII		13 EN 13	183-181			-				
PULJ7_HSVEB			Ţ	111.145	614.641	215.350	781-822			
PULJ7 HSVSA	GENE 21 PROTEIN	AIN AUST	T	241					-	
PLAL37 VZVD	GENE 61 PROTEIN		T							•
BIR TE HOLVA	GENE 11 PROTEIN			178:08/						
MA 1 VZVD	ROTERIOLS	ΗΊΝΑΝ CYTONEGÂLOVIRUS (STIAIN AD169)	16-51							
NA AS LIEVES	2		٦							
TOTAL POPUL			134-168	221-263						
FOLKS RISVED	2	ECKINE HERPESVIRUS TYPE I (STRAIN ABAP)	138-172							
MONTH HONA			33.109							
PULAS HSVEA			17.61							
מעצע נאזוע	MOLOG									
PULAS HSVIK	GENE 15 MEMBRANE PROTEIN		600							
PLR 45 HSVIM		2	10-6							
PIR 43 RCLAVA		HERVES SDIOLEX VIRUS (TYPE I / STRAIN NO)	20.0							
2000		HUMAN CYTONEGALOVIRUS (STRAIN AD169)	114-165	41.415	745-856					
וואכנו איווי	200	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	473-518							
HAN EN		HERPES SINDLEX VIRUS ITYPE I / STRAIN F	113-64			-				
CLAN HSVBP		PONTE PROSECULATION TO COMPANY PROTECTION PR	\$61-612			•				
PULAT HSVEA		DOVING THE PERSONNEL TYPE A CET BAND 19431	Τ	582-620	823-666					
PULAT_HSVEB			T	121417	917.866					
PLL 47 VZVD			T		100					
ACTACH SO ROAVA	PROTEIN	VAUCELLA-ZOSTER VIRUS (STILAIN DUNIAS)		407-061						
50 THE CO. THE CO. II		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	155-189							-
CR 41 1151054		HERPES SINDLEX VIRUS (TYPE I / STRAIN I?)	11:169							
משלים היינים	2	EQUINE HEAPESYIRUS TYPE 4 (STRAÑA 1942)	121-162							
PULSI PLYES		EOUTHE HEAPESVIRUS TYPE I (STRAIN AB4P)	120-161			-				
ULSI VZVD		VARICELLA. 20STER VIRUS (STRAIN DUNIAS)	122-163							
PULS2 EBV	CENE FROIEIN	EPSTEIN-BARK VIRUS (STRAIN 895-8)	168-255							
PULSZ HSVII		HEAPES SOULEX VIRUS (TYPE 1/STRAIN 17)	189-323			<u> </u>				
PULSZ HSVEB		EQUINE MEMPESVIRUS TYPE I (STRAIN ABAP)		929.970						
20.54	NE S6 PROTEIN	HERPESYDUS SADMIN (STRAIN 11)	43.483							
0134 424	T	VAUCELLA-ZOSTER VIRUS (STIAIN DUNIAS)	301-342							
PULSS RUMAN		HIDRAN CYTOMEGALOVIRUS (STRAIN ADISS)	13-48							
UL 35 RSV2H		HEIDES SOCILEX VIRUS (TYPE 2 / STRAIN HGS2)	131-185							
PULM HCMYA	TROITER CLOS	HIDAAN CYTOMEGALOVIRUS (STRAIN AD169)	11-11							
PUL70 HCMVA	٤	HIBAAN CYTOMEGALOVINUS (STRAIN AD169)	19.99							
PULYA HOMYA	PROBABLE DAY MELLANISM TANKS TO THE TANKS TO	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	43.79							
PULLEY HSV6U	HTTOINE III AL TAOI EIN UE :	KERPER SOUTH X VIRUS (TYPE 6 / STIAM UCANDA-1102)	129.770							
PULIT HSVSA	HTTOINE TROITING	HERPESYTELIS SADVOU (STRAIN 11)	366-400	919-295						
CLES HOWA	HTOTAL OCCUPANT	HIMAN CYTOMEGALOVIRUS (STIARIY AD169)	161-181							
PUL91 HSVSA	HTTOTHETICAL PROJEIN OLS	MERMESVIRUS SAIMIN (STRAIN !!)	24-58							
TULY EBY	HTOTHER GALL JOSEPH TO EN	PPSTEIN-BAKK VIRUS (STRAIN B95-8)	107-144	181-222						
PULM HOWA	HITOING TAOLEN BOX	MIMAN CYTCKEGALOVIRUS (STRAIN AD169)	79-116							
PULPE HSV6U	ATTORICAL PROTEIN OF	HEAPES SUPLEX VIAUS (TYPE & / STAATN UGANDA-1102)	101-145	912-761						
PULM, HSVSA	ATTOINGIESE TAOLEILE SE	HERPESYTHUS SAIN(THU (STRAIN 11)	11-133		-					
PULD HOWA	HTOTHER OCAL STREET	HEIMAN CYTONEGALOVIRUS (STIVAIN AD169)	13-57	186-667						
PULS HOWA	PROJECT DEPT	HIRIAN CYTOMEGALOVIRUS (STRAIN AD167)	16-71	189.793						
MALOS HSVED	HTDIRE MALTAGES OF S	STEPPES CINIM EX VIRUS (TYPE 6 / STRAIN (IGANIA)-1102)	13.151	213-270						
PULTE HONYA	IIYTOTIETICAL PROTEIN IJA	INTERIOR CYCLOSTIC CALOVINIS (NIRALY ADJUS)	15:5							
PULSE HISVED	INFORMETICAL PROTEIN UITA	HERTER SINFLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	E							
PULSE HSYSA	IIYOTIETEAL PROTEIN IAA	STEATS SAININ (STRATH II)	45.100							
PULAZ HCHVA	HIYOHE IKAL GENE 23 FKOLEN	INDIAN CYTOMEGALOVIRUS (STRAIN ADIAS)	6-40	758.792						
PULA HOUVA	HYPOTHETICAL PROTEIN UCIUS	THE INCOME. CALOVIETE (STRAIN ADICO)	-36	170-171	110.364	439.403	\$41.575			
FULTO HCMVA	VIRION PLOTEIN ULION									

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PUCTAGE	ATTENDED	Manual Control of the Person of the Control of the								
FILE NAME	PROTEIN	VIRUS	ABEAI	48643	1054	- 20		,		
PUNO_HSV1	HYPOTHETICAL PROTEIN ULISO	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	Γ			-	Τ	T	T	1
PUNG_HSV1)	URACIL-DNA GLYCOSYLASE	HERPES SUPLEX VIAUS (TYPE I / STRAIN 17)	227.268			-				1
PUNG HSV2H	URACIL-DNA GLYCOSYLASE	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN 111)	111-229			-		Ī	1	
PUNG HSVSA	URACIL-DNA GLYCOSYLASE	HERVES SINULEX VIRUS (TYPE 2 / STRAIN HGS)	141.119						F	<u> </u>
PUNO STAKA	URACIL-DNA GLYCOSYLASE	HENESVINUS SAINUM (STRAIN 11)	921-561							
PUSOZ HSVEB	URACIL-DNA GLYCOSYLASE	SHOPE FIBROMA YRUS (STRAIN KASZA)	81118							
PUSOZ HSVEK	GENE 64 PROTEIN	EQUINE HEXPESYIRUS TYPE I (STILAIN AB4P)	021.62							
PUSO HCAVA	USI PROTEIN	EQUINE HERPESYIRUS TYPE I (STRAIN KENTUCKY A)	16-120							
PUSII HOLVA	HYPOTHETICAL PROTEIN HOLFS		1.16				-			
PUSH HOWA	HYPOTHETICAL PROTEIN HOG.F.I	HIMAN CYTONEGALOYIRUS (STRAIN AD169)					-			
PUSIS HONYA	HYPOTHETICAL PROTEIN HYLF4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	15.0							
PUSZJ HOMVA	LENDRANE PROTEIN HWLFS	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	107-225				İ	ĺ		ľ
PUS34_HCMVA	HYPOTHETICAL PROTEIN HIGH?	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	T	535-578				T		Ī
PUSZE HOLIVA	HYPOTHETICAL PROTEIN HOLFS	HIMAN CYTOMEGALOVIRUS (STRAIN AD169)	T			-		T		
PUSZZ HONYA		HUNLAN CYTONEGALOVIRUS (STRAIN AD169)	535-584							
PUSSO HCAYVA	G-PROTEIN COUPLED RECEPTOR HOMOLOG US17	HUMAN CYTOMEGALOVINUS (STRAIN AD169)	6.40			-		Ì	Ì	
PV135 DAME	HYPOTHETICAL PROTEIN HORUS	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	135-169	274.312		-				
PVIO NPVAC	135 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 425 / ISOLATE LEIDEN	18.52	126-367	191-649		-			
PVISK_TRVPS	HELICASE	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	313-350	1114-1150	1179-1213			T		
PVICK TAVSY	16 KD PROTEIN	TOBACCO MATTLE VIRUS (STILAIN PSG)	73.117				T	T		
PVIA_BBMV	16 KD PROTEIN	UN SYN)	78-117				 -	T	<u> </u>	
PVIA BMV	IA PROTEIN	VIRUS	21.55	349-405	492-526	10-731	137.484 19	190.924		
PVIA COMV	IA PROTEIN	BROME MOSAIC VIRUS	3	117-876			-			
PVIA CAMPA		COYPEA CHLOROTIC MOTTLE VIRUS	6.53	242-276	346.319	417.596				
PVIA CLIVO		CUCUMBER MOSAIC VIRUS (STRAIN FNY)		Г	584-619	16:916				
PVIA CANO	IA PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)			514-619	916-191				
				193-414						
TALL TALL	TA TRUILIN	(AIN I)		П		-				
TIACLE STATE	2		1	192411	157-923					
MAN MAN		DORACT PERCESVIROS (STRAIN 112)								
TV23A DEVAL		т		130-171						
PUZER PLAN	23 KD FROIEIN	LA POLYHEDROSIS VIRUS	4-50							
PUTON ACET (POTATO LEAR MOLL VIRUS (STRAIN I)	2 2							
PVZ9K PEBV			201				1	1		
PV29K_TRVSY			12.0			1	+			T
PV29K_TRVTC		AND (STRAIN PSG)	167.201			T		1	1	T
PVIA COMV	2	GA.	45.79	T						Ī
PV2A_CHVFN			768-806			Ī		\mid		
PV2A PSVI		IN FNY)	316-420			T		T		Ī
١		የሊ ነህ <u>በ</u>	12.71				-		T	
ا	2A PROTEIN		32-226		-					
1			105-218	·						
				131-193					l	
اء				161-212	290-124					
١		VIRUS (STRAIN BATIV)	183-199							Π
PYJA CHYTH			11-45						İ	
PVJA CHYM		2	215-255							
PVJA CHVO			215-255							
PV3A CAMY	JA PROTEIN		215-255					-		
PVSIK ACLSV		CUCUMBER RIOSAIC VIRUS (STRAIN Y)	215-255	1		1	-			

		The state of the s				A S F A A				
PCCEME	ALLMOTIS		I	1000	7000		Γ			
ED E MANG	ZAOTEN	CHLOROTIC LEAF SPOT VIRUS	Т	***	137.70					
PVSIK BWTVP	XX I I VIVI EIN	LATE FL-1)	1	Ţ	137.00					
PVSIK BWTVO	SI KD PROTEIN			62-041						
PVSK PLRVI	SI KD FROIEIN		Ī							
PVS6K PLKVV	No ALL TAULTIN	AIN WAGENINGEN)	T							L
PVSIK BYNY	Marionalda		101.07							
TYDOK BY IVE	64 2 KD PROTEIN	LATE PL-1)	94.144	514-548						
AND IN ARCH	AS 7 KD PROTEIN		96.144	Γ	514-548					
100 ANA 100 AN	AND PROTEIN	T	107.141							
2000	SOUTH THE PROPERTY OF THE PROP	A.A.I.E. LEIDEN	1 1 1	311.275						
22707	PROTEIN A4	T		316-116						
2000	PROTEIN A4		1 7 6	310.265						
LAVA AVA	PROTEGNA A		20.77							
2000	PROTEIN A6	ENHAGEN								
מייי אייי	PROTEIN AG	(STRAIN WR)		11.34			_			
2000	PROTEINA		20.76				_			
יייייייייייייייייייייייייייייייייייייי	SPOTED AT	VACCINIA VIRUS (STRAIN COPENHAGEN)	200							
PVAUS VALV	SPORTED AS	VARIOLA VIRUS	80						L	
אאס איררר	PROTEIN A	VACCINIA VIRUS (STRAIN COPENHAGEN)								
PVAUP VAKY	A VIETO	VANOLA VIRUS		1	210.211					
PVAII VALLE	CACIENT AND AND AND AND AND AND AND AND AND AND	VACCINIA VIRUS (STRAIN COPENIAGEN)	***	T				_		L
PVAII VARV	TROIGIN ALI	VARIOLA VIRUS	200	220-712			-	-		
PVA13 VACCC	PROTEINAL	VACCINIA VIRUS (STRAIN COPEMIAGEN)	2			-	-			
PVA13 VARV	TROIEMAN	VARIOLA VIRUS	2					-		L
PVA11 VACCC	SE EN ABORTIVE LATE PROTEDA	VACCINIA VIRUS (STIVAIN COPENIAGEN								L
אירר אירר אירר אירר אירר אירר אירר אירר	A K D ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN WR)	17.104	197						
AVA STAN	15 KD ABORTIVE LATE PROTEIN	VAUOLA VIRUS								4
VANO VARV	PROTEIN AZD	VACCINIA VIRUS (STROM COTEMINALITY)	9							1
PVA32 VACCC	PROTEIN A20	VAUOLA VIRUS	38.69							
PUASS VARV	PROTEIN A3	VACCINIA VIKUS (STRAIM COFERENCES)	19.10							
AVA 1 VACC	PROTEIN A22	VALOCA VIRUS	25.143	173.207	335.219	344.382				
VAN VARV	PROTEIN A7)	VACCINIA VIRUS (STRAIN CUTERIACES)	25.50	Γ	255-219	344-382				-
PVA11 VARV	PROTEIN A33	VARIOLA VIRUS	200	T						4
VAJ1 VACCV	PROTEIN A11	VARIOLA VIROS								1
PVAJ2 VARV	PROTEIN A12	VACCINIA VIRUS (3) INAIM WAY, AND (3) INSING CO.	217.251						1	1
PVAJ VAKV	PROTEIN AZ	VAUOLA VIRUS	16.19							-
PVA WACCV	PROTEIN AJ3	VARIOLA VIRUS	26.63	109-155						$\frac{1}{4}$
747	PROTEIN AJ6 PRECURSOR	VACCINIA VINUS (STRAIN WRI, AND (STRAIN COLLEGE)	16.67			L				4
SAN VACCO	PROTEIN AJ6 PRECURSOR	VARIOLA VIRUS	99							
VACCV	PROTEIN A17	VACCINIA VIRUS (3 IRAIN COTENANCES)	34-65							-
2004	PROTEIN A17	VACCINIA VIRUS (STRAIM W.K.)	5			_				4
PVATE VACCV	PROTEIN A38	VACCINIA VIXUS (STRAIN COTENTIACES)	5			_				-
PVA18 VARV	PROTEIN A31	VACCINIA VIXUS (STRAIN W.K.)	16.91							1
PVAJ9 VACCC	PROTEIN AJS	VAUOLA VIXUS	13.31							4
PVA39 VACCV	PROTEIN AJ9	WACCING COLOR (STEAD) WITH	15.109						1	1
PVA 46 VACCC	PROTEIN AJ9	VACCINIA VIAUS (STRAIN TO)	200							1
PVA46 VACCV	PROTEIN A46	VACCIDIA VIRUS (STRAIN COLLANDALY)	61-136							\downarrow
PVA46 VARV	PROTEIN A46	VACCINIA VIKUS (STRAIN WK)	9:13g						-	+
PVA47 VACCC	PROTEIN A46	VARIOLA VIRUS	8:3	143-184					4	$\frac{1}{1}$
WAAN VACCV	PROTEDN A47	VACCINIA VIAUS (3) INALIA CONTRACTOR	63.96	10:10	L	_			_	_

PUGENE	ALLMOTIS	ises (no bacteriophages)	T		ABEAN	ABFAA	ABEAS	ARFAG	AREA 9 A
FILE MARIE	PROTEIN		Ī	Т	Ī	Т	Т	Γ	Π
PVA40 VACCC	PROTEIN A47			101010					Ì
PVA40 VACCV		VACCINIA VIRUS (STRAIN COPENHAGEN)		128-160				1	
PAY O VAN		VACCINIA VIRUS (STRAIN WR)	3-40	126-160					-
יייייייייייייייייייייייייייייייייייייי		VARIOLA VIRUS	3-40	126-160					
אייייייייייייייייייייייייייייייייייייי		VACCINIA VIRUS (STRAIN COPENHAGEN)	91-132						1
איזיי איניני		VACCINIA VIRUS (STRAIN WR)	91-132					1	
7777 67476	CHANT ATE KINASE HOMIDLOG	VACCINIA VIRUS (STRAIN COPENHAGEN)	134-168						
PVAL LICVE	CHANN ATE KINASE HOMIOLOG	VACCINIA VIRUS (STRAIN WR)	134-160						
W 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AL PROTEIN		230-269			•			1
2000	A1 000 150		226-262						
PYAL RISKS	AL PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	226-262						1
יייייייייייייייייייייייייייייייייייייי	711000	SOUASII LEAF CURL VIRUS	117-131						
2011	711011	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	191-225						
1000	11 PBO 11 1	ABUTILON MOSAIC VIRUS (ISOLATE WEST INDIA)	14-78	13-124			•		
100	AL STOCKER	BEAN COLDEN MOSAIC VIRUS	84-78	83-124					
2012 1170	ALL PROTEIN	POTATO YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)		17:121					1
2001		SQUASH LEAF CURL VINUS		91-125	٠				
100 T 100 T		TONIATO GOLDEN MOSAIC VIRUS	44.78						
2000	CALISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM-1141)		14:13					
PVAT CAMVE	APHID TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DM)							
PVAT CANON		CAULIFLOWER MOSAIC VIRUS (STRAIN BBC)		93-127					
PVAT CANIVE		CAULIFLOWER MOSAIC VIRUS (STRAIN NYBIS))		93-127					
PVAT CAMIVS	APRID TRANSAIISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN PVIA?)		13.137					
PVAT CAMIVW	APHID TRANSMISSION PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	T	43-130					
PVAT CERV	APHID TRANSHISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W260)	36-70		1				
PVB03 VACCV	APHID TRANSMISSION PROTEIN	CARNATION ETCHED INNO VIRUS	3.5			İ			1
PVBO4 VACCC	PROTEIN B3	VACCINIA VIRUS (STRAIM WR)	Ī	T					1
PVB04 VACCV	PROTEIN De	VACCINIA VIRUS (STRAIN COPENHAGEN)	T	T	016-044				
PVB04 VARV	PROTEIN B4	VACCINIA VIRUS (STRAIN WR)	I	T					
PVB05 VACCO		VAUOLA VIRUS		324-372	492-530				
PVB05 VACCC		VACCINIA VIRUS (STRAIN LC16MO)	234-298						1
PVR05 VACCL	OTEIN PRECURSOR	VACCIMIA VIRUS (STRAIN COPENHAGEN)	254-298						
PVR05 VACCV		VACCINIA VIRUS (STRAÍN LISTER)	254-298						
PYTO VACCV	OTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	234-298						
PYDOS VACCC	PROTEIN BY PRECURSOR	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENIAGEN)	70-17						
PVT00 VACCV	PROTEIN BE PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	3 5						Ì
PVB16_VACCC	PROTEIN BE PRECURSOR	VACCINIA VIRUS (STRAIN WR)	31.5	401,013					
PVB18 VACCV	PROTECN BIS	VACCINIA VINOS (STRAIN COTENHACEN)	Ī	33.18					
PVBIG VARV	PROTEIN BIS	VARIOUS VIRIALIS	I	491-532					
PVB19 VACCC	PROTEIN BILL	VACCINIA VIRUS (STRAIN COPENHAGEN)	13:131						
A A A CO	SON ACE ANTICEN SON CONTRACTOR	VACCINIA VIRUS (STRAIN DAIREN I)	18-119						
TABLE VALLE	SUBSACE ANTIGEN SPRECURSOR	VACCINIA VIRUS (STRAIN WR)	13-119						
מלילי הייני	PROTEDURY	VACCINIA VIRUS (STRAIN COPENIAGEN)	48.85						
NATIONAL PROPERTY.	PROTEIN B2	VACCINIA VIRUS (STRAIN WR)	69 2						1
200	NI PROTEIN	BEAN GOLDEN MOSAIC VIRUS	159-193						
FVBL 3LL	AT 1 PROTEIN	SQUASH LEAF CURL VIRUS	159-193						
VANCE BOOK	AL I PROTEIN	TOMATO COLDEN MOSAIC VIRUS	159-193						
A SILVE	BRI PROTEIN	BEAN COLDEN MOSAIC VIRUS	17.78						
PVBL TCMV	BRI PROTEIN	SOUASH LEAF CURL VIRUS	- S						
PVC02 VACCC	BA! PROTEIN	TONIATO GOLDEN MOSAIC VIRUS	85.52	363.100	101.447				1
PVC03 VACCV	PROTEIN C2	VACCIMIA VIRUS (STRAIN CUPEMHAGEN)		20.00					

		YACCHIA VIRUS (STAAIN WIT) SHOPE FIBROBIA VIRUS (STAAIN KASZA) VACCHIA VIRUS (STAAIN KOPENKAGEN) VACCHIA VIRUS (STAAIN COPENKAGEN) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN KASZA) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN WR) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) SHOPE FIBROBIA VIRUS (STAAIN COFENKAGEN) VACCHIA VIRUS (STAAIN COFENKAGEN) EFSTEIN-BAJA VIRUS (STAAIN COFENKAGEN) FRANKAN CYTOMEGALOYRUS (STAAIN ASSA) FRANKAN CYTOMEGALOYRUS (STAAIN ASSA) FRENES SIDPLEX VIRUS (STAAIN STRAIN 19) FRENES SIDPLEX VIRUS (STAAIN STRAIN 19) FRENES SIDPLEX VIRUS (STAAIN STRAIN 19)		13-121 13-121 16-226 16-226 131-159 131-159 101-709 101-709 101-235	289-315 289-315 289-315 119-340 120-394	535 412 575 412			
		E PREADLY VIRUS (STACIN KASZA) INIA VIRUS (STACIN VASZA) INIA VIRUS (STACIN VASZA) INIA VIRUS (STACIN VASZA) EN STACIN VASZA) E FIRECOLA VIRUS (STACIN KASZA) GE TIRECOLA VIRUS (STACIN KASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN VASZA) TOTA VIRUS (STACIN COPENIAGEN) CINIA VIRUS (STACIN COPENIAGEN) CINIA VIRUS (STACIN COPENIAGEN) CINIA VIRUS (STACIN COPENIAGEN) TOTA VIRUS (STACIN COPENIAGEN) TO	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		19-313	335413 335413			
		INTERVALUS (STRAIN COPENHAGEN) INTA VALUS (STRAIN COPENHAGEN) INTA VALUS (STRAIN WA) OLA VIRUS OLA VIRUS TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN COPENHAGEN) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN COPENHAGEN) TERROGALA VIRUS (STRAIN COPENHAGEN) TERROGALA VIRUS (STRAIN COPENHAGEN) TERROGALA VIRUS (STRAIN COPENHAGEN) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN COPENHAGEN) TERROGALA VIRUS (STRAIN KASZA) TERROGALA VIRUS (STRAIN ESTRAIN ADISO) TERROGALA VIRUS (STRAIN ESTRAIN ADISO) TERROGALA VIRUS (STRAIN ESTRAIN ADISO) TERROGALA VIRUS (STRAIN ESTRAIN II)		9 9 9	18-740	335413			
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		PARA YRUS (STALM WE) THA YRUS (STALM WE) THA YRUS (STALM WASZA) THE FIREQUIA VIRUS (STALM KASZA) THE FIREQUIA VIRUS (STALM KASZA) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM WE) THA YRUS (STALM WE) THA YRUS (STALM WE) THA YRUS (STALM WE) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM COPENAGEN) THA YRUS (STALM WESA) THA CYTOMEGALOVIRUS (STALM AD169) THA CYTOMEGALOVIRUS (STALM AD169)	0 • 0 • 5 5 5 5		18-110 18-140	735412			
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		FERROLLA VIRUS (STANIN KAZA) FERROLLA VIRUS (STANIN COFENHACEN) FOR VIRUS (STANIN COFENHACEN) FOR VIRUS (STANIN COFENHACEN) FOR VIRUS (STANIN WR) FOR VIRUS (STANIN WR) FOR VIRUS (STANIN WR) FOR TORONIA VIRUS (STANIN COFENHACEN) FOR TORONIA VIRUS (STANIN COFENHACEN) FOR TORONIA VIRUS (STANIN COFENHACEN) FOR TORONIA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN COFENHACEN) FOR TOROLLA VIRUS (STANIN STANIN TOROLLA VIRUS (STANIN STANIN TOROLLA VIRUS (STANIN STANIN TOROLLA VIRUS (STANIN TOROLA VIRUS (STANIN TOROLLA VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIRUS VIR	63-106 12-116 13-116 136-170 136-170 1-56 100-133 100-133 100-134 110-134 136-174 136-174		18-313 18-310 18-340	33413			
		FE FIREGRAM VIRUS (STRAIN RAZZA) CHIA VIRUS (STANN COPENHAGEN) CHIA VIRUS (STANN WE) CHIA VIRUS (STANN WE) CINIA VIRUS (STANN WE) CINIA VIRUS (STANN WE) CINIA VIRUS (STANN COPENHAGEN) EF FIREGRAM VIRUS (STRAIN COPENHAGEN) CINIA VIRUS (STRAIN COPENHAGEN) CINIA VIRUS (STRAIN COPENHAGEN) CINIA VIRUS (STRAIN COPENHAGEN) CINIA VIRUS (STRAIN COPENHAGEN) CINIA VIRUS (STRAIN COPENHAGEN) TEN-BAAR VIRUS (STRAIN B95-1) TEN-BAAR VIRUS (STRAIN B95-1) TEN-BAAR VIRUS (STRAIN B95-1)	13-116 13-116 13-110 13-170 13-170 13-170 14-171 10-173 11-273 11-273 11-174		19-310	333413			
	3	CINIA YMUS (STRAIN COFERIACES) CINIA VIRUS (STRAIN WR) CINIA VIRUS (STRAIN WR) CINIA VIRUS (STRAIN WR) CINIA VIRUS ET IRROUN VIRUS (STRAIN KASZA) ET IRROUN VIRUS (STRAIN KOZZA) CINIA VIRUS (STRAIN COFENIAGEN) CINIA VIRUS (STRAIN COFENIAGEN) CINIA VIRUS (STRAIN COFENIAGEN) CINIA VIRUS (STRAIN COFENIAGEN) CINIA VIRUS (STRAIN COFENIAGEN) CINIA VIRUS (STRAIN BIS-1) TEN-BAJU VIRUS (STRAIN BIS-1) TEN-BAJU VIRUS (STRAIN BIS-1) TEN-BAJU VIRUS (STRAIN BIS-1) TEN-BAJU VIRUS (STRAIN BIS-1)	13-116 136-180 136-170 13-176 1-146 14-178 100-18 16-77 218-23 116-174 116-174		116-3140	133413			
4 3 4 3 9 4 3 9 5 9 5		CDALA VIRUS (STALIN WE) CINIA VIRUS (STALIN WE) CINIA VIRUS (STALIN WE) OLIA VIRUS FIRIDOILA VIRUS (STALIN WE) CINIA VIRUS (STALIN WE) CINIA VIRUS (STALIN KASZA) FIRIDOILA VIRUS (STALIN KASZA) CINIA VIRUS (STANIN COPENIAGEN) FIRIDOILA VIRUS (STANIN COPENIAGEN) FIRIDOILA VIRUS (STANIN COPENIAGEN) FIRIDOILA VIRUS (STANIN COPENIAGEN) FIRIDOILA VIRUS (STANIN COPENIAGEN) FIRIDOILA VIRUS (STANIN COPENIAGEN) FIRIDOILA VIRUS (STANIN ENSYN) FIRIDOILA VIRUS (STANIN ENS	136-180 136-170 136-170 1-16 143-176 100-133 16-97 16-173 136-174 136-174		116-340				
		CIMIA VIRUS (STAAIN COPENHACCIA) CINIA VIRUS (STAAIN WA) FINA VIRUS (STAAIN WA) FINA VIRUS (STAAIN KASZA) FINA VIRUS (STAAIN COPENHACEIA) CINIA VIRUS (STAAIN COPENHACEIA) CINIA VIRUS (STAAIN COPENHACEIA) FINA VIRUS (STAAIN COPENHACEIA) FINA VIRUS (STAAIN COPENHACEIA) FINA VIRUS (STAAIN COPENHACEIA) FINA VIRUS (STAAIN COPENHACEIA) TEIN-BAAR VIRUS (STAAIN B99-1) TEIN-BAAR VIRUS (STAAIN B99-1) ANA CYTOMEGALOVIRUS (STAAIN AD189) ANA CYTOMEGALOVIRUS (STAAIN AD189)	136-176 136-176 13-36 13-36 100-135 100-13 100-13 110-134 136-17		19-740				
		CINIA VIRUS (STALIN WR) GILA VIRUS FE FIRONIA VIRUS (STALIN KASZA) FE FIRONIA VIRUS (STRAIN KASZA) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) TEN-BARA VIRUS (STRAIN B95-1) TEN-BARA VIRUS (STRAIN B95-1) TEN-BARA VIRUS (STRAIN B95-1) TEN-BARA VIRUS (STRAIN B95-1) TEN-BARA VIRUS (STRAIN B95-1)	136-170 1-146 1-46 1-46 100-155 100-155 100-155 110-151 116-114		18-240				
		TOLA VIRUS FE FIBEORIA VIRUS (STRAIN KASZA) FE FIBEORIA VIRUS (STRAIN KASZA) CENIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) FEIN BAJAI VIRUS (STRAIN KASZA) FEIN BAJAI VIRUS (STRAIN KASZA) FEIN BAJAI VIRUS (STRAIN B95-9) FEIN BAJAI VIRUS (STRAIN B95-9) FEIN BAJAI VIRUS (STRAIN AD169) FEIN BAJAI VIRUS (STRAIN B95-9) FEIN BAJAI VIRUS (STRAIN B95-9)	1.36 1.46 142-176 100-155 10-98 16-97 110-184 130-184 110-174		19-240				
		PE TIDROMA VIRUS (STRAIN KASZA) PE TIDROMA VIRUS (STRAIN KASZA) PET RIDROMA VIRUS (STRAIN KASZA) CHALA VIRUS (STRAIN COPENIAGEN) CHALA VIRUS (STRAIN COPENIAGEN) PET RIBROMA VIRUS (STRAIN KASZA) PET RIBROMA VIRUS (STRAIN KASZA) TENA AVIRUS (STRAIN EOPENIAGEN) TENA BAJA VIRUS (STRAIN B93-9) TAN CYTOMEGALOVIRUS (STRAIN AD169) TAN CYTOMEGALOVIRUS (STRAIN 11)	1.46 142-176 100-155 40-98 56-97 218-253 150-184 136-174		160.194				
		FE FIDRONÍA VIRUS (STRAIN KASZA) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) CINIA VIRUS (STRAIN COPENIAGEN) FE FIBROSIA VIRUS (STRAIN KASZA) FE FIBROSIA VIRUS (STRAIN KOPENIAGEN) GINIA VIRUS (STRAIN SOPENIAGEN) ANA CYTOMEGALOVIRUS (STRAIN AD189) ANA CYTOMEGALOVIRUS (STRAIN AD189)	142-176 100-155 100-155 100-155 150-184 110-174 110-175		160-194				
		CINIA VIRUS (STAAIN COPENIAGEN) CENTA VIRUS (STAAIN COPENIAGEN) CENTA VIRUS (STAAIN COPENIAGEN) FETIBACALA VIRUS (STAAIN KAZA) FETIBACALA VIRUS (STAAIN RASA) TEIN-BALA VIRUS (STAAIN B99-1) TEIN-BALA VIRUS (STAAIN B99-1) TEIN-BALA VIRUS (STAAIN B99-1) TEIN-BALA VIRUS (STAAIN B99-1) TEIN-BALA VIRUS (STAAIN B99-1) TEIN-BALA VIRUS (STAAIN B99-1)	100-155 40-98 56-97 218-253 118-174 116-175	123-159 670-709 191-223	260-194				
		CINTA VIRUS (STRAIN COPENHAGEN) CINTA VIRUS (STRAIN COPENHAGEN) PETIBLOGIA VIRUS (STRAIN KASZA) PETIBLOGIA VIRUS (STRAIN KASZA) TEINA VIRUS (STRAIN COPENHAGEN) TEINA ANUS (STRAIN BIS-1) TEINA CYTOMEGALOYRUS (STRAIN AD18) PES SIRUELE VIRUS (TYPE I STRAIN 11)	100-133 40-98 56-97 216-233 136-134 116-173	670-709 191-225 104-336	160-194				
		CINIA VIRUS (STRAIN COPENIAGEN) PE FIBRORIA VIRUS (STRAIN KASZA) CINIA VIRUS (STRAIN COPENIAGEN) TEIN-BAJA VIRUS (STRAIN B93-1) AN CYTORIEGALOYBUS (STRAIN AD169) BES SIRPLEX VIRUS (TYPE 1 / STRAIN 17)	10-74 56-97 216-253 150-184 136-174	670-709 191-225 108-336	360-394				
		FEFIBROAIA VIRUS (STRAIN KASZA) CINIA VIRUS (STRAIN COPENHAGEN) TEIN-BAJA VIRUS (STRAIN BS)-1) AJA CYTONEGALOYIBUS (STRAIN AD189) PES SIGNEGA VIRUS (TYPE 1 / STRAIN 17)	26-97 216-233 150-164 136-174 116-175	670-709 191-225 108-336	260-294				++++
		CINIA VINUS (STRAIN COPENNAGEN) FEN-BAJA VIRUS (STRAIN 895-1) FAN CYTOMEGALOVIRUS (STRAIN AD169) PES SIDPLEX VIRUS (177E 1 / STRAIN 17)	116-174	670-709 191-225 101-336	260-194				
		TEIN-BALA VIRUS (STRAIN BIS-1) IAN CYTOMEGALOVIRUS (STRAIN ADIS) PES SIDPLEX VIUS (1YPE 1/ STRAIN 17)	136-174	191-235	160-194				$\frac{111}{111}$
		ILEN CYTONIEGALOYRUS (STRAIN AD169) DES SINDLEX VIRUS (TYPE I / STRAIN I?) DES SINDLEX VIRUS (TYPE I / STRAIN I?)	116-174	104-335	×47-007				\mathbb{H}
		DES SINDLEX VIRUS (TYPE I / STRAIN 17)	16.13	1101:330					+
		STAD SIVE EX VIEW						-	-
1111 111111			136-174	230-266	727-17		-	-	_
		COLONE MERPESVIRUS TYPE I (STRAIN ABAP)	130-114	304-352	90. 315				
	1	PERFECUELY SABILIA (STRAIN II)	479-520	*17.774					
		SEI MORABLES VIRUS (STRAIN INDIANA S)	105-160	792-378					
$\Pi\Pi\Pi\Pi\Pi\Pi$		SECTION OF THE STAND OF THE STA	_1	315-330			-		
		WANTELLY ON ITORNICA MUCLEAR POLYHEDROSIS VIRUS	-						
		ACTUACO STRADA PP.1)	_						_
		CONTRACTOR OF THE ATA COPENIAGEN	123-157						
	WA .	VACCINIA VIRUS (STRAIN WR)	133-157			1			
\prod		A VIRIN	13-13						4
П	1	VACCINIA VIRUS (STRAIN COPENHAGEN)	136-160						
Π		CAPCINIA VIRUS (STRAIN WR)	176-180						_
	170	VARIOLA VIRUS	2						4
	100	FOWLPOX VIRUS (STRAIN FP-1)							$\frac{1}{1}$
	HS.	SHOPE FIBROMA VIRUS (STRAIN KASZA)	101.54						+
	*	VABIOLA VIRUS	-						+
٦		CAULTIOWER MOSAIC VIRUS (STRAIN CHILLS)	5				+		$\frac{1}{1}$
		CAULIFLOWER MOSAIC VIRUS (STRAIM LIM)	١						+
		CAULIFLOWER MOSAIC VIRUS (STRAIN BBC)							+
		CAULIFLOWER MOSAIC VIRUS (STRAIN NYELS)							+
П		CAULIFLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	20,316	+				1	+
PVEDY VACCE DNA-BINDING PROTEIN		VACCINIA VIRUS (STRAIN COPENHAGEN)						-	+
Γ	(A)	VACCINIA VIRUS (STRAIN WR)	217.77	+					+
	\(\hat{\lambda}\)	VARIOLA VIRUS		-		-			+
EVENT VACCE PROTEIN ES	3	VACCINIA VIRUS (STRAIN COPENHAGEN)	:	-	1				$\frac{1}{2}$
		VACCIDITA VINIS (STRAIN WR)	10.7	-					

	ALLAIOIIS		Ī		ABEAT	ABFAK	ABFA S	AREA 6	AREA 7	AREA
EILE HANE	PROTEIN	YIRUS	9 5							
PVE05 VACCC	PROTEIN ET	CATE AIM COPENHAGEN	28-93							
PVE05 VACCD	PROTEIN ES		18.101						_	
PVE05 VACCV	PROTEIN ES		14.101							
PVEOS VARV	PROTEIN ES		26.183							
PVEOR VACCC	PROTEIN ES	(STRAIN COPENIAGEN)	103-139	232-266						
PVEOS VACCV	PROTEIN ED		105-139	133-266						
PVEOS VARV	PROTEIN ES		961-501	367-401						
PVEIR NPVAC	CAN VIEW CONTINUE	ALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	113-163							
PVEI MPVIA	C. MOTEN	_	17.171							
rvei lirvii	ES PROTEIN		26.90							
TAPE CANAL	STUBBLIEN.		11-67	133-167						
STAR HEAL	ELPROTEN		26-90							
TACK TO A	FI PROTEIN		2.8							
BVEL HBV43	EI PROTEIN		2.5	312-346						
PVE! HPVS!	EI PROTEIN		15-47							
PVEL HPV68	EI PROTEIN		1.63	19.1%						
PVE! PAPVE	EI PROTEIN		263-299							
PVEM MPVAC	EI PROTEIN	+	2							
PVE1 CRPVK	EARLY 25.9 KD PROTEDM									
PVE2 HPVOS	PROBABLE E2 PROTEIN	ILLUMA IAUS (SI KAIN KANS		276.110	142.183	417.471				
PVE2 HPV08	PROBABLE EZ PROTEIN			141.183						
PVE2 HPV16	PROBABLE E3 PROTEIN		١	115.140						
PVE2 HPVII	E2 PROTEIN	HUMAN PAPELDAIAVIRUS 1 TTE 10	T							
PVE2 HPVIA	E2 PROTEIN		1 2	150-101						
PVE3_HPV2A	E2 PROTEIN			159-193						
PVE2 HPV31	E3 PROTEIN									
PVE2 HPV33	ET PROTEIN		101-3	166-762						
PVE2 HDV35	E2 PROTEIN			158-192						
PVE2 HPV39	EZ PAOTEJN		74-110	323-357						
PVE2 HDV41	ES PROTEIN		6-54							
PVEZ HOVA?	ETROIEM		5.59	148-182						
PVEZ HPVSI	ES PROTEIN	HUNAN PAPELLOMAVINUS TYPE 11	184-191							
EVEL POST	ESPECIEN		13-47	3.35						
PVE? HPVSB	E2 PROTEIN		3:36							1
PVE2 PAPVD	PROBABLE ET PROTEIN	JS TYPE SB	18.0							-
PVEL PAPVE	PROBABLE E2 PROTEIN		107-141							
PVE2 PCPVI	PROBABLE ES PROTEIN		200							
PVE2 AUDVI	E3 PROTEIN	VIKUS I TEE I	43.106	167.141						
PVEJ9 NPVAC	E2 PROTEIN	INTESUS PAPILLONIA VIANO E LE BOY VAFOROSIE VIEITE	20.00							L
PVE19 NOVOP	EARLY 39 KD PROTEIN	15								
PVE4 HPVIS	EARLY 39 KD PROTEIN									
PVE4_HDV41	PROBABLE E4 PROTEIN	HUMAN PATELONA VINOS LITE IN	61.97							
PVES_HPVSB	PROBABLE E4 PROTEIN	INDIANA PAPER I CALAVIEUS TYPE 58	ş	96-130		_				
PVEF_GVTN	PROBABLE ES PROTEIN		611.119							
PVENY BEV	ACTOR (VEF) IIM NO.		195-239							
PVENY DHVII	ENVELOPE PROTEIN		118-364							
PVENV MCVI	MAN TO STATE OF PROTEIN (4) KD PROTEIN) (P4)K	MOLLUSCUM CONTAGIOSUM VIXUS SUBTYPE I (MCVI)	252-216							
PVENY MICVA	WAIDS ENVELOPE PROTEIN (4) KD PROTEIN) (P43K)	HOLLUSCUM CONTAGIOSUM VIRUS SUBTYPE 2 (MCVII)	253-316							1
NEW THE	ENVELOPE OF YOUR DECUMSOR (SURFACE	THOCOTO VIRUS (THO)	20-01							

	TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN (1) KD PROTEIN) (P) IX TELOPE PROTEIN PRECURSOR OR NELSIBRANE PROTEIN PRECURSOR OR NELSIBRANE PROTEIN PRECURSOR OR NELSIBRANE PROTEIN PRECURSOR OR NELSIBRANE PROTEIN PRECURSOR (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	AGEN) 12 12 12 13 14 14 15 16 16 16 16 16 16 16 16 16		AREA1 A. [18-156 [124	A LANGE					
	FLOPE PROTEIN (17 KD PROTEIN) (P) IX FLOPE PROTEIN (17 KD PROTEIN) (P) IX FLOPE PROTEIN (17 KD PROTEIN) (P) IX FLOPE PROTEIN (17 KD PROTEIN) (P) IX II DPE PROTEIN (17 KD PROTEIN) (P) IX II PROTEIN ETS II PROTEIN PRECURSOR OR NELSBRANE PROTEIN PRECURSOR OR NELSBRANE PROTEIN PRECURSOR OR NELSBRANE PROTEIN PRECURSOR OR NELSBRANE PROTEIN PRECURSOR III II	OCYTECHOSIS VIRUS (1) AND VACCINIA VIRUS 1 1 1 1 1 1 1 1 1 1 1 1 1								
	* * * * * * * * * * * * * * * * * * *	0 CYTE DROSIS VIRUS [] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2				11111			-	
	XXXX	OLYTEDROSIS VIRUS (1)				+++++		1111		
	FEE	MIAGEN) MIAGEN MIAGE								
	REEL LINE LINE TO A CONTROL OF THE C	ENTAGEN FENTAGE								
		EMIAGEN) EMIAGEN EMIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN FINIAGEN								
		ALFORNICA NUCLEAR POLYIEDROSIS VRUS (I STRAIN COFEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1 STRAIN COEMIAGEN) 1								
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	TEN FILL		ΠT	TT	199.236	350-361	344-581			
	TEN 13 TEN 73		11		100.316	130-364	144.581			
	TEN FIZ		T							
\prod	TEN FIL				200					
٦	TINET		<u> </u>							
l	THE PERSON NAMED IN COLUMN 1		155.194							
	I EIN THE		146.194							
PVF16 VARV PROT	PROTECUTIO		5							
	PROTEINFIG		T	16.016						
	PROTEINFF									
T	PROTEINIPA		25.5							
T	PROTECUEN									
T	CHI FET PROTEIN (FILACINIENT)	NIAGEN)	3							
T	A PROTEIN		70-64			1				
	STRINGS PROTEIN	JANNEL CATFISH VIRUS) (CCV)		513-363	100					
1	TANDERS OF THE PROTEIN	Г	966-106							L
٦	POINTING ST.	- Constant	240-278							
VICOL VACCV PRO	PROTEING		101.110							1
Γ	PROTEIN GI (FRAGMENT)									1
	PROTEING	VIRUS TYPE I (STRAIN AB4P) (EHV-1)				-				
Ţ	CENE SPROTEIN	(EHV-1)	10:01				L			
Ţ	CENTE 1 PROTEIN (OM L.1)		64-98			-			L	
T		VAUGLA VIAUS	117-158	255.289	AF-CE			-	_	L
	O. P. C. C. C. C. C. C. C. C. C. C. C. C. C.	VACCINIA VIRUS (STRAIM COLECTIONS)	117.150	155-219	155-349			+		L
	PROTEINO	Т	81:18							
PVCOS HSVII PAC	PROTEIN GS	Τ	69.103		-				-	1
	HYPOTHETICAL GENE & MEMBRAILE SECTION	7		134.150	_					1
[HYPOTHETICAL GENE 1 MEMBILAND PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)				 -				
I	PROTEIN GT	100 A SPECIE			1	-				
T,	00 March (2)	VACCOLA CINCOLA IN COPENIAGEN	304-331			1	1			
T	CONTRACTOR CONTRACTOR	VACCINIA VIAUS (SI PALIA COL	304-338			1	+	-		L
	PROJEIN PLICATE CONTRACTOR	VACCOMA VINUS (STRAIN WA)	304-338					-	-	
PUGOS VARV PR	ROTEIN FI (FROIEIR CF)	VARIOLA VIRUS	61.63	L						ļ
	PROTEIN FI (PROTEIN CF)	ICTALURID HERPESVIRUS I (CHANNEL CATITISTI VIANALICALITY	17							-
	ENE 10 MEMBINGS	SPIROPLASMA VIRUS SPVI-RBAZ B				L				1
	GENE 13 PROTEIN	MELDES YOU'S SAIMIN (STIAM II)	_	137.211						1
	KYPOTHETICAL GENE 16 PROTEIN	ICTALINED HEAVES VIRUS I (CHANNEL CATFISH VIRUS) (CCV)	Т	2003	-	-				1
T	HYPOTHETICAL GENE 17 PROTEIN	ICTALLIA DE LA ESVIRUS I (CILANNEL CATTISH VIRUS) (CCV)	Т		-	-				
]	HYPOTHETICAL CENE 11 PROTEIN	AMERICA MOOREI ENTONIOPOXVIRUS (ANEPV)	407-441							
TO TOO	Matter and									

FILE NAME	PROTEIN	All Vicuses (no batterlaphages)	ARTAI	AREAT	ARTA 3	48644	7 7 7			
PVGI SPV4	CAPSID PROTEIN	SPIROPLASMA VIAUS SPVI.RE42 D	11:10	156.241	28.52	ļ		Τ	Т	-
PVG22 115VII	CAPSID PROJEIN	SPIROPLASNIA VIRUS 4 (SPV4)	=======================================							
N.C.24 115V11	INPOSSE INCAL GENE 23 PROTEIN	ICTALURID HERPESVIRUS I ICHANNEL CATFISH VIRUS) (CCV)	13.13	417.679	660.192	109.1055			-	
LVG27 HSV19	HYPOTHETICAL GENC TAPROTEIN	ICTALURID HERPESVIRUS I ICHANNEL CATRISII VIRUSI (CCV)	2	74.108						
	TITOTILI PLAL CLAE LI PROTEIN	ICTALCATOR IN THE SVINUS I (CHANNEL CATFISH VIRUS) (CCV)	2							
	THE PROPERTY OF THE PROPERTY O	THE CLASSING THE PROPERTY OF T	M. C.							
	THE THE THE TANK THOUSING	ANISACIA PIOCREI ENIGNIGIO AVIRUS (ANILLY)	77.6)	186-218						
	CENE I FROIEIN	SPINOPLASKIA VIAUS SPVI-RIAZ D	111.156	215-316						
	CANE J PROTEIN	SPIRITE ASSIS (TRUS 4 (SPV4)	33.110							
120	HYPOTHETICAL GENE 3) PROTEIN	CTALUNIO HERPESVIRUS I ICHANNEL CATRISH VIAUS) (CCV)	14.103							
PVC.15 115V.11	INPOTITE FICAL GENE 14 PROTEIN	ICTALUNIO HEM ESVIRUS I (CHANNEL CATFISH VIRUS) ICCV)	145-179							
PV617 115VII	INTO THE THEAL GENE 19 PROTEIN	ICTALURID HERPESVIRUS I ICHAMMEL CATHISH VIRUSHICCVI	17.90							
P. C. 3 1157.11	HYPOTHETICAL GENE 17 PROTEIN	ICTALURID HERPESVIRUS I ICHANNEL CATFISH VIRUSI ICCV	135.433							
P16.10 115VII	INPOSITE HEAL GENE DEPROTEIN	ICTALURID HERFESVIRUS I ICHANNEL CATFISH VIRUS) (CCV)	===							
PIGI SPVIA	INPOTITE FICAL GENE 19 PROTEIN	ICTALUNID HERDESVIRUS LICHANNEL CATFISH VIRUSHICCY)	134-151	366.300						
PVG) SPV4	GENE) PROTEIN	SPIROPLASMA VIRUS SPVI-RIAZ II	=	162-196	201-104					
PVG41 ISVII	CENE I PROTEIN	SPIROPLASALA VIRUS 4 (SFV.4)		17:11						
PVG45 HSVSA	INPOTHETICAL GENE 43 PROTEIN	ICTALUAID HERPESYIRUS I [CHANNEL CATFISH VIRUSI (CCV)	116-130	262.296	124.161	641.677				
PVC44 IISVII	HYPOTHETICAL GENE 43 PROJEIN	HERPESVIAUS SAIMINI (STRAIN 11)	121-162							Ī
PVG46 HSVII	PROBABLE MAKUR GLYCOPROFEIN	ICTALUMD IERPESVIRUS I (CHARNEL CATTISH VIRUS) (CCV)	15.16	939.1078	131-131					
PVG46 HSVSA	HYPOTHETICAL GENE 41 PROTEIN	ICTALUNID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	10.301							
PVG19 115VSA	HYPOTHE FICAL GENE 48 PROTEIN	IERPESVIRUS SAINIIRI (STRAIN II)	160-413	11.464	111.347					
PL CAR ANTEPV	JIYPOTIG.TICAL GENE 49 PROTEIN		61.102							
PVC4 SPV4	GAR PROTEIN	KUS (ANEPV)	1							
PVGSI IISVII	GENE + PROTEIN		19.130						Ť	
PVGII IISVSA	HYPOTHETICAL GENE SI MENIBRANE FROTEIN	HANNEL CATTISH VIRUSHICCVI	15.2	19-123					Ī	
PVGS1 HSVII	GENE 11 GLYCOPROTEIN	IERPESVIAUS SAINIIN (STRARP 11)	29.70	13.137	162.1%					
PVCS4 IISVII	HYPOTHE HCAL GENE 31 PROTEIN	1.	11.131							
PVGSS IISVII	HYPOTHE HICAL GENE SO PROTEIN	-	155.386					Ī	Ì	
PVG19 IISVSA	HYPOTHETICAL GENE SS PROTEIN	<u> </u>	101.13							
PVG36 115VII	HYPOTIETICAL GENE 35 PROTEIN		176-176							
PVGIV HSVII	HYPOTHETICAL GENE SA PROTEIN	ICTALUTUD IERFESVIRUS I (CITANNEL CATEISII VIRUS) (CCV)	151-172	578.612	644.678	750-714	146-190	1111-1145		
PVG1 CPVIB	GENE G PROTERY		20	2						
PVG61 115VII	GENE 1 PROTEIN		107-70							
PVG63 115VII	IIYPOTIETICAL GENE &! PROTEIN	MEL CATFISH VIRUSI (CCV)	1 1 1 1 1				1		1	
PVG65 IISVII	HYPOTHETICAL GENE 61 PROTEIN	1	36.514					1	1	1
PVC64 HSVII	HYPOTHETICAL GENE 65 PROTEIN	ï	T	20.00					I	
PVG67_JISVII	HYPOTHETICAL GENE 64 PROTEIN		36.11	977						
PVG68 HSVII	HYPOTHETICAL GENE 61 PROTEIN	П	139-413	301.346	1321-1369	1078-1341			T	
PVG71 JISVII	HYPOTHETICAL GENE 64 PROTEIN									
VCM IISVII	HYPOTHETICAL GENE 12 PROTEIN				912.949					
T VIJE STVIR	HYPOTHETRAL GENE 13 PROTEIN	VEL CATFISH VIAUS) (CCV)	2	=======================================						
1000	CORPORATION			7	٦					
PVGID IICHIVA	TI PROIEIN	IN BEAUDETTE)	5	130	1119-1156	1111-1474	1478-1513	1517-1556	1761.1795	
יייייייייייייייייייייייייייייייייייייי	CLICORDIEN PRECIESOR MANAGER CO	PACALLY I CARE CALLOVIACIS (STRAIN AD189)								
	ET CLYCOPROTEIN PRECUESOR (SPIKE CLYCOPRO)	INVINE CORONA VIRIS SCHAME IS		1						
I.	ET GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO	VINE CORONA VIRUS (STRAPH L9)	T	100.100	101.01	50:00		1	j	
1	ET GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO BG	WINE CORONAVIAUS (STRAIN LY-134)	T	T	T	1001				
L	ET CLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO	VIDE CORONAVIAUS (STRADY MEBUS	Τ	T	Т	2 2			1	
1	EZ CLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO	WINE CORONAVIRUS (STRAIN QUEDEC)	T	T	Т	600	1	1		
			7	7	7	101-101		1	1	7

CINE	ALLAIOTIS	All Virures (no batteriophages)	П	IJ	ABEAL	AREA	ARGA	AREAL	197	9
ILE KANE	NICOSI	MANUA CORONAVIRUS (STRAIN VACCINE)	969-639	ī	80 - 100	126)-1303				
	I SPINE GLYCOPE		170.916	1055-1112					1	
VC 2 CVR	ET GLYCOPROTEIN PRECUASOR ISPINE GLYCOPRO	ī	643.614	1001-1111	1370-1315					
	ET GLYCOPROTEIN PRECURSOR (SPIKI: GLYCOPRO	ı	31 62	949-1079	1310-1363					
	EI GLYCOPAOTEIN PRECURSOR (SPIKE GLYCOPRO	MUMINE CONORATIONS THE CONTRACT CL.2)	10.03	1111-1001	1370-1315					
ינים ז כאוווו	ET CLYCOPROTEIN PRECURSOR (SPINE CLYCOPRO	ī	\$01.54	966-991	1129.1174					
1	ET GLYCOPACIEN PRECURSOR (SPIKE GLYCOPRO	ST SUBMANISTS	61:59	441-413	111-111	119-933	1040-1164	132-1319		
ı	ES CL VEOPROTEIN PRECURSOR (SPIKE GL YCOPRO		40.110	441.413	602.713	119-933	1040-1166	133-1369		
- 1	CONTRACTOR SPINE GLYCOPRO				116 007	16.71	1011-1114	138-1317		
CVPYR	E. O. T. CAROLEIN MECHANISME CLYCOPRO		10.110	200			101	1330-1387		
CVPTU			49.110	010-020	6 VO: 131					
CVPRE	ET CLYCOPROTEIN PRECURSOR (SPINE OF LOPING	5	114-158	468-509	49.599	74.01				
CVPRA	ET CLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRU		174.230	461.909	643-630	116-962	2			
CVERT	ET CHYCOPROTEIN PRECURSOR ISPINE CLYCOPRO	12	69.10	446-410	16.069	126-711	1038-1184	1350-1317		
120	ET CLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO		48.102			L				
İ	SOUTH FARMENE GLYCOFROTEIN		100	461.404	643.736	643.926	1043-1119	1315-1392		
١	CVENT SEA MINISTER OF THE PROPERTY OF THE PROP	Ī								
-		╗	2		0000					
BVD	ET CL TCUTCHE IN TRECUMPOR	9		2	200					
PVGL 2 IBVD2	ET CLYCOPROTEIN PRECURSOR		111-905	1057-1091						
EVK	ET CL YCOPROTEIN PRECUASOR	٦	417.416	173.904	1056-1090					
	ET CLYCOPROTEIN PRECURSOR	Ī	23.438	13.804	1036-1090					
	CONTRACTOR OF PRECURSOR			130.143	117-117	144.171	L			
	SOSTILLE SECTION OF STREET				11.478	31.485	863.879			
_										
2	GLYCOTHING THE CONTROL		28-890							
	GLYCOPROTEIN BY RECURSOR		117-119							L
PVGL B HSVIK	GLYCOPROTEIN B PRECURSOR	2	137.009							
VOLB HSVIP	GLYCOPAGIEIN B PRECURSOR	ON)	120.100							1
VCI B HCV21	GLYCOPROTEIN B PRECURSOR		120.190							
HEADING TO A	CH YCOPADIEIN B PRECURSOR	HEAPES SAULEX VINDS (1 TTE 4' STACK VILLE	11.100							
11.00	CI YCOPROTEIN B PRECURSOR		100			_				
	CI VEOPEOTEIN B PRECURSOR	Ī		100						
	- No. 100 -	47 STRAIN UCANDA-1102)								L
III A	STATE OF THE CORP.		11.46							_
PVGLB HSVB1		BOVINE ICENPESYINGS IYPE I (STRAIN BAIN)	40.474	700.						L
NGLB HSVBC	CLTLUFACIEN BILLIAN CONSCI	BOVINE IERPESTAUS TYPE I (STRAIN COOPER)	863.v00							
VGL B 115VE	CLYCOPROTEIN I PALLUANOR	COUNTY HE PESVIRUS TYPE 1 (ISOLATE 11VS19A)	341-576	111.001						
PYCL B HSVE4	CLYCOPROTEIN B PRACTURESON	BOUINT HERPESVIRUS TYPE CISTRAIN 1942)	3	147.900						ļ
HSVEA	GLYCOTAG I I'M & PARCONSON	TOTALINE LIFTURE SVIRUS TYPE 1 (SIRAIN ADI)	342.516	181						1
VGLB IISVEB	GLYCOPROTEIN B PARCUASOR	FOUNT HE RESCRIBES TYPE ! (STRAIN ABAP)	943-576	11.00						1
PVGLB HSVEL	GLYCOPROTEIN B PRECURSOR	COURSE LIEBBE CVIBILS TYPE I ISTRAIN KENTUCKY U)	343-376	910-940						
PUCLB HSYND	GLYCOPROTERY B PRECURSOR	STATE OF THE DESCRIPTION (STRAIN RB-10)	190-01	119-617	787-845					
PI'GLE HSVSA	GLYCOPROTEIN B PRECURSOR		110.012	104-403						1
PACIFICATOR	GLYCOPACIEIN B PRECURSOR	TERMINATION OF THE PROPERTY OF THE PARTY OF	206.360	417-475	661.136	144.778	160-194			
NO. PRVU	GLYCOPROTEIN B PRECURSOR	MUMPE CYTONIEGALUVINO IS INAINA ENTRINE								
4777	CL YCOPROTEIN GII PRICURSOR	PSEUDOICABILES VICTOS (3) FALS INDIVINS SUST		019.90	100.167					
	CI VIORBOIETH B PRECUTSOR	VARICELLA-20STER VIRUS (STRAEN DUNIAS)								
	CI COMPOTEN C PAECURSOR	HERPES SINDLEX VIRUS (TVPE I / STRAIN I !)		1		-				
PVGIC HSVIK	TOY WILLIAM TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO	IERPES SINDLEX VIRUS ITYPE I / STRAIN KOS)				 - -	\ \-			L
- EX	CLYCOTHOLEIA CHARCON	IN LATES SUPLEX VIRUS (TYPE 2)	2			\ \-	1	+		L
ואפור אנו	CLYCOPHUIEIR CYALUTION	HEADES SUPLEX YIAUS (TYPE 27 STAKIN 111)	=			-	1	+		Ļ
PICIC HISMBC	GLYCOPROTEIN C PALCURSON	BOVING IERPESVINUS TYPE I (STRAIN COOPER)				1	1	1	_	+
PVGLC HISVEB	GLYCOPROTEIN GIII PRECURNA	ROUNS IS REES VIRUS TYPE I (STRAIN ABIP) AND (STRAIN KEN	113-311					1		1
PULC HING	GLYCOPAGIETH C PRECURSOR	-					1	_	_	\downarrow
PVGLC 115MD	SECRETORY GLYCOPADTEIN GP31-63 PRECURSON	_	6)-93				_	1		4
DIAM DIE	SECRETORY CLYCOPROTEIN CP37-65 PRECURSOR		10.13	L	_					4

PC: NE	ALLMORIS	All Viruses fra batteriaphopes								
III. EAVE	RITION	VAL	CHES.	ARTAL	AKEN	SEE.	AREAS	AREAS	AREAT	AREA
PVGLC PRVIF	SECRETURY CLYCOPROTEIN GP17 61 PRICURSOR	MAREK'S DISEASE MERPLISY IRUS (STR. VI.) AIDS)							Π	
2000	CL YCOTAGIEN GIII PM CCR50A	PSELDORALIES VIAUS (STA 41N INDIANA-FUNNITAUSER / BECKE	==							
PVGLD IISVEA	STATE OF STA	VARICELLA 2 OCTRE VIRES (STATES)							1	
	CLYCOPROTEIN DPRECLESOR	FOUNT IN PRESENTATION OF LICENSIN ALLE								
L	GLYCUPROTEIN D PRECURSOR	FOUNT HERPESYTRUS TYPE LESTERAL ABAPT AND STRAIN HEN	_							
ĺ	GLYCOPROTEIN D PRICERSOR	EQUINE HERDESVIRUS TYPE LISTRAIN KENTUCKY AL								
l	CA VCCPROTEIN E PRECURSOR	HEADES SIMPLEX VINUS (17PL 1/51RAIN 17)	11.13							
PVCH PRSVA		HERPES SIMPLEY VIRUS (TYPE 2)								
١,	SUR	BOVINE RESPIRATORY SYNCY HAL VIRUS (STRAIN AS1908)	-	504-545						
PICAT BASIT		BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENIAGE		.67.302	506.547					
0/07 17/4		POVINE RESMEATORY SYNCYTIAL VIRES STRAIN BROSE		191.191	100					
PICH HASVI	PUSIUN GLYCOPROTEN PRECLASOR	CANINE DISTENDER VIRUS (STRAIN ONDERSTEROORT)		1100						
PICH INSVA		HUNIAN RESPIRATORY SYNCYTIAL VIRIS (SUBCROLP BY CIRAL	9	101.101			1			
Mar ium		INIAN RESPIRATORY SYNCYTIAL CIRIS (CIRAL) AS		101	200					
Print Have		HUNIAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP AVSTRA)		141.103	104.403					
		HUNIAN RESPIRATORY SYNCYTIAL VIRUS ISTRAIN BES. 21		100	200					
PICAL MEASI	PUSION CLYCOPROTEIN PRECURSOR	MEASUES VIRUS (STRAIN FONOASTON) AND (STRAIN 1/4 + F)		200	200.000					
Picar Surasy		ALEASLES VIRUS (STRAIN IP.) CA)		1	101.101					
-		MEASIFS VIRUS (STRAIN YANIAGATA-I)	19:11	220.269	13.500					
PACIF ARIABAI		FUNITS VINUS (STRAIN SOL.1)	20.54	01.170	116.311	417.507				
PVIN F NICKPR		IURIPS VIRUS (STRAIN MITTAINAN VACCINE)	20.54	ī						
PLUIT PRINTS	ON GL YCOPROTEIN PRECURSOR	AITAIPS VIRUS (STRAIN RW)	20.00	T		706.100			Ì	
7.127 KOVA		MUNDS VIRUS (STRAIN SOL)	3	Ī			1			Ì
PLILE NOVE		ASTRAIN ATISTRALIA.VICTORIA/12		Ī		200				
מונים איניונו				Ī	776.111		1		Ì	
PICE NOW!		EWCASTLE DISEASE VIRUS (STRAIN HER/1))	1.1	Ī	77.	1				
PVCLF NOVI		MEWCASTLE DISEASE VIRUS (STRAIN DI-HITCHINERAT)	2	Ī	26.51		İ		1	
P. C.L. NOV.			2	Ī	200.00		Ì	Ì		
PI GLF, NOVA			T	T		İ		İ		
			T	Ι	426.513		Ì		İ	
		MEWCASTLE DISEASE VIRUS (STRAIN QUEENSLANDOS)	T	T	43.513	İ	T			
MOVIG			Ī	T	476-517		Ì	1		
2/0	PUSION CLYCOPROTEIN PRECURSOR	/48)	Ī	T	115-313	T	İ	Ī	İ	
2		S (STRAIN ULSTERN)	132-163	211:311	436-512					
L L L L L L L L L L L L L L L L L L L			19-61			118:00				
TACE PLAN		(STRAIN CIP)			459-503					
PYCLE PINET	STREET OF VONE OF PACCASOR	INMAN FALAINFLUENZA 2 VIRUS	Ī	417-528						
PVGLT PILB			Ī	477.538						
PVGLF PINE										
PYCAL RINDK		30007 1100 700 0130	Ī	Ī	-					
PVCAL BINDL			Ī	Ī	216-232					
NG4 SENDS			Ī	Ī	46.49					
PVG F SENDE	STATE OF THE PROPERTY OF THE P	1000	Ī	Ī	48.306					
PV CL F SENDAI			Ī	T	3					
		110		ī	60-33	7	1	1		
		150	Ī	Ī	65.533					
		SENDAL VIRUS (SIRAIN HAI)	-	٦	19:53					
.,.				T	463-333					
.1-			Т	106-201						
<u>``ı :=</u>		TURKEY RIENOTRACIOLITIS VIBILS		Ţ	20.00	1	1	1		
1			7	7			1	1	1	7

İ					0.210	. 270			
TIKE ST.			206-612	Γ					
1	SPIRE GLYCOPROTEIN PRECURSOR		Ī	104-131					
i	CANA CIRCACE CLYCOPROTEIN G		Ī					-	
1	S NI SI CILICATO S S S S S S S S S S S S S S S S S S S	2							
	CALCAST CONTRACT OF THE PROPERTY OF THE PROPER	RESPIRATORY SYNCYTIAL VIRUS ISTRAIN RSBOTT							
ı	CONTRACTOR CONTRACTOR	Ĭ							
VGLG HESV	S NEW CORPORT OF THE PROPERTY	ILLIAN RESPIRATORY SYNCYTIAL VIRUS ISTRAIN REBILLY	100	-					
- 1	MAJOR SURFACE OF TOO POST OF THE POST OF T	١	2				1		
	NIAION SURFACE CLYCOROICIA		10 01						
	NIAIOR SURFACE GLYCOPROTEING	Γ	19:00						
	NIATOR SURFACE CLYCOPROTEING	INTERIOR STATE VIEW CONTRACTOR BY STRAIN	10.01						
P. C. C. IRSVA	MIAJOR SURFACE CLYCUTADIEIN G	_	190						
	MIAKUR SURFACE GLYCHIPROTEIN G	-							
	ALA ICIA SLIKE ACE CIL YCOPROTEIN G	HUNIAN RESPIRATORY SYNCYTIAL VIRUS INDIRACOUT A . 3 . A.							
	TO SELECT TO SEL	-							
VCI C SIGNA	CLY CAROLEIN O'NELCONO	_	14.31	167.731		Ī			
	SPIKE GLYCOPHOTEIN PRECURSOR	LOW MET VIRITE	11.523						
	SPIKE GLYCOFROTEIN PRECURSOR	TANA CIRTIS (STRAIN 07.71)	163.197						
	SPIKE GLYCOPROTEIN PRECURSOR	7	28.510						
1	COIKE GLYCOPROTEIN PRECURSOR	The second secon		101.05	114.180	651-694			
	CI VENDE OFFIN GPIS PRECURSOR				76.107				
١.									
PUGLIH HICKING	CLTCOTROLEIN II TRECOTROL		97:116	697-160					
VOLTH MSVII	GLYCUPROTEIN II PRECIONATE		147.411						
PVGLII HISVIE	GLYCOPROTEIN IF THE LURSON	_	187-481						
PVGLII IISV6G	GLYCOPROTEIN II PRECURSOR		191.406						
V.CLII IISVBC	GLYCOPROTEIN H PRECIMSOR	1	919-94						
NOTH IIS VE	GLYCOPROTEIN H PRECUPSOR		14.179	416.655					
PVCLII HSVED	CL YCOPROTEIN H PRECURSOR	AKINIKOI ATE HV	Ī	407-448					
PVC4 II IISVSA	GLYCOPACIETY II PRECUTSOR		7	134.453	664.712				
SALCO IN MICHAE	GLYCOPROTEIN IN PRECURSOR								
VC2 II PRVKA	GLYCOPROTEIN H PRECURSOR		076.360						
PVGL II PRVNJ	GLYCOPROTEIN H PRECURSOR		34.366						
VCI II PRVIII	GL YCOPROTEIN II PRECURSOR		97.76						
565	CI VCOPROTEIN H PRECURSOR								L
200	PROPARI E CLYCOPROTERY M PRECURSOR		20.00						
VOL. 1101	IN SERIATE EARLY GLYCOPROTEIN PAECURSOR	US (STRAIN AD169)	Ī	111-114					
PVCLNI BURGE	N. BOL VEROTE N. PRETLINSOR		П	613-737	7971-977				
200	N. BOL VABOLETA PRECIESOR	\TE L74)	20.00	916-930					
VGLPI BLANSII	The state of the s		3						L
ACCES BOOM	CO COLUMN SECULO	BUNYANWERA VIRUS	340.374	204-363	40.00				ļ
VGLM DUGBV	N COLUMN TO SECOND TO SECO	DUCAE VIRUS	111.919	1239-1300					1
VCLN HANTB	NI POL TROIEIN PRECORSON	US (STACIN B-1)	693-727						
PVGLM SIANTH	IN POLITICAL STATE OF	(6	12.106						
PVCLNI HAMIL	A TOLITACIENT PACCONSOL		13.106						1
PVGLM HANTV	A TOLITHOLEM TRECONDO	6	- 10 - 10						-
PVCI N INSV	N TOLITECHEN TRECONDE	IMPATIENS MECROTIC SPOT VIRUS	1067-1101						1
PVGLM PHV	M FOL TEROIEM FACTORSON		1:1					-	
PVGLM PIPV	M FOL VERGIEIN FACTORSON	VIRUS	149-151						
PVGLM SEOUS	M FOLVEROIEIN FACCINASON		111-111						1
PVCLM SEOUR	N POLYFROIEIN PRECUASOR		694.726						
PVGI.NI SEOUS	N POLYMOIEIN PRECORSOR	SFOUR VIRUS (STRAIN SR-11)	693-330						1
PVGLY BEFV	IN POLITICAL PROCESSOR		11711	<u>\$</u>					1
PVGLP BEV	MONSTRUCTIONAL DESCURSOR		=	20.00	622-656	1178-1730			1
PVGLX PRVI	TELLUNEA CLICA ROLLING	PSEUDORABIES VIRUS (STRAIN NCE)	130-461						

PCGENE	TALLAIDTIS	All Viruses (ne bacteriaphages)								
TILE MANIE	PROTEIN.	YIRUS	AREA	AREAJ	AREAD	AREA	ARCA S	ARFAG	ARFA?	ABFAE
PVGLY LASSI	GLYCOPROTEIN POLYPROTEIN PRECURSOR	LASSA VIRUS (STRAIN GA191)	317.360	11733			Т			
PVGLY LYCVA	GLYCOPROTEIN POLYPRUIEIN PRECURSOR	LASSA VIRUS (STRAIN JOSIAH)	18:36	319-423						
PVGLY LYCVW	GLYCUPAGIEIN POLYPROFEIN PRECURSOR	LYAPIIOCYTIC CHONOLIEMINGITIS VIRUS (STRAIN ARXISTRON	13:31	195-412					-	
PVGI.Y AIOPEI	GLYCOPROTEIN POLYPROTEIN PRECURSOR	LYRCHIOCYTIC CHORIOMENINGITIS VIRUS (STRAIN WE)	136-156	131.367	117-11					
PVGLY PIARV	GLYCOPROTEIN POLYPROTEIN PRECURSOR	AIOPEIA VIRUS	116-359							
PVGLY TACV	GLYCOPAGIEIN POLYPROTEIN PRECUASOR	PICHINDE ARENAVIRUS	316-375							
TOTAL PLAN	OLICOPROJEIN POLITROJEN PRECINSOR	IALAUBE VIRUS	313-363							
NOT ACK	GLYCOTROLEIM FOLVFROIEIN PRECURSOR	TACAMBE VIRUS (STRAIN VS)	101-151	382-416						
PIGLY TACVI	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACAUSE VIRUS (STRAIN V?)	302-150	381-418						
A CINB CPAIV	GLYCOPROTEIN FOLVPROTEIN PRECURSOR	TACAUBE VIRUS (STRAIN TRVL, 11990)	303-351	167-416						
A CENT	GENOME POLYTROTEIN II	COWPEA MOSAIC VIRUS	135-869							
TCHAI CPSAIV	GENORIE POLYPROTEIN AI	COWPEA MOSAIC VIRUS	160-301							
-VENT REALV		COWPER SEVERE MOSAIC VIRUS (STRAIN DG)	192-226	158-792	874.915					
PVGPI COV	GENOMIE POLYPROTEIN M	RED CLOVER MOTTLE VIRUS	123.431	913-946						
PVGP EBOV	PROBABLE MEMBRANE ANTIGEN GP19	EPSTEIN-BARA VIXUS (STRAIN B95-1)	94-149							
PYGP MABYAI	STRUCTURAL GLYCOPROTEIN PRECURSOR		260-328	134.368	469.303					
PVGP MABVP	STRUCTURAL GLYCOPROTEIN PRECURSOR	KE)	343.596							
PV1102 VACCC	STRUCTURAL (12 YCOPROTEIN PRECURSOR		\$62.596							
PVINJ VACCV	LATE PROTEIN HIS	VACCIMIA VIRUS (STRAIN COPENIIAGEN)	58-92							
PVIIO3 VARV	LATE PROTEINIUS	VACCINIA VIRUS (STRAIN WR)	58.94							
PVIIDS VACCC	LATE PROTEINIT	VARIOLA VIRIJS	58-92							
PV1105 VACCV	PROTEINITS	VACCINIA VIRUS (STRAIN COPENIAGEN)	111.183							
PUINS VARV	PROIEINIII	VACCINIA VIRUS (STRAIN WR)	11:113							
PVIIEL LSV	PROTEINHS	VAUOLA VIRUS	136-203							
PUINT VACCO	PROBABLE HELICASE	LILY SYND TONGLESS VIRUS	126-160					Ī		
PUIN VACEV	HOST RANGE PROTEIN	VACCIMIA VIRUS (STRAIN COPENHAGEN)	316-379							
PVIO) VACCC	HOST RANGE PROTEIN	VACCINIA VIRUS (STRAIN WR)	316.379							
PVI01 VACCV	PROJECT	VACCINIA VIRUS (STRAIN COPENHAGEN)	Ī	110.344					T	
PVIO) VARV	PROTEIN 13	VACCINIA VIRUS (STRAIN WR)	120.00	210-244						
PVIDE VACCV	PROJECTI	VANOLA VIRUS	30-193	210.344			 	Ī		
PVIOS VARV	PROTEINIG	VACCINIA VIRUS (STRAIN WR)	16:11			Ī		Ì	Ť	Ī
PVIOT VARV	PROJEIN 16	VARIOLA VIRUS	26.81					Ī		1
PVI08 VACCC	PROTEIN 17	VARIOLA VIRUS	133-401				İ			
PVIOR VACEV	PUTATIVE ANA IELICASE II	EMIAGEM	4.580					T	T	Ī
PVIOL VARV	PUTATIVE RNA IGENCASE IS	S (STRAIN WR)	516-519	Ī						Ī
PVIET INCMVA	PUTATIVE ANA IELICASE II		41.519				İ	İ		
rviet inchivi	SAD INDICIDIATE EARLY PROTEIN		78.113	Ĩ	168-402	95791		İ		
PVIET MOVING	MARKETAL EAST VOICE		=	20,20	161-402	416-450				
POTEN MENAC	MACCINETE FARE V PROTEIN IF 1									
PVIF CAFVC	NAMEDIATE SARY A REGISTANCE OF TENERS	ALTOCA APHA CALIFORNICA MULTILARSIO POL TIEDROSIS VIKUS		200						
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PVIF FIVSD	VIRION INFECTIVITY FACTOR	T		1				1		
PVIF IIVIAZ	VILION IN ECTIVITY FACTOR	T	1	Ì				1	1	
PVIF HVIBI	VINION BY ECTIVITY FACTOR	Ė	Ī	12	1					
PVIF HVIBS	VIAJON INTECTIVITY FACTOR					1	\dagger	1	1	
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PVIF IIVIA	VIXION INFECTIVITY PACTOR	Ī	Ī	2 3		T	\dagger	\dagger	T	
PVIF HVING	VIRION INTECTIVITY FACTOR		Γ	95.19		T	T			1
PVIF IIVINN	VILION INFECTIVITY FACTOR		3.6							
PVIF HVINS	VILLON INFECTIVITY FACTOR		1-43	61.96					İ	
PVIF IIVINA	VILION INFECTIVITY FACTOR	HUMAN INDITINODEFICIENCY VIRUS TYPE I (NEW YORK-5 ISOL 1	2	94-29						T

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PYTIGI VACET: LEG PROTEIN TIPULA INDESCENT VIRUS			٦		1]	

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FROTEINNI	VACCINA VIETE (S) & AIM CONTINUES CONT	4	ANGAL	4866	A SEE	MEAS	OREA	4864	OREAL
R VIRION STRUCTURAL PROTEIN PIU. 2	REOVINGS 177E 1 STRAIN LANG	200							
R VIRION STRUCTURAL PROTEIN MIU-IA	U.IC REOVINUS (1 YPE 1 / SIRAIN DEABING)		410 643						
N VIRION STRUCTURAL PROTEIN NIU-IA	U.IC REOVINUS (TYPE 1/ STRAIN DEADING)								
VIRION STRUCTURAL PROTEIN MULIA	U-ICAEOVIAUS (TYPE 2 / STRAIN DIJIONES)	99	1						
R VIRION STRUCTURAL PROTEIN NIU-IAI	U-IC REDVINUS (TYPE 1 / STRAIN LANG)	25	618.662						
MAJOR HONSTRUCTURAL PROTEIN AND NS	REOVINUS (TYPE 1/STRAIN DEARING)	3.18	15.5	28.03	618.490				
MATRIX GLYCOPROTEIN MIS	BOVINE RESPIRATORY SYNCYTIAL YIRUS (STRAIN AS1906)	8:5							
MATRIX GLYCOPROTEIN MIT	HUBIAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	8							
MATRIX GLYCOPROTEIN MI	TURKEY MIINDIRACHETTIS VIRUS	5.30							
HATRIX PROTEIN	CAMINE DISTRAIPER VIRUS (STRAIN DNDCRSTEPOORT)	3.3							
NIAIRIX (NI) PROTEIN	INFLUENZA C VIRUS (STRAIN CIIDSO)	_	131.201						
NIATRIX PROTEIN	NEW CASTLE DISEASE VIRUS (STRAIN AUSTRALLY, VICTORILATION	•							
X PROJECT	NEW CASTLE DISEASE VIRUS (STRAIN BEAUDETTE, CAS)								
MATRIX PROTEIN	BOVINE PARAMYLUENZA J VIRUS	=	204.353						
MATRIX PROTEIN	PIUNIAM PARAINTLUENZA 3 VIRUS (STRAIN KINI 47815)	=	30						
X PROTEIN	RADIES VIRUS (STRAIN AVOI)								
MATRIX PROTEIN	RADIES VIRUS (STRAIN CVS.11)	9							
MAIRIX PROTEIL	RABIES VIRUS (STRAIN ERA)	101							
IX PROTEIN	AABIES VIRUS (STRAIN MISHIGANIARA RCEIN	9							
MAIRIX PROTEIN	RADIES VIRUS (STRAIN PV.)	9							
MAIRIX PROIEIS	RABIES VIRUS (STRAIN SAD BIN)	69.103							
MATRIX PROTEIN	SONCINUS VELLOW NET VIRUS	14.30		-					
NATRIX PROTEIN	VESICULAR STONIATITIS VIRUS ISCAULY IE INDIANA / STRAIN								
COPROTEIN	BONINE CORONAVIRUS (STRAIN KIEBUS)		-						
EI GR YCOFROIEIN PRECI. RSOR	PORCINE TRANSMISSIBLE GASTAGENTERUTIS CORONAVIRUS (S		112.337						
COPROTELY PRECERSOR		113-131							
COPROTEIN PRECURSOR	PORCINE RESPIRATORY CORONAVIRUS (STRAIN RVII)	111.137				Ī		Ì	
COFROILS		18-42	175.200					Ī	
EI GLICOPROTEIN PRECURSOR	146)	111.157							
COPROTEIN	AVIAN INTECTIOUS BRONCHITIS VIRUS ISTRAIN 6/12)	1.33	117-2118						
E CE YCOPROTEIN		2:3 2:3	177.318			1			
COPROTEIN	AVIAN IN ECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE AL	======================================	111:311						
EI GLYCOFROIEIN	AVIAN INTECTIOUS BRONCHITIS VIRUS (STRAIN KB0523)	131.211							
PROBLE NEXIBRANE PROTEIN	EPSTEIN BARR VIRUS (STRAM 845-1)	16.74					Ī	Ì	
NOT MENT PROTEIN	CALLITOWER MOSAIC VIRUS (STRAIN CH. 1841)	10.334	230.324					İ	
ANOVENIENT PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN DAI)	187.234	170.134						
NOVI NEW PROJECT	CAULITOWER MOSAIC VIRUS (STRAIN BDC)	181-334	370.324					İ	
ENTPROTEIN		187-25¢	130.134						
ANOVEMENT PROTEIN		117-254	170-314						
STATE OF STA	1.A.IN W.760)	ž	270.124				-		
	CAUNATION ETCHED RING VIRUS	2							
NOTE AND THE PROPERTY.		2							
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MAKEN ALBEATE ANTICEN PRETINGO			134.361						
TOTAL MACIENT STATES	New Heavening a vision of the Collect		27.750						
MANOR SURFACE AND COMPANY OF THE COM		2	10-121						
PIANOR SULFACE APPLICENT PRECURSOR		33:31	114.361						
SUM ALE AMILIER PRECURSOR	TIS VIAUS	20.24						İ	
NAME OF SURFACE ANTIGEN PRECURSOR		294-328							
MANOR SIMEACE ANTICEN PRECINCOL	WOOLHOLK HETAINS VIRUS !	206-303						- 	
SOM ACE ACHIEF NAME CORSON									

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נונגאאנ	LEOJI C.	CHUCK HEPATITIS VIRUS 7	2		-					
INISA WHYBI	MAJOR SURJACE ANTIGEN PAECURSON	I (IN ECTIOUS CLONE)	11:13							
VALLE DIVI	PROBABLE MAJOR SULVACE AN HOLY PRECONSON		101.335						-	
PINITI IANN	MATRIX PROFFIN			13.23						
VAUL LANAN	MATRIX (NI) PROTI IN			= =	1					
PV11111CAO	MAINIX (NII) PROTEIN	INTEREST A VIEUS (SIRAIN ACAMILANONGOLIANS)	į							
1411 1411W	NATRIX (MI) PROTITIO			≅ ≅						
111111111111111111111111111111111111111	VIA JEIN (NII) PROTEIN		91.136	25.22						
VIIII FULL	NATRIX (NII) PROTEIN	MET HE NEA A VIRUS (SIRAIN ANOWL PLAGUE VIRUSAVEVIRUS		75.33						
VMII INI EI	MATRIX (MI) PROILIN		93.134	174-111						
	MATRIX (MI) PROTEIN	=	47:116	134-222						
TANK INA	VIATRIX (NI) PROTEIN	1875078)	!	14-212						
1.411 IVEK	MAIRIX (MII) PROTEIN	1	97-176	3.5						
VIII 100E	VIATRIX (Sti) PROTEIN		93:136	14-212						
2017 1100	MAIPIX (MII) PROTEIN		97.136	35.22						
PASTE TAME	VIATRIX (NII) PROTEIN	AND AND CALIFORN	97-136	14.22 14.22						
1271	NIA TRIX (ALL) PROJECTS		36.00	134.323						
PV VIII INDAC	MATRIX (MI) PROTEIN		300							
QVEN I	NATALX (NII) PROTEIN		36.300							
107	MATRIX MILITAGER	account to the second								
	ALA TRIX INIII PROTEIN									
	NI JUNE IN THE PROPERTY OF THE	INFLUENZA B VIRUS (STRAIN BISINGAPORE/12/19)	607-60					L		
	PROPERTY AND PROPERTY	INTERENTA B VIRUS (STRAIN BYANN AUBORUMS COLD ADAPTE								
	PROBABLE ALATRIX (PLI) PROTEIN	BOWING IWILD-LTPEII								
NAME OF THE PARTY	PROPERTY CALLY CALLY PROTEIN	INTLUENZA D VIRUS (STRAIN B.LED40)								
150 N. 15	PROBLES MATRIX (NI) PROTEIN	PORECIUM				-				
2000	V. 10 PLOTEIN									L
A JUNE A PORT	PROTEIN	ENIAGEN)								
38108	PROTEIVE									
2010	KONSTRUCTURAL PROTEIN MS 14			131.160						
LAVE VAN	NOWSTRUCTURAL PROTEIN NS14	C/STRAIN COWOLN								
N. 73.	DNA REPLICATION PROTEIN	D VIRUS 2						L		
DEVAY PAYED	NIAJOR MONCAPSID PROTEIN	NCE STRIPE VIRUS								
PVYCS ADVG	PROBABLE MONCAPSID PROTEIN MP.	BOVINE PARVOVIRUS		170.104			L			
PANCS AEDEV	HONCAPSID PROTEIN MS-1	16	176.110	21.52	98.640	113.760	110.649			
PVNCS (PVI)	MOMCAPSID PROTEIN NS-1		-							
PLYCS MEVA	MONT APSID PROTEIN NS.1	FELINE PANCEUROPENIA VINOS (STANIA VINOS)	-							
PVNTS AILMAN	MONCAPSID PROTEIN MS-1	MINK ENICKLIS VINOS (STRAIN AUTOMATIC	19.	100						
PVNCS MUMITY	NOWCAPSID PROTEIN MS-1	AIURINE BINGLE VIROS (STRAIN BY PRI)	=	198.101						
PVNCS PAVBO	MONCAPSID PROTEIN MS-1	MINIOUNE PRINCIPLE	181.323							
PVNCS PAVON	PROBABLE NONCAPSID PROTEIN NSI	SOCIONAL SANCOCION	21.01							
PUNCS PAVIOR	WONCAPSID PROTEIN NS-1	HIGHAN PARCOVIRUS BIP	116-170							
PVMCS PAVIOL	NONCA SID FROID IN NO.	HAAISTER PARVOVIAUS III	13.76	159.297						1
PVNCS PAVPN	MONCAPSIO PROTEIN NS.	PORCINE PARVOVIAUS (STRAIN NADL-1)	34.33	169.210	3	-				1
PVKS BIVID	MONE THE PROPERTY NO.	BLUETOMGUE YIAUS (SEROTYPE 107 ISOLATE USA)	103-14			1				1
	LONGIE LEGIEN PROTEIN NS	BLUETONGUE VIAUS (SEROTYPE 17/150LATE USA)	101.10							<u> </u>
	MONSTRUCTURAL PROTEIN NS!	BLUE TONGUE VIAUS (SEAOTYPE I / ISOLATE AUSTRALIA)	2							
100	NOMS I RUCTURAL PROTEIN MS I	BLUETONGUE VINUS (SEROTYPE I / ISOLATE SOUTH AJ INCA)			1	+				
200	HOMS I RUCTURAL PROTEIN MS!	BLUETOMOUE VIRUS (SEROTYPE 19/150LATE AUSTRALIA)			1					
NAM.	NONSTRUCTURAL PROTEIN HS!	EPIZOOTIC IEMONUAGIC DISEASE VIAUS (SEKULTIFE ZI SIINA			1					L
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VIRUS INTLUENTA A VIRUS ISTRAIN ACTICKENGERATANY NAME	INTLUENZA A VIRUS (SIRAIN ACHICKEWIAPAW24)	INTLUENZA A VIRUS (SIRAIN ADUCKVALBERTANSOTA)	INT. UENZA A VIRUS (STRAIN ADUCK/ENGLAMD/1/34)	METUCASA VIXUS (STRAIN ADUCKARRAINE/IN)	INTERNAL VINESTATION AND STATE OF THE STATE	INTUENZA A VIRUS (STRAIN AGONT PLACIFIC VIRTIE PROFICE	INTLUENZA A VIRUS (STRAIN AA ENINCIACY 1247)	INFLUENZA A VIRUS (STRAIN AA ENINGRADISMI)	INTLUENZA A VIRUS (STRAIN AALALLARDVAL BERTANSCIS	INTLUENZA A VIRUS (STRAIN ARIALLARDINEW YORKATSOTE)	INTLUENZA A VIRUS (STRAIN ARIALLARDAEW YORKAITANS	INTLUENZA A VIRUS (STRAIN ANIYNAUMANEDA-TITAU)	INTLUENZA A VIRUS (STRAIN APINTALUAL BEATAITION	INTERESTATIONS (STRAIN APINTALLAL BERTALLING)	INCHES A COURTER AND AND AND AND AND AND AND AND AND AND	INTLIENZA A CIRIO GIRAN AGIRDIO DICORDA	INTUENZA A VIAUS (STRAIN ACTIONS VARITIES BIRCH CLINING)	INTLUENZA A VIRUS ISTRAIN ACTURKE Y/CANADAMI	INTLUENZA A VIRUS (STRAIN ATTURKE Y/ORF GOWILL	INTLUENZA A VIRUS (STRAIN ATERWSOUTH AFRICASH	INTLUENZA A VIRUS (STRAIN ATERNATURX MENIALIST)	MILLENZA A VIAUS (STRAIN ASWINEADWAIS)	INFLUENZA B VIRUS (STRAIN BIANN ARDONING (COLD. ADAPT	INTLUENZA B VIRUS (STRAIN B/GA/16)	HAT LUENZA B VIAUS (STRAIN BAIONG KONGWIY), AND (STRAIN	MELITERZA B VINUS (STRAIN BRITAL)	DELLENZA B VIRUS (STRAIN BA ERIAN	INTLUENZA B VIRUS (STRAIN BAIARYI ANDVIO)	INFLUENZA B VIRUS (STRAIN BPA/79)	INSTURNZA B VIXIUS (STRAIN BALVIER)	INGLUENZA B VIRUS (STRAIN BASINGAPORE/112/19)	IN LUENZA B VIRUS (STRAIN BASINGAPOREMA)	INTELLEGIZA B VIRUS (STRAIN BANCTORIAN)	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 6)	BLUETONGUE VIRUS (SEROTYPE 17/15OLATE USA)	BLUETONGUE VIRUS (SEROTYPE 10)	AIURUNE CORONAVIRUS ABIV (STRAIN DRI)	PALLICATION OF THE STREET OF T	INTERPRETATION AND STRAIN ALLASKANTI, AND STRAIN AL	PRELIENZA A VRUS (STRAIN AVANNA ARROGAMA) AND COTA	INTLUENZA A VIRUS (STRAIN ACTUR PAINT)	INTLUENZA A VIRUS ISTRAIN ACTITICA PAGEBALANY ALABO	INT. L'ENZA A VIRUS (STRAIN ACHICKENIJAPANZA)	INTLUENZA A VIRUS (STRAIN ADUCKVAL BERTAKONS)	PIFLUENZA A VURUS (STRAM ANDUCKJENGLANDVINS)	PRICENTA A VIBILE COTTACT A CALCULATE AND COLOR
NONSTRUCTURAL PROTETN MS!	NONSTRUCTURAL PROTEIN NS	MONSTRUCTURAL PROTEIN NS	MONESHIEF THAT PROTECT AS	NONSTRUCTURAL PROTEIN NO	NONSTRUCTURAL PROTEIN NST	NONSTRUCTURAL PROTEIN NS!	MONSTRUCTURAL PROTEIN NSI	MONSTRUCTURAL PROTEIN NSI	MONSTRUCTURAL PROTEIN NSI	HONSTRUCTURAL PROTEININS!	NONSTRUCTURAL PROTECTIVES	NONSTRUCTURAL PROTEIN NSI	MONTH OF A PROPERTY AND A PROPERTY OF THE PROP	NONSTRUCTURAL PROTEIN NO	NONSTRUCTURAL PROTEIN NST	NOWSTRUCTURAL PROTEIN NSI	HONSINGCIURAL PROTEIN NSI	NONSTRUCTURAL PROTEIN HS!	HONS IRUCTURAL PROTEIN NSI	MONSTRUCTURAL PROTEIN NS	NONSTRUCTURAL PROTEIN NSI	MONSTRUCTURAL PROTEIN HS!	MONS A UCTURAL PROTEIN WS	MONSTELL TITLE AT PROTECT MS	NONSIERCE LEAL PROJECT NE	NONSTRUCTURAL PROTEIN NS	MONSTRUCTURAL PROTEIN MS!	MONSIAUCTURAL PROTEIN HSI	MONSTRUCTURAL PROTEIN NS	MONSTRUCTURAL PROTEIN MS!	MONSTELL THAT PROTEIN WE	NONSTREET IN PROTECT WE	MONSTRUCTURAL PROTEIN NSI	NONSTRUCTURAL PROTEIN NSS	NONSTRUCTURAL PROTEIN NS2	HONSTRUCTURAL PROTEIN NS	MONETHING IN ALL PROTEIN UST	NONSTRUCTURAL PROTEIN NO	HONSTRUCTURAL PROTEIN HSZ	HOWSTAUCTURAL PROTEIN MS2	HONSTRUCTURAL PROTEIN HS2	NOWSTRUCTURAL PROTEIN NS.	HONSTRUCTURAL PROTEIN HS1	NONSTRUCTURAL PROTEIN NS2	MONSTRUCTURAL PROTEIN NS2	HONSTRUCTURAL PROTEIN MS2
1	TANK TANK	PANEL LANGE	PVNSI IAFON	PVNSI 1410W	PVNSI LIFFE	PVNSI JALEI	PVHSI IALEN	PVNSI JANIA6	PVIVSI TANTAN	71.51 14AAO	PVNSI IAAIYN	17.00	1	5	PANSI JAPUE	PVSSI IATEB	PYNSI IAIKC	AIKR	IATRS			PVNSI INBAC	1		ļ	Ī				SEA SEA	Ī		Ī		Ī	TANKS CANCIN	Ī	Ī	Ī	Ī	PVNS1 IACKG					PVNS3 IAFOM

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NONSTRUCTUAL FOOLEN NST NOLURIAL A VIRUS STAND ALVESTAMENT 14.1	NS2 IATRS	MONSTHOCK INC.	THE LIENZA A VIRUS (STRAIN ATERNSOUTH AFRICANT)	2			1	+			
POST STATE CLUAL FOLEN NST POTENT NST STATES ST	NS1 IAUSS	HOMSTRUCTURAL PROTEIN MAS		(6.9)				1			
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ORDISTRICTIONAL PROTEIN NO. ORGINICATION NO. ORGINICATIONAL PROTEIN	NS2 PABYA	HONSTRUCTURAL PROTEIN MS2	11,11			-					
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MONSTRUCTURAL PROTEIN FELNE ENTERC CORDONAVRUS (STRAIN PR-166) 1-4 MONSTRUCTURAL PROTEIN FELNE ENTERC CORDONAVRUS (STRAIN PR-166) 1-4 MONSTRUCTURAL PROTEIN FELNE ENTERCHOUS PRATIONITIS VRUS (STRAIN PR-166) 1-4 MONSTRUCTURAL PROTEIN FELNE INDIVIDUAL PROTEIN FELNE INDI	/NS) CVCAE	NONSTRUCTURAL PROTEIN MS		7							
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MONSTRUCTURAL PROTEIN C	ANST FIPV	MONSTRUCTURAL PROTEIN	TO SEE THE COLOR PERILONITIS VIRUS (STRAIN 79-1146)	7							
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NOSS INCCTULAL FROIGN C NEASLES VIRUS GIRANN TALLOS	WSC MEASI	NONS TRUCTURAL PROTEIN C		3							
NONSTRUCTURAL PROTEIN C NICASLES VILLA PARAMETRICERA NICAS GRAIN CESS 111-167	VNSC BIEASY	MONSIAUCTURAL PROTEIN C			<u> </u> 	<u> </u>					
	GILLS LINE	HONSTRUCTURAL PROTEIN C			1						L
HONS INCTUTAL PROTEIN C HUMAN PAKINS LUERA VRUS (STACK C. 97) 13-167	VNSC PINC	HONSTRUCTURAL PROTEIN C	HUNDAN PARAING LUENZA I VIRUS (STRAIN C.13)		<u> </u> 			İ			
INDIAN PALINE LURA VRUS (STANTCHOS) 10-15	911	MONSTRUCTURAL PROTEIN C			<u> </u> 					-	
NONSTRUCTURAL PROTEIN C NUMBER 1 VRUS (STRAIN CL-103) 19-13	11 PE 11 PE	KONSTRUCTURAL PROTEIN C		Ī	<u> </u> :			Ì			
MONSTRUCTURAL PROTEIN C MIDALAN PALAMNILUENZA) VIRUS (STAZIN MILLORIZA) WINDS (STAZIN WINDS (STAZIN MILLORIZA) WINDS (STAZIN WINDS	200	KONSTRUCTURAL PROTETN C	HUNIAM PARAINS LUTHZA I VIRUS (STRAIN CI-1401)	1		<u> </u>					
NOWSTRUCTURAL PROTEIN C SEMBAI VARUS (STAAM AN4) 11-161	A STATE OF THE PERSON NAMED IN	MONSTRUCTURAL PROTEIN C	HUNGAN PALAINTLUENZA 3 VIRUS (STRAIN MILLATORS)	Ī.		+		T			
NONSTRUCTURAL PROTEIN C SEPONT VIRUS ISTAMIN INANSS 111-167	TOTAL SERVICE	KONSTRUCTURAL PROTEIN C	SENDAI VIRUS (STRAIN 474)		1		1				L
NONSTRUCTURAL PROTEIN C SEMBAT VIRUS (STAAN Z) 11-10-10-10-10-10-10-10-10-10-10-10-10-1	1000	NONSTRUCTURAL PROTEIN C	SENDAI VIRUS (STRAÍN HARRIS)		-	1	<u> </u> 				
HOWSTRUCTURAL PROTEIN NS. A HOPATIENS MCROTIC SPOT VINUS (NSS) 1-15 1-1	2000	KONTHUCTURAL PROTEIN C	SENDAI VIRUS (STRAIN Z)	Ī		<u> </u>		$\overline{ }$			
NOWS FRUCTURAL PROTEIN WS. S BUNYAVIRUS CELAUSTON NOWS FRUCTURAL PROTEIN WS. S BUNYAVIRUS LA CROSSE NOWS FRUCTURAL PROTEIN WS. S NACOLALA VIRUS NOWS FRUCTURAL PROTEIN WS. S NACOLALA VIRUS NOWS FRUCTURAL PROTEIN WS. S TOSCANA VIRUS (100) NOWS FRUCTURAL PROTEIN WS. S TOSCANA VIRUS (1	A LAS MILES	NOWCIELTIMAL PROTEIN NS.NI	INDATIENS MECROTIC SPOT VIRUS (INSV.)	Ť	2	1		1			
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HONSTRUCTURAL PROTEIN HS S BUNYAVIRUS LA CROSSE HONSTRUCTURAL PROTEIN HS S KACIAAN VIRUS (FOS) HONSTRUCTURAL PROTEIN HS S TOSCANA VIRUS (FOS) A HONSTRUCTURAL PROTEIN HS S TOSCANA VIRUS (FOS) A HONSTRUCTURAL PROTEIN HS S PSEUDOMARIS VIRUS (STIAM KAPLAN) (PAN) A HONSTRUCTURAL PROTEIN ANTIGEN PROTEIN POLICE (STIAM POLICE)	VNSI BUR	SOLICE TO BE AT PROPER USES	BUNYAVIRUS LA CROSSE (ISOLATE L'14)	=	1	1	1	\dagger			ļ
HONS INCCTUTAL PROTEIN NS STANDARDA VIRUS (EOS) HONS INCCTUTAL PROTEIN NS TOSCANA VIRUS (EOS) A WONS TRUCTUTAL PROTEIN NS STREED VIRUS (OR) A WONS TRUCTUTAL PROTEIN NS STREED VIRUS (STANDARDAN) (PRV) FROM ABLE MUCLEAR ANTIGEN THOSE ABLE MUCLEAR ANTIG	VYST BUNC	NOTICE AND PROPERTY.	BUNY AVIAUS LA CROSSE	1:3	<u> </u> 	1		1			-
CA HOWSTRUCTURAL PROTEIN HS TOSCANA VIRUS (105) NORSTRUCTURAL PROTEIN HS S UNKUNITURI (10K) TOROGABLE MUCLEAR ANTIGEN PROTEIN TOROGABLE VIRUS (STRAIN EAPLAN) (PRV)	VKST BIAGV	S S N N S I COM THE STORY	NAGUAD VINUS	92	1	1		T			
MONSTRUCTURAL PROTEIN HS.5 UGRUNIEM VIRUS (ATRAIN FAMAN) (PRV) PROBABLE MUCLEAR ANTIGEN PROBABLE	VNSI 10SV	SUNTERIOR OF THE PROPERTY OF T	TOSCANA VIRUS (TOS)	=======================================		1	+	Ť			ļ
PROBABLE MUCLEAR ANTIGEN PROBABLE MUCLEAR ANTIGEN PROBABLE MUCLEAR ANTIGEN PROBABLE MUCLEAR ANTIGEN	LNST GOK	TOTAL PROJECT NEWS	UURUNIEMI VIRUS (MAK)	139-173			+	T			
PROBABLE TOUR CONTRACTOR OF THE PROPERTY (STRAIN PROJUCE) (DHO)	NYUA PRVKA	MONSTAN AND SA	PSEUDORABIES YURUS (STIAMY KAPLAN) (PRV)	1134-1175			+	1			1
	יאיאת סוויאי	PROBABLE MOLLEAN ANIMES	INGORI VINITE (STRAIN DOIAN(1)1941) (DHO)	200-243			-				

PCGFNF	TALL BUILDING	All Vieutes (no basteriochans)			-					
FILENANE	PROJEIN	VIRUS	AREAI	AREAT	Π	AREA 4	AREAS	ARTAG	ABEA ?	ABEA
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PVNUC IAANN	NIKCLEOPROTEIN	INFLUENZA A VIRUS ISTRACA AVANAS ACITTAPRINIORIE/681/741	Ī	Ī	157.401		T			
PVNUC IABRA	NUCLEOPROTEIN	INCLUENZA A VIRUS ISTRAIN AVANN ARBORUGEO		53-408			T		1	
PVNUC IABUD	MUCLEOPROTEIN	IMILUENZA A VIRUS (STRAIN ADRAZIL/IIMI)	Ī	157-408					Ī	
PVNUC IACAL	MUCLEOPROTEIN	MPLUENZA A VIRUS (STRAIN A/BUDGENGALNIOKKAIDOVIAT)		86-154	157-406					
PYNUCIACKG	MUCI EOPROTEIN	INFLUENZA A VIRUS (STRAIN ACALIFORNIA/10/11)		12.40						
PVNUC JACKP	MUCLEOPROFEIN	ING LUENZA A VIRUS (STRAIN A/CIIICK EN/GERALANYA/44)		96-154	357-404					
PVNUC JADAU	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ACHICKENTENNSYLVANIA/1/8))	143	96-154	157-406					
PINUC INDBE	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCIVAUSTRALIA/14/10)	6	21.3	337-408					
PYNC IADCZ	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCK/BEIIING/I/TI)		¥-134	137.408					
PVNUC IADEI	MUCLEOPROTEIN	MFLUENZA A VIRUS (STRAIN ADUCK/CZECIIOSLOVAKIA/S)		25.35	960-606					
PVRUC IADES	MICLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKÆNGLANDVIVS)		\$.53	357-406					
PVNIX JADIOK	SECT EOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCK/ENGLAND/182)	3	100	157.408					
PLNUC IADMI	NUCLEOPAGIEIN	INFLUENZA A VIRUS (STRAIN ADUCKATONG KONGAMS)	17:	86-154	337-404					
PVNUC JADAIA	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKAIEMPHIS921/10	~	20.00	357-408					
PUNUC INDIVI	NUCLEOPROFEIN	INFLUENZA A VIRUS (STRAIN ADUCKALANITOBAVISI)	29:1	¥1.8	357-406					
PVNUC IADUZ	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKANEW ZEALAND/11/14)	3	96-134	357.408					
	NICI.EDFROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKAUKRAINE/2060)	36-154	337.408						
	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AENCLANDAINS)	10.1	117.409						
	NUCL EOFROTEIN	MELIENZA A VIRUS (STRAIN AFORT MONNIOUTH/1/17)	7	337.400	İ					Ī
PVNUC IN PD	HUCL EOPROTEIN	INTLUENZA A VIRUS (STRAIN AFORT WARREN/1/50)	337-408							
	MUCIEOPROFEIN	INFLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUS/DOBSON	7	25.58	157-408					
	NUCI EOPROTEIN	INTIUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSROSTOCK	3	96.134	160.401					
l	NUCI EOPROTEIN	INTLUENZA A VIRUS (STRAIN AKREY TEAL/AUSTRALIA/UT9)		13:18	157.401					
	HUCI EOFROTEIN	INFLUENZA A VIAUS (STRAIN A/GLA LAIARYLANDY)	~	337-406			Ī	Ī		
	MUCLEOPROTEIN		26 134	357-400						
	MUCLEOFROTEIN	MILLENZA A VIRUS (STRAIN AGLILLALARYLANDVIDZUTI)	6	1 2 2	157-409					
	MUCLEOPROTEIN	MPLUENZA A VIRUS (STRAIN AGULLAKARYLANDYIIISM9)	-	96-154	157-400				-	
١	NUCLEOFROTEIN	INFLUENZA A YIAUS (SIRAIN AGULL/ASTRAKHANZI7/11)			157-409				-	
PVNUC IAGUN	MOCLEOPROTEIN	INFLUENZA A VIRUS ISTRAIN AGULLAIASSACHUSETTSJØNIO)	-43		137.409					
אוועי אאני	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/GULL/MINNESOTA/MIS/IID)	1.62 / 91	96-154	937-409					
PVNC IAU	MUCLEOPADIEM	MELUENZA A VIRUS ISTRAIN ATUCKOX/40)	-43	157-409						
PWIC INEO	NUCLEOPROTEIN	MELUENZA A VIRUS (STRAIN AEQUINEJILLINVIRS)	-43	96-154	157-408					
PVNUC IAIRI	NUCLEOPROTEIN	MELLENZA A VIRUS (STRAIN AEQUINEALONDONVIGIATI)			137-408					
LANCE IMIDI	MUCLEOPROTERN	DIFLUENZA A VIRUS (STRAIN AEQUINEALIANIVIA))	7	16-154						
PWRUC IAIOS	NOCLEOPROTEIN	PIFLUENZA A VIRUS (STRAIN AARONG KONGUME)		37.400						
TANUC INITE	MULLEUTROILIN	INTUENCA A VIRUS (STRAIN AMUNG RONGYAT)		337.409		1				
PVAIL LAKE	Name of the Party			Ī						
PVNUC 14LEN	MIXTEDPROTEIN	(STRADIACIEVISTO)		200	37-408	1	İ	1	1	
PWNC IMIA	MUCLEOPROTEIN	NFLUENZA A VIRUS (STRAIN ALENINGRAD/S4/1)		137.40	+	1	1	Ì		
PVNUC JAMAN	MUCI EOPROTEIN	INFLUENZA A VIRUS		Ī	137-401		İ	1		Ī
PUNC IAM	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ARIALL ARDINEW YORKS 13071)		Ī	157-404	T		T	1	
PYNUC IANEJ	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AMUNICSWEDENGS)	20.	96.154	157-408			T		
PVNUC_IANT6	MUCLEOPROTEIN	INFLUENZA A VTRUS (STRAIN AMEW TERSEYANS)	43	94-154	157-408					
PVNUC IAOIT	MXLEOPROFEIN	INTLUENZA A VIRUS (STRAIN ANT/60/68)	-43 35	157-409						Ī
PUNUC IAPAR	MUCI EOPROTEIN	NG LIENZA A VIRUS (STRAIN AOHIO/441)						T		
PVNUC IAPUE	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN APAÙROTALSTERTI)		96-154	157-408					
P VACC TARUD	MUCIEOPROTEIN	=:								
PVNUC IASEO	NUCLEOPROTEIN	뼰			157-408					
PVNUC IASHD	MUCLEOPROTEIN	_		П	357-408					
PUNIT IASIN	MICLEOFAGIEIN	INTLUENZA A VINUS (STRAIN ASHEAAWATENAUSTRALIA72)	<u>=</u>	121-408						

4714	A1 NO 73	All Virgini (no bacteriophogni)	П		1964	VREA 4	AREAS	AREA	AREA?	AREAI
THE RANG	PRO)[13		1	80713	1			Γ		
PARIE INTE	NUCLEOPROTEIN	INITUENZA A VIRUS (STRAIN AUSINGAPURE/1197)		11.40	117.404					
PANEL INTEN	NICTEOFROTEIN				100				-	
PUNITE IN IKO	MUCLEOPROIEIN			2	117.401					
PUNIC IAIRS	MIXCLEOPROTEIN				140.404					
PVAILE IATRI	NUCLEOPROTEIN				113.403					
PV-NUC IATX7	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ATERIATURANEMIATOR		153.400						
	NUCL EOPROTEIN	INTELLENZA A VINUS (STRAIM ALEAANIM)		11.400						
PVMUC IAUSS	NUCLEOPROTEIN	INTI LENZA A VIRUS (STRAIN AUDUMASOVI)	1	10773						
PUNIC IAVI6	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AUSSIVACIT)	107.5							
PVNUC IAWIR	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AVVICTORUA 3482)		21.40	147.400					
PUNIC IAWID	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AVWHALLEAIAINEZZENY)		27.7	107 631					
PUNIT IAWI	MICLEOPROFEIN	INTLUENZA A VIRUS (STRAIN ANNIAL EPACIFIC OCEANUMIS)		100						
SIAVE JINA	MICLEOPROJEIN	INFLUENZA A VIRUS (STRAIN AMILSON-SAIITHUU)	-	337-403						
27.74	MICHEOFROTEIN	NATUENZA A VIRUS (STRAIN AMISCONSIMITATO)		2	100					
	Maiore	INGLUENZA A VIRUS (STRAM A/SWINE/1997)	ç	- C	331-408					
300	VI310403 CIS	INGLUENZA A VIRUS (STRAIN A/SWIND/41/49)	~	20.52	337-408					
LAKE WELL	NOCECUTA STATE OF THE PARTY OF	INTLUENZA A VIRUS (STRAIN A/SWINE/CAABRUDGE/1/15)	=	157-409						
LANCE INCOM	ACTION OF THE PROPERTY OF THE	DIFLUENZA A VIRUS (STRAIN ASWINE/DANDONG/1911)	7	127-409						
ו אישור ואיציוני	MOLLEGY NOTE IN	MOLLENZA A VIRUS (STRAIN AJSWINE/GERMANY/2011)	1-13	96-154	157-408					
PUNDE JAZIEI	MULEUROIEIN	INTITION A VILLIS (STRAIN A/SWINEARONG KONGA/A)	171	117-409						
PVAUC 14211)	MUCLEOFFOIE	ING LIENZA A VIRUS (STRAIN A/SWINE/HONG KONC/126/82)	2	16-154	197-408					
PVRUC IAZIIA	MUCLEOFICIEN	MATHEMPA A VIRUS (STRAIN ASWINEARONG KONG/127/82)	70-1	96.134	157-408					
PYTHUC IAZII	MUCLEOFICIEIN	DELITENZA A VIRUS (STRAIN A/SWINE/10WA/1970)	7:	96-154	157-408					
PVMIC IAZIZ	NUCLEOPROTEIN	MELIENZA A VIRUS (STRAIN ASWINEADWAITPANI)	7	151-34	357-408					
PYRUC IAZI)	MUCLEOWIGIEIN	MET TENZA A VIRUS (STRAIN A/SWINE/YOW A/46)	2	21.24	357-408					
PVNUC 1AZ11	MUCL EOFICIEIN	MELIENZA A VIRUS (STRAIN ASWINEATAL YM)776)	7	¥-154	157.408					
PVNUC IAZIZ	NOTE OF THE PARTY	INTLIENZA A VIRUS (STRAIN ASWINEATAL VIDTO)	1.23	96-154	157-408					
PVRUC IAZII	ADCIECT TO SELVE	INGLUENZA A VIRUS (STRAIN A/SWINE/13 AL Y/14/14)	1.42	¥-5	357-408					
TAMOS IN THE	Maccondition	DRELIENZA A VIRUS (STRAIN A/SWINEATAL YAINAN)	₹	<u>₹</u>	337-408					
PVRUC IAZIA	NAC CORDIECT	INTLUENZA A VIRUS (STRAIN ASWINEJIANGSBURGW2)	7	ž - ž	151-408					
TYRUC IAZAIA	NI COLOR CONTRACTOR	INTILIENZA A VIRUS (STRAIN A/SWINEALAYNY)	3	¥-5×	351-408					
NAME AND I	MACLEOPROTEIN	MILLENZA A VINUS (STRAIN A/SWINEMETHERLANDS/12/15)	7	Z .	200					
NO CALL DISCON	MIXTEOPROTEIN	NGLUENZA A VIRUS (STRAIN A/SWINE/OHIO/21/15)	<u> </u>	2	27.40					
PUNIC IAZE	NACLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/SWINEJOHTADIOD/II)	7	× -	104					
PVNIC IAZWI	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ASWINE/TENNESSEE/2471)	7	200	137-408					
PVNUC IAZW2	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN A/SWINE/WISCONSIDVINS)	7		200					
PVMC INBAA	NUCLEOFKOTEIN	MALUENZA A VIRUS (STRAIN ASWINE/WISCOMSIMIAI)	2		207.466					
PVNUC INBAC	MUCLEOPROTEIN	INTLUENZA B VIRUS (STRAIN BLANN AUBONING)		7150						
PYNUC INBAD	MUCLEOPROTEIN		1	110.914						
PVPIUC INBLE	NUCLEOFROTEIN	CONTRACT OF CAMERA OF THE CAME	1 2 2	50.514						
PVNUC INBSI	MICLEOPROTEIN	THE LUCINES A VIRILE (CIRAD REPORTATION)	2.5	100						
PVNUC INCCA	MUCLEOPROTEIN	THE LIENZA C VIBIG (STRAIN CALIFORNIATE)	102.50	106.447						
PVNUC MABVM	MUCLEOPROTEIN	ALABRIDG VIBILS (STRAIN AUSOKE)	131.703	332407						
PVNUC MABY	MUCLEOFROIE	MARRIED VIRUS (STRAIN POPP)	13.20	111-401						
PVD01 VACCC	MUCLEOTROIEIN	VACCINIA VIJUS (STRAIN COPENIAGEM)	103-145	345-279	141-382	\$11-118			·	
PV001 VARV	PROTEIN OI	VARIOLA VIRUS	103-145	245.279	341.302	301-618				
PVOR! FXDAY	TRUISING!	FOXTAE MOSAIC VIRUS	181-181							
PVOE SAV	Najora Carre	MARCISSUS MOSALC VIRUS (MAIV)	1319-1375							
PVORT PMV	THE KIND OF THE PARTY OF THE PA	PAPAYA MOSAIC POTEXYIRUS (PMY)	1-39	199-337	1474-1532					
1000	111 KD PROTER	POTATO VILUS M (STRAIN RUSSIAN) (PVIN)	397-431	62:33						
NOK.	STORE STORE	POTATO VIRUS X (PVX)	916-550							
PVORI PVAC	I TO THE THE THE THE THE THE THE THE THE THE									-

111111	אוראוטווז	All Virutes (no batteriophoges)								
חיבירונ	raultiz	TRUTT	1,36,1	AREAJ	SKC1.	AKEAS	AREA 3	AREAG	AREA?	AREAT
A CHILL	NI STORY OF THE PARTY OF THE PA	PUINTU VIRUS X (STRAIN CP) (PVX)								
	THE PROPERTY OF THE PROPERTY O	SHAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SNIVE	_:	931.965				,		
MAN WALLE	TO THE PROPERTY	WILLE CLOVER MOSAIC VIRUS (STRAIN MI) (WCMIV)	1340-1289							
20.00	THE POLICE	WILLE CLOVER MOSAIC WRUS (STRAIN O) (WCMY)	_							
PV PIG BROOK	751044614	AUTOCAATIIA CALIFORNICA NUCLEAR POLYIEDROSIS VIRUS								
P. PIO REDV	PROJECT STO	BICE AL ACK CIRE A MED DIVABLE DIRECTOR	2							
Pipe will	NONSTRUCTURAL PROJECY PASTO	RICE GALL DIVABLE COLUMNS (1830 V)		147-614	96.58					
P. PII RDV	NONSTRUCTURAL PROTEIN PUSIO	WOUND TURIOR VIRIS (W.TV)								
P. P.I. W.TV	NONSTRUCTURAL PROTEIN PUSIT	NCE DWAN VIRUS (ADV)								
FIFT RDV	NONSTRUCTURAL PROTEIN PAST	WOUND FUNIOR VIRUS (WIN)								
7 E E	NONSTRUCTURAL PROTEIN PIL	RICE DWARF VIRUS (ADV))	100							
PLPIE WINN	NONSTRUCTURAL PROTLIN PASTS	WOUND TUNIOR VIRUS (WIV)	101.10							
PA PIO HSVED		WOUND TUNIOR VIRUS (STRAIN NI) (WTV)	46.100							
PY P.D. HCNIVA	CAPSID ASSESSIBLY AND DNA MATURATION PROTE	EQUINE HERPESVIRUS TYPE I ISTRAIN ABAPITETIV.	118-231							
P. P. 1 115V6U	PROBABLE CAPSID PROTEIN VP21	IUNIAN CYTOMEGALOVIRUS (STRAIN AD169)	2	144.115						
P. F. 24 F HOV	PROPABLE CAPSID PROTEIN VP31	HERDES SIMPLEX VIRUS (TVPE 6/ STRAIN UGANDA-1102)								
F. F. & 115. CB	ED STRUCTURAL PROTEIN V	EBOLA VIRUS	900							
71 F26 HSVSA		EQUINE HERPESVIRUS TYPE I ISTRAIN ABILITERIY.	19.10							
TIPIO NOTOR	CAPSID PROTEIN VP26	HE LPESVIAUS SAINING (STRAIN 11)	17.14							
0121 9:414		APSID POLYHEDROSIS VIRUS								
PLF1 AHSV4		-								
7. F1 B1V10	OUTER CAPSID PROTEIN VP2	ATRICAN HORSE SICKNESS VIRUS (SEROTYPE 47 STRAIN VACCI		10,107	410.441					
YP2 BIVII		BLUE TONGUE VIRUS (SEROTYTE 10/150LATE USA)	Ī					7/0-1030	1	
1 P. J. B I V 1.7		BLUE TONGUE VIRUS (SEROTYPE 11 / 150LATE 115A)	Ī	140.401						
VP1 BTVIS	OUTER CAPSID PROTEIN VP3	BLUETOMGUE VIRUS (SENOTYPE 1771SOLATE USA)	T	41.70					Ì	
VP1 EMDVI	2	ANCAL			101,100		T			
VP2 ROIBE	1	SE VIRUS (SEROTYPE I) (END)	T	10.10	101.441	141 491		Ī		
VP1 ROTBU			Ī	915.0	11.40	T				
1 F1 ROIPW				Τ	157	T		1		
VP2 ROIPC			18.1	Τ	111.547	Ī	775.344			
P. P. ROTSI		NA COWDEN		T	164.231	T	Ť	276	1	
VP10 ASFE!	1/7]		16.94	_	T	T	1		1	
VPII FACIV		VER VIRUS (STRAIN E-15) (AST V)		Τ	Τ			1	1	
(P)) ASFB)			117.261				Ī			
1713 EBOV		NE FEVER VIRUS (STRAIN BATIV) (ASFV)	19.69						\dagger	Ī
TO STATE	POLITICAL CONTLEY PROTEIN (7)	_	10.119			Ì			T	
This VACCO		200						Ī		-
VP39 VACCP	VELOPE PROFESSION	VACCINIA VARIEGISTA IN CORESTA CORE	Ī	20.20						
VP15 VACCV	T			İ						
VPIS VARV				Ì			1	1		
VP3 AHSV4	ENVELOPE PRUTITIN P11							Ì		
	VP) CORE PROTEIN	SICKNESS VIRUS (SPROIVPE 47 STRAIN VACCT	T	16.31	100	İ			1	
			ī	T	3	İ		-		
DIVIA			Ī	1		Ī	T	İ	İ	
VP) EIDVI			110 333	13.00		İ	1			
VP1 EIDVA		É	Τ	T	11.00	T		T	\dagger	
vPI GFLV	ROIEIN	VIRUS	301.246	Ī	Τ	- E	Ì	İ	Ì	
PVP1 ROV	ALAKO TEKTINAL PROTECT	GRAFEVINE FANLEAF VIRUS (GFLV)	П	Π						
PVP1 ROISI			_							
			200	130.363	139-195	9 902-902	119-041			
		•								

	CAPID PROTEIN VP.	SIMILAN II ROTAVIRUS (STRAIN SATI) FISTERNARA VIRUS (STRAIN SOFT DIGITALIA PERSYIRUS) FISTERNARA PARAMITETY PERSYIRUS) FISTERNARA PARAMITETY PERSYIRUS)	П	344.338	31.363	451.492	247.79			
	APSID PROTEIN 170									
	APSIU PAOIEIN PAO	-	413.467							
			100	190.6					-	
	CAPSID PROJETY PAG									
	CAPSID PROTEIN P40	-		536.603						
	CAPSID PROTEIN P40	A HIOKAL A							-	
	APCID PROTEIN P40	+								
	APCID PROJETY P40	:		777		-				
	TOTAL STREET,	AUTOGRAMIA CALIFORNICA NUCLEAR POLYHEDROSIS VIAUSI	13:166						Ì	
	STRUCTURE AND THE COMMENT OF THE COM	≕	≘	5:3	23.670					
111	OUIER CATSIO PROJECT			333.516	331-646					
T	UTER CATSID PROTEIN VI	EN)	181-189	110.363	794-828	127.891				
Ī	MAJOR COXE PROTEIN FAR PRECURSOR		363-396	359-359	111.763	794-828	157-001			
l	MINJOR CORE PROTEIN PAR PRECURSOR		35.310	736.784	103:019	198-892				
	MAIOR CORE PROTEIN PAR PRECURSOR		11:13	296-330						
Γ	MATOR CORE PROTEIN PAR PRECURSOR		11.	125.163	10.30					ļ
PLP IS VACCY	MAJOR CORE PROTEIN PAD PRECURSOR	MINGEN		3	149.783					
Ī	NIAIOR CORE PROTEIN PARTICUSOR	(STRAIN WR)		1977	140.381					
	NIAJOR CORE PROTEIN PAB PRECURSOR									
	VP4 CORE PROTEIN	BLUETONGLE VINUS (SEROLTTE 1971)SULVIE USA)	100	170						
	PP CORE PROTEIN			177 007						
	VP4 CORE PROTEIN		199	177 007						
ACDV 1979	VP4 CORE PROTEIN	ī								
Ī	DUTER CAPSID PROTEIN VP4	A VIRUS (STRAIN NCDV-LINCOLN)		200	1	-				
	NONSTRUCTURAL PROTEIN PNS					1	131.411			
Ī	CALIFER CAPSID PROTEIN VP4	STRAIN BEAT	=							
	CALIFE CAPSID PROTEIN VP4		2		978-630					
	WHEN CAPTED PROTEIN VP4		6		1					
	OUTER CAPSID PROTEIN VP4		<u> </u>		1	207.60				
1	CAPSID PROTEIN VP4		13.131	14-314			17, 92,			
	CUTER CAPSID PROTEIN VP4		2							
Ī	DUTER CAPSID PROTEIN VP4		2					777 113		
	CHITEL CAPSID PROTEIN VP		3	113-166	11.11					
Ī	CATES CAPSID PROTEIN VP4	I STRAIK DSI)	≘	116-273	37.71		200			
I	CHARL CAPCID PROTEIN VPA		5	20.00	200	100	320-310		1	
Ī	CATES CAPED MOTEIN VA	IUNIAN ROTAVIRUS (STRAIN KU)	=	=======================================	40.517	237-652				
rve koru	CATE CASCIDAROIEN VP4	IIUNIAM ROTAVIRUS (STRAIN L76)	≘	2	117.178	40.51	537-653			
	TON NEW YORK WAS A STORY	INDIAN ROTAVIRUS (SEROTYPE 1/ STRAIN MI))	1.33	117-116	40.317	330-643				
	COLER CASID FROIEN VA	INDIAN ROTAVIAUS (SEROITPE IT STRAIN MCNIS)	1.35	117.274	138-379	414-518	531-445			İ
T	COLUMN TO THE PROPERTY OF THE	ILINIAN ROTAVIRUS (SEROTYPE) / STRAIN P)	1.35	116-273	137.378	413.17	337-65:			İ
	COLER CASIO FROIEIN VIA	HUMLAN ROTAVIAUS (SEROTYPE 3 / STRAIN MAY)	1.30	991-16	111.114					
	COLER CASE OF CHEMICAL COL	HUNIAM ROTAVIRUS (SEROTYPE 4/ STRAIN ST THOMIAS 3)	1.15	236-223	111-111	41.31	330-444			
1.	CASE CASE SECTION AND AND AND AND AND AND AND AND AND AN	HURIAN ROTAVIRUS (SEROTYPE 4/ STRAIN VA10	<u></u>	3.5	144-376	55.57	237-425			
Ţ	CARLE CASED BROTED VPA	HURIAN ROTANTRUS ISEROTYPE I / STRAIN WAS	.35	<u>=</u>	34-378	49.517	117-651			
	STATES CARSID PROTEIN VPA	1	13:146	3	\$31-629	-				
	Course Cascill and felt Vita	6	6.40	133-161	21.278	30:03	200			
	COLER CASID FROIDING VAL	PORCINE ROTAVIRUS (STRAIN GOTTI RED)	1.35	136-173	117.111	481-517	230-364	369-636		
	COLER CAREN PROTEIN VP.	PORCINE ROTAVIRUS ISTRAIN YNI)	1.35	113-146	217.274	94.51	528-679			
	COLER CASIO PROTEIN VP	ALCESUS ROTAVIRUS	7	113-166	117.174	28.33	44-522	21-440	Ī	
	STATE OF STA	SINIAN II ROTAVIRUS (STRAIM SAIL FENI)	=	=	518-630					
10133	DE CITES CAPCILIPEDIEN VP4	SINIAN II ROTAWRUS (STRAIN SAIL SCN)	≘	3	13.13	484-518	211-446			
	SNA NISIONA IVERTAINA	WOUND TUNIOR VIRUS (WTV)	3	365.621						
	CATES CAPEID PROTEIN VP.	AF ALCAH HORSE SICKNESS VIRUS (SEROTYPI: 47 STRAIN VACC	=	12:22						
200	CONTRACTOR DESCRIPTION OF THE PROPERTY OF THE	BROADHIAVEN VIRI S (ORD)	45.86	99.236		-				

PCGENE	ALLAIOTIS	All Viruses for bucteriophoges					П	П	П	
TL XANE	PROJECT	STEETS.	ABEAL	1438	SEE	ABEAs	AREA S	PER	ABEAZ	AREAI
PVPS DIVII	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 10/150LATE USA)	14.50	93-150	154.222	64 438				
PVPS BIVIS	OUTER CAPSID PROTEIN VP3	BLUETONGUE VIRUS (SEROTYPE 11/150LATE USA)	14.58	92-150	134-222	404-445				
PVP5 BTVIA	OUTER CAPSID PROTEIN VFS	BLUETONGUE VIAUS (SEROTYPE 137/SOLATE USA)	14-58	154.222	104.438					
FVP 01VIS	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	14.58	93-143	148.323	£ 71				
PVPS D1V2A	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	14.51	93-143	141-272	1770				
PVPS EIIDVI	QUIER CAPSID PROTEIN VPS		14-58	91-111	17.00					
PVPS RUV	OUTER CAPSID PROTEIN VPS	: DISEASE VIRUS ISEROTYPE I) (EIIDV	14-51	92-136	163-213	291-325	199-413			
PLPS WTV	OUTER COAT PROTEIN PS		10-06	95-136	150.594					
PVP61_BTV10	OUTER COAT PROTEIN PS		114-303	185-196	181-180					
PVP61 AIRDV	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10/150LATE: USA)	163.315							
PVP61 NPVAC	PROBABLE NOWSTRUCTURAL 41 8 KD PROTEIN		131-701							
PVP62 BTV10	61 KD PROTEIN	DSIS VIRUS	20.56	381-186						
PUPER NPVOP			5.5	159.201	214-251					
PVP67 NPVAC	MAJOR ENVELOPE GLYCOPROTEIN PRECURSOR	ROSIS VIRUS	196-361	411-110						
PUPET NPVGNI	MAIOR ENVELOPE GLYCOPROTEIN PRECURSOR	AUTOGRAMIA CALIFORNICA MUCLEAR POLYIII: DROSIS VIRUS (14.70	289-364	443.433					
PVP6 BIVII	MAJOR ENVELOPE GLYCOPROTEIN	GALLERIA AIELLONELLA NUCLEAR POLVIILDROSIS VIRUS IGNIY	206-281							
PVP4 BTVI3	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1171SOLATE USA)	159.211							
PAPE BIVIS	VP6PAGTEIN	BLUETONGUE VIRUS (SEROTYTE 11/150LATE USA)	134.211							
PVP6 BIVIS	VPA PROTEIN	BLUETONGUE VIRUS ISEROTYPE 17/150LATE USA)	10.103	159-211						
PVF6 BTV2A	V PE PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1/150LATE SUCTII AFRICA)	===	161.211						
V 26 ADV	VP4 PROTEIN	Ī	64.10	11:41						
PI PA W. CV	STREET LEAF PROTEIN PA		130-191	296-364	360.401					
PLPS WIVE	STRUCTURAL PROTEIN PO	IN.	46.73	316-334	7(7007					
PLP34 NPVAC	STREET PROFES PA	WOUND TUNIOR VIRUS (STRAIN NI) (WTV.)	46.131	216.334						
N PAGE	PAPAGIEN	A VIRCINIOSIS VIRUS (27.12						Ī	
PV P15 115VSA	P24 PROTEIN	75	105.450							
PLPIN NPVAC	PROBABLE MENIBRANT ANTIGEN 75	-	8.0	Γ	931.984					
l	79 KD PROTEIN	•	14.78	161.197	108-410					
PAPE BEVIE	VP) CORE PROTEIN	(SCROTYPE	104-236							
İ	VP1 CORE PROTEIN		101-215							
P. P. BIVIA	IN CORE PROTEIN		114-720							
P. P. BIVIS	VPT CORE PROTEIN		14-335							
Pi Pi BTV2A	IPT CORE PROTEIN	III AFRICA)	184-228							
PLP1 EHDVI	VP CORE PROTEIN		184-228							
אמו ידיי	VPT CORE PROTEIN	COISEASE VIRUS (SEROTYPE 1) (LIIDA	16.50	134-138						
PIP WIV	NOVSTRUCTURAL PROTEIN PAST			132.33						
PLP80 NPVAC	HOYSTRUCTURAL PROTEIN PKS?				138.495					
PLEST NPVOF	CAPSID PROTEIN PIO		T	1	26.704	221-278				
PVPE BTV10	CAPSID PROTEIN POT	ORGYIA PSEUCOTSUGATA MULTICAFSID POLYIIEDXOSIS VIRUS	201	10-121						
11.78 BTV11	SOSTRUCTURAL PROTEIN PL		T							
11/41	MONSTRUCTURAL PROTEIN PI	BLUE LUTCUE VIRUS (SENOITYE 11715ULA 1E USA)	T							
171	SONSTRUCTURAL PROTEIN PE			13.710						
PVPC BTVIA	KONSTRUCTURAL PROTEIN PO	ELUETONGUE VIRUS (SEROTYPE 17/150LATE USA)	2013					İ		
PVPI BIVIS	NOWSTRUCTURAL PROTEIN PE	T								
PVP0 BTVJA	NOWSTRUCTURAL PROTEIN PI	BELUE LONGOE VIRUS (SERO) THE L'ISOLATE BOUTH AFRICA)								
2000	MONSTACE LUNCE PROTEIN TO		20.00							
	STACK LOWER TO THE STACK STACK	Section 21		76.53					Ī	
ALM MAIN	MONSTRUCTURAL PROTEIN PRIST	100		***************************************						
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	771000	VIRUS		106-165						
	TO POLITICAL PROTEIN		=							
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	VAR PROTECT		1	1						
	VV PAOTEIN			1	Ť					
DELVI DAVA	LTU PROTEIN		<u> </u>	1						
NEU INIBA	LPU PROTEIN	THE PROPERTY VIEWS TYPE I (BRAIN ISOLATE) (I 4.)	6.50							
NAME AND PARTY.	VPU PROTEIN		1.12							
Ī	Maiore		3							
i										
-	V V V V V V V V V V V V V V V V V V V	HIMIAN INDICANDEFICIENCY VIRUS TYPE I (ELI ISOLATE) (III)		1	Ī					
PLPU IIVIII	CPU PROTEIN	THAT A MAN PARADE FICIENCY VIRUS TYPE I (HIXEL ISOLATE) (HIS)	2	1	İ					
IN IN	VTU PROTEIN	THE PART NODE OF THE VIRUS TYPE I (III) ISOLATE) (IIIV 12.	2.50	1						
	THE PROPERTY		4.59							
	2010	_	9							
P FU SIVINA	TO THOUSE									
N PU IIVING	VPU PROTEIN	_						L		
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A PAT HIVIRM	CPUPROTEIN		1.30							
	VALUE PROTEON	INDIAN INITION COEFFICIAL COEFFICIAL COEFFICIAL ATELLINA	57							-
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A BSNIV	VPX PRUIEIN		40.74	197.191						
101.00	ALPIIA.A PROTEIN		141.217							
	LOCATEDICTURAL PROTEIN NCVP2		175							1
	A 40 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BOVINE ROTAVIRUS (GROUP L' STANIS SIMILEDIES BOTTES	69.144							
PY SOB MOTOR		יין (אסטרו מוששערע אמני		197,79						
PY SOL ROTGE	NA PROCESS									
PV SOS ROTHC	VP&FROIRIN	IN BUSTOL)								
PV SOL ROTPC	VP6 PROTEIN	-								
PVS07 ROTBI	VP6 PROTEIN		*	200						L
PVS01 ROTBU	CL YCOPROTEIN VP		2	2						
PY SOT ROTPS	HONSTRUCTURAL PROTEIN ALVES	S / STRAIN OSU)	10.162	20			-		-	
PYSOJ ROISI	MONSTRUCTURAL PROTEIN MLVF		11:13	j				-		L
N SON ROTBU	MONSTRUCTURAL PROTEIN MCVP3		3.70		60.336				1	-
PV COL BOISI	NONSTRUCTURAL PROTEIN NS2VP*		97-8	144.212	117.255					-
Section BOTH	NONSTRUCTURAL PROTETN NCVP4	SPRIAM II RUIN TAND LESS TANDES A COM A LONG	***	283.330					+	
COS BOIRS	GLYCOFROTERN VP?	BOVINE RUIN WOULD STREET	17.	262-330						1
	CL VICTORIOTEDA VP	141717	15.	211.120						
101 65.44	CL CCORD TEOL VP	STAMINOLA		11.110	1					
KOLBA	Constitution of the second of			077						4
VS09 ROTES	CLYCOTON CO.	STRAINULL		91.1						
PVSOP ROTOK	GLYCOTROIRING						-			
PVSOF ROTEN	GLYCOPROTEON VY	2						-		L
PUSOR ROTET	GLYCOPROTEIN VP	TRAIN TARS)	2	225.72						
PVS09 ROTBU	GLYCOPACIEIN VP7		١	200			-			L
PVSON ROTC?	CL YCOPROTEIN VP	CHICKEN BOTAVIBUS A (SEROTYPE 1 / STRAIN CILL)	313-326							
PV CON ROTEL	GLYCOPROTEIN VP1	CALCASTA VIEW CATE AIN 131	262-320				+			-
N. COB BOTCA	GLYCOPROTEIN VP1	AVICADULT DIAMBIEA ROTA			i					-
PVCOB BOTG	GLYCOPROTEIN UP? PRECURSOR	ACIA TORON BOY STRAIN IDIR	63.79				-	-	-	-
NOTICE BOTT	GLYCOPROTEIN VP ? PRECURSOR	ROLAVISOR (SEEDTIVE AVERALA SEEDTIVE AVE	(7)	113.330				-	+	-
MILLS 80118	CL YCOPROTEDN VP1	HUNDER ROLL VINCE CONTROL OF STRAIN RKP)	203-330							
ALL OF STATE	CL YCOMOTEDN VP1	HIGHEN ROLL VALUE (SERVICE) ATTACK HUS)	21:38				-			1
20 m	GLYCOPROTEDIAP?	HUNLAN KOLAVIKUS (SEADLINE OF CREAM DIS)	3	281-330					+	1
	CA YCOPROTEIN VP?	INMAN ROLAVIROS (SENOTIFE EL TITADOS)	87:22							+
VSO KULL		MURITAN ROLANIAUS (SENOTETE AV BENAME)				-	_	_	_	
						_				

PCGENE	(ALLNOTIS	IAH Viruses (ne batteriophages)	-							
FILENAME	PROTEIN	VINUS	ABIA! A	ABEA!	SPELL	AREA 4	AREAS	AREAS	AREA?	AREA
PI SOF ROTIES	GLYCOPROTEIN 177	HUNIAN ROTAVIRUS (STRAIN 1.26)							П	
P1 509 ROTIO	GLYCOPROTEIN VP?	HUMIAN ROTAVIRUS (SEROTYPE 1/STRAIN NIT)	1.43	:13.330						
PYSON ROTHP	GLYCOPROTEIN VP7	INDIAN ROTALIRUS (SEROTIPE ILSTRAIN NO AND STRAIN D)	3.43	113-330						
PVS00 ROTHR	GLYCOPHOTERN VP1	HIDAIAN AOTAVIRUS (SEROTYPE 1/STRAIN P)	283-330							
PV 509_R0111S	GLYCOPROTEIN 172	IRDARN ROTAVIRUS (SEROTYPE 1/STRAIN RAV)	182-320							
P1 509 ROTHT	CLYCOPIOIEIN VP?	HUDIAN ROTAVIRUS (SEROTYPE 2/STRAIN S2)	91.330							
PVS09 ROTHY	GLYCOPROTEIN VP?	HEMIAN ROTAVIRUS (SEROTYPE (/STRAIN ST THONIAS))	20 20 20	206-242	182-320					
P. S.M. ROTIEW	GLYCOPROTEIN VP?	HUBIAN HOTAVIRUS (SEROTYPE 4/STRAIN VATO)	25.11		112.170					
	GLYCOPROTEIN VP?	HOBIAM ROTAVIRUS (SEROTYPE I / STRAIN WA)		183-330						
	GLVCOPADTEIN VP?	PORCINE AOTAVIAUS (SEROTYPE 37 STAAIN AT/76)	201-170							
PI SOF ROTPA	CLYCUMOTEIN VP2	PORCINE ROTAVIRUS (SEROTYPE 37 STRAIN CAW-1)	22							
	GLYCOPROTEIN VP!	PORCINE ROTAVIRUS (SEROTYPE 4/STRAIN OSU)		106-242	183.320					
	GLYCOPROTEIN 177	PORCINE ROTAVIRUS (SEROTYPE S/STRAIN OSU)	202-370							
l	GLYCOPROTEIN VP)	PORCEME ROTAVIRUS (SEROTYPE 57 STRAIN TER-41)	313-330							
P1 509 RO1PK	GLYCOPROTEIN VP?	PORCINE ROTAVIAUS ISEROTYPE 47 STRAIN BEN: 144)	10.56 20		282-320					
PY SOS ROTPAI	GLYCOPROTEIN VP1	PORCINE ROTAVIAUS (STRAIN K)								
PI SOF ROTPY	GLYCOPROTEIN VP?	PORCINE ROTALIRUS (SEROTYPE 4/STRAIN BAIL-1)	11.54 20		113.330					
PV SDP ROTRU	GLYCOPROTEIN VP)	POACINE ROTAVIRUS (STRAM YAI)		281-320						
PI SOF ROTS!	CLYCOPROTEIN 177	AMESUS ROTAVIRUS	20.32e							
PI SIO ROTON	GLYCOPROTEIN VP?	SIMIAM II ROTAVIRUS (STRAM SAII)	202-330							
PVS10 BO185	HONSTRUCTURAL GLYCOPROTEIN ACVPS	BOVINE ROTAVIRUS (STRAIN NCDV)	73.161							
PVS10 ROIBU	NINOR OUTER CAPSID PROTEIN	BOVINE ROTAVIRUS (GROUP C./ STRAIN SHINTOKU)	17.58							
PVS10 RO1112	NOWSTRUCTURAL GLYCOPROTEIN NC175	BOVINE ROTAVIRUS (STRADA UK)	19:161							
P. S10 ROTH	MONSTRUCTURAL CLYCOPROTEIN NCVPS		13.162							
PVS16 ROTH	HONSTRUCTURAL GLYCOPROTERM HCVPS		1)-161							
PVS18_ROTHC	MONSTRUCTURAL CLYCOPROTEIN NEVTS		73-162							
VSIG ROTHW	NINOR OUTER CAPSID PROTEIN	67	131-131							
VS10 ROTS1	NOMSTRUCTURAL GLYCOPROTEIN NC175	CAIN WA)	7:1X							
PVSII ROTGA	NONSTRUCTURAL CLYCOPROTEIN NCVP1	_								
PVSII ROTGI	NONSTRUCTURAL PROTEIN	VIADULT DIARRUEA ROTA		8.130						
NSTI ROTHS	NONSTRUCTURAL PROTEIN	ROTAVIRUS (CROUP B / STRAIN IDIR)	7	İ	1		1		1	
VSII ROLIB	MINOR COLER CASID PROTEIN		27.10	1	T	1	1		1	
PVCII BOTTED	MINOR OUTER CAPICOPROTEDA		200	T			T	1	1	
PVSII ROTIIW	MINDA OUTER CAPSID PROTEIN		51:11	Ī			T	T		
PVSII ROTSI	MINOR OUTER CAPSID PROTEIN	RAIN WA)	111.143							
VS48 TBRVC	NINDA OUTEA CAPSID PROTEIN		11-145							
VSH MUMB!	SATELLITE RNA 48 KD PROTEIN		217-365							
VSH MUNITS	SMALL HYDROPHOBIC PROTEIN	FIGURES VINUS (STRAIN SOCIE), AND RICHARS VINUS (STRAIN SOCIETY		Ì	1					
VEH AIIADA	SALAL MYTHORNORUS PROTEIN			T		Ī			Ī	
VSII MUNITE	SALALL HYDROPHOBIC PROTEIN		250	T				Ī	T	
PVSII MUMPE	SMALL HYDROPHORIC PROTEIN	ANDAIPS VIAUS (STRAIN BELFAST)	15:1							
PVSII MUNITI	SNALL HYDROPHOBIC PROTEIN	ANALIS VIRUS (STRAIN ENDERS)	97-6	İ						
PVSH MUNDE	SALALL HYDAOPHOBIC PROTEIN	MAROS VIRUS (STRAIN JERYL-LYNN)	3							İ
PVSH NUMBE	SMALL HYDROPHOBIC PROTECH		1.51							
PVSII MURUM	SMALL HYDROPHOBIC PROTEIN		13.55							
PVSH MUNDT	SMALL HYDROPHOBIC PROTEIN	ACCINE)	17:58							
PVSII MURDU	SMALL HYDROPHOBIC PROTEIN		171							
PVSII REOVD	SMALL HYDROPHOBIC PROTEIN	E AMP)		1						
PVSII REOVI	SIGMA I PROTEIN PRECURSOR	REDVINUS (TYPE 3 / STRAIN BEARING)		2.23	\$	1		1	1	
PVSII REOVL	SIGMA I PRUTEIN PRECURSOR			1	1	1	1	1	1	7
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				AREA 2 1A	ARCAS	48.43	2			
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III, E.NAME	TAROUTH.	AUS (TYPE I / STRAIN LANG)	1							
II REOVD		(Ç	20.00	İ						
PVS12 REOVE			20.314							
00000	SIGNIA 2 PROTEIN		2113							
1020	12		7							
10000			111.152							
201211	CONTINUE PROTEDY 2 PRECURSOR									
TVS17 IEVBE	STATE OF SECUTION 2 PRECURSOR			İ						
VSI3 IEVAIV	TOTAL STREET,			İ						
PYSII HEVPA	STRUCTURAL PROJECT A STREET OF	,	200	Ì			İ			
PVS13 HEVILH	STRUCTURAL PROTEIN 2 PLECURSOR		116-220							
PVIJA CAPVI	PROTEIN 2		120-158							
VAL CAPVI	PROTEIN 13A		00-130							
CABVE			14.120							
		CAPRIPOXVIRUS (STRAIN RS-1)	L	101.430		L				
LA LOS	PACKAGING PROTEIN	VICENCES VINOS VI	Τ	117						
VIER INCHIA	MOLECULA CAST AND STATE OF THE		Ţ							L
VIER HSV6U	PROBABLE DRA PACKAGING PROTEIN	LMDA-1102)	46.502							
VIER HSVED	PACGABLE DNA PACKACING PROTEIN	7								
VIER HISVII	PROBABLE DNA PACKAGING PROTEIN	(A) (CC/V)	91.136	698.744						
N.TER HSVSA	PROBABLE DWA PACKAGING PROTEIN		116-167							
VIEW VZVD	PACDABLE DNA PACKAGING PROTEIN	VOID LAST LYZON	119-015							
2000	PROBABLE DNA PACKAGING PROTEIN	TAL VIOLET	17.							
1	70.000	VIRUS (STRAIN TOSINIA)			!					
PLYI SENDO	A CALLETIN									_
Y 101 SSV1	VI TRUITM		20.0							
VIOL SSVI	ATTOMA CO. SO. ST. ST. ST. ST. ST. ST. ST. ST. ST. ST				1					
1 SSVI	HYPOTHE IKAL IN THE PROPERTY		2							L
Y119 SSVI	HYPOTHETICAL IT BRUTANESS	-	200							
YIIK TYDVA		STRALBAITADVI								
YIJK FCVC	HYPOTHETICAL II I KU PROJETS	TELENE CALICIVIANS ISTRAMS CENSO FIVERICY	1.18							
YIZK FCVF9	PROTER	TELINE CALICIVIRUS (STRAIN FO) (FCV)	-							
YIJK NOV	PEDTE	PARRIT IE MORAIACIC DISEASE VIRUS IRIDVI	2							
VISK RUDVS		RABBIT IENIORUIACIC DISEASE VIRUS ISTRAIN V.1111 INHIUV.)	2							
YIJK CLVK		CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 114)	6,3							
THE CLAY	HYPOTHETICAL IN TRIP PRINTERS	CARRACA LATENT VIRUS (STRAIN NICERIAN)	43.11							
PVIJK NPVOP	HYPOTIETICAL II I KD PROILIN	CHECKIA PSELIMOTSUGATA MILLTICAPSID POLVHEDROSIS VIRILY	10.67						1	
		CHI FOR COURT VIRUS LIKE PARTICLE SSVI	3.36	2.50						
İ	HYPOTHETICAL IN TRUTCHE	COR COLOR MAIS INT PARTICLE SSVI	1.10							ļ
_	NAPOTHE INCAL 13 7 KD PROTEIN	SOUTH OF THE TABLE AND THE PARTY OF THE PART	119.164							
PY 16K 55V!	HYPOTHETICAL PROTEIN C.168	STATE CHANGE LIKE PARTICLE SAVI	1.15	11.11	ļ					1
	HYPOTHETICAL 19 6 KD PROTEIN	STATE OF THE PARTICLE SSVI	50-1	119.153						1
YIIK SSVI	HYPOTHETICAL ITERDITORIES	STATE OF CHILL IKE PARTICLE SSVI	102-136							ļ
7. 20K 55VI	INPOTIGETICAL IS & KD PROTEIN	SULTOLOGICA LIBITATION PARTICLE SSVI	13.101							1
17.21K \$5.VI	HYPOTHETICAL 20 4 KD PROTEIN	NOTICE COMPANY OF STREET BY CALL	23:12							
VI COCIIV	IN POTIGITICAL 18 5 KD PROTEIN	SULFOLDED VINUS LINE PARINE LE STITE	13.134							
1000	ILYPOING THOME PROTEIN 3	SOYDEAN CILCUXOTIC NOTICE VINOS	10.0	198						
	IIVPOTIG TICAL 31 \$ KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE 35VI	18.31				_			
1111	INTOTHE TICAL 11 7 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI								
1	IN BOTHS INCAL 17 TED PROTEIN	AUTOGRAPHA CAL IFORMICA MULLEAR PULTIFEDESSES								
X	INSPORTED FAULT PROTEIN	SOVE EAN CHE DROTTE MOTTLE VIRUS								
VIK9 53VI	SOUTH THE SAME PROJECT	SULFOLOBUS VIAUS-LIKE PARTICLE SSVI					-			
VI SOCIAL	INDOCESTICAL PROTEIN ?	SOYBEAN CHEOROTIC MOTTLE VIRUS		117.15	146.503	658.700				
7018 3301	SINDOTHE TICAL BY 7 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI				_				
VI SOCALV	AND PROTEIN	SOYDEAN CHLOROTIC MOTTLE VINUS				-	_	L	_	_
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INTOINITECAL BARBIN ONLY FOOLING CONTROL WILLIAM INCOLUDIO 17-15	AME	RULLIN		T	T	1	20.3	27707	2000	0400	
INTODITE ICAL BARBING OFF FROLES TOWARDS VIRELES FROM THE PATHUNSCHIP 13-13 11	FOWPN	HYPOHE HEAL BANGH ORF FROTFIN			16:19						
INTOINING TALK BARBIN ONLY FOOLING CONTROL WILL STRANGE CONTRO	OWPM	HYPOTHETICAL BANGHORF PROTEIN		Τ	İ						
	OWPSI	HYPOTHE TICAL BANGH ON F PROTEIN			İ						
	NAMO	HATOME IN ALL BANKS OF PROPERTY		62:331							
INTOINITIES A. BATTOTOTIC NOTE TO THE CONTRACT STRAND BY AND STRAND BY	2000	INPOLITE TICAL BANGIL CREEN PROTEIN	OWLPOX VIAUS (ISOLATE 19-41)(AILUNICII)		13:51						
INTODITE TEAL BILLT PROTEEN 16.204 10.118	2	HYPOTH TICAL BANGH ORF IS PROFEIN		33:16)							
	1919	INPOSITE REAL BELLT PROTEEN	7	58.500							
	I MO	NDIGN	-	10.111							
INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHENT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS LIGHT SUBSTITUTION 11-21 INTODITE IGA. 11 SED PROTEIN PAGENOUS PAGENOU	IISVAID	HYPUTHE HEAL 30 9 KD PROTEIN	Ī	60.204							
INTRODITE ITEAL 11 SE DROTEIN PROJECT VICTORA VRUS STRAND WAS DEADLE TO THE PROSTRUCT OF	ISVANI	HYPOTHETICAL 21 4 KD PROTEIN IN GLYCOPROTE!		16-211							
INTROTITE ICAL 11 TEO DUCTION CROOTEN INTROTITE ICAL 11 TEO DUCTION CROOTEN INTROTITE ICAL 11 TEO DUCTION CROOTEN INTROTITE ICAL 11 TEO DUCTION CROOTEN INTROTITE ICAL 11 TEO DUCTION CROOTEN INTROTITE ICAL 11 TEO DUCTION INTROTITE ICAL 11 TEO PROTEIN IN TOU PROPERATE ALL ITORNO VIRUS (STAND SALE) (TEOLORY OF SALES (STAND SAL	VACCV	INPOTIETICAL 23 6 KD PROTEIN IN GLYCOPROTEI									
INTOINE IRCAL BRAIN TOWER 214 KD PROTEIN VACCEINA VINUS ISTAND 893 JJIIILOJAN ILRPESVIUUS 1941	VACCV	HYPOTHE FICAL 21 7 KD HINDIN-C PROTEIN		1	98-139						
INTOPOTIETICAL BY ALD PROTEIN CONDELLINA VILLOGANIST (STAND REALINGUAN) ILLAND 19-11	CBV			٦	111-227						
INTODITETICAL BILD PROTEIN INTODITETICAL BILD BILD BILD BILD BILD BILD BILD BIL	ADEA		BOS-DJ (INUSIAN INCRPESVIRUS 4)								
	, A		_	=							
	CONNIV	HYPOTHETICAL BUREY PROTEIN	_	÷							
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TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

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YANDO, A VIBLOS EQUIPE REDESINUS TYPE I ISTRAINS ADM and Kr A) IERDESINUS SABINUS STALIN II) ALABSTER POL YOMAVIRUS BUDGEBLAR ILEBOLING DISEASE VIRUS BOVING POL YOMAVIRUS	112.339 127.134 159.186 180.187								
EQUINE HEAPESVIRUS TYPE I ISTAAINS ADMP and Ky A) TEAPESVIRUS SADAIN (STAAIN II) HAMSTER POL TOMAVIRUS TEAPESVIRUS TEAPER NOT THE TEAPER TO STAAIN III) BOYDERICAN TEAPER	127-134								
FEMPESYRUS SABIRIO (STRAIN 11) HAMSTER POLY OMANYRUS BUDGERDAR FLEBACHING DISEASE VIRUS BUNGERDAR FLEBACHING DISEASE VIRUS	137.154							T	
HANGER WAD SOME OF THE STATE OF	159.186			į					
MAASTER POLYDMANNIN WOGGENGAR HEDGLING DISEASE VIRUS ROTHER POLYDMANNING	190.10								
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BOVINE POLICEM VIACS			_						
	3:5								
POLYOMAVIAUS AC									
I YAPHOTA OPIC POLYONIA VIRUS	ò								
LANGE BOY VOMAVIRUS ISTRATA KILIJANI)	13-49							İ	
20 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	178.205	`	_				j		
STATE OF THE PARTY	130-147							Ī	
ADENO-ASSUCIATED VIRGS 6	1.10								
THE RAIOPROTEUS TENAN VINUS I (STRAIN BRATI)									
ALEUTIAN MINK DISEASE PARVOVINUS (STRAIN G)	2								İ
BEAN LEAFROLL WRUS	1								
TARE STOUTH MOSAIC VIRUSISTRAIN CALIBAL		193.320	101-111						
CAUCAGE AND	Γ	184-221							
CAULULUM EN PROJECT VINCOLO PORTO DE LA COMPANIO DEL LA COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANION DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPA	97.5	191.320							
CAULIS LOWER MOSALC VIRUS (STRAIN BOL)			117						
CAULDIOWER MOSAIC VIRUS (STRAIN NYSISS)	2								
CAULULOWER MOSAIC VIRUS (STRAIN STRASBOURG)	ž.	2						T	
CARNATION MOTTLE VIRUS	Î							Ī	
AND ANACOMA BITTA CARIA CHO ORELLA VIRUS I	97-19								
TAXABLE TO COLOR OF THE COLOR O	321.362								
CUCUMBEN PERSON	97.59				L				
CHLONIS STRATE MOSAL VIRUS	W. 46.								
CLOVER YELLOW MOSAIC VIRUS									
FELINE CALICIVIALUS (STRAIN CFIMS FIV)	No.				-				
FFI DE CALICIVIDUS (STRAIN IAPANESE F4)	316-343	2				Ţ			
GET TAT I CIVILITY ISTRATIVE OF	319-546	269-603						1	
STOWNER TOPE OF THE PAIN DAY	220-247	131.313							
FOR THE POST CANADA CAN	93,70	346.273							
LELY STATIONELESS VIAUS									
MUSCANTHUS STREAK YOLUS	2								
ODONTOGLOSSUM NINGSPOT VIRUS	8								
HIDAAN PARVOVINUS B19	324-551	2						Ī	
POPL AN MOSAIC VIRUS (ISOLATE ATCC PV275)	<u>-</u>								
SOME ALCID DECINE MOTTLE VIRUS	121.162								
SOURCE CHANGE OF COMMENT	31.48								
LANCHES MONTH AND THE PROPERTY OF THE PARTY	3:50	L			L				
TOMATO ASPEAME VINOS	97.	19:19							
TOWATO BUSH'S STUM VIRUS (STINAIN BS:3)	7				-				
TOMATO BUSHY STUMI VIRUS (STRAIM CHEROLT)									
	POLYMEAU BUTCH AND SECURATION OF THE SECURAL STANDAY OF SECURAL SECURATION OF SECURAL SECURATION OF SECURAL SECURATION OF SECURAL SECURATION OF SECURATION O		137.154 19.166 19.166 17.204 	137.154 150.164 150.164 176.	13-154 13-154 15-154 1	13-154 13-154 15-154 1	13-154 13-154 15-154 1	13-154 13-154 15-154 1	13-154 13-154 15-154 1

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POAT TACALL	COAT PROTEIN	IUKNIK CIUNKLE VIAUS	133.359			,	-		1	Т	300
PCOAT TAV	COAT PROTEIN	TOBACCO MILLO CALEM MOSAIC VIRUS	<u>=</u>					İ	İ	İ	i
PCOAT TMVCO	COAT PROTEIN	TOPACCO MORAIC VIROS (VULGARE)	2						İ		
PCOAT THYDA	COATPROTEIN	TOBACCO MOSALC VIBILS AS TO THE SASTEST	2								:
PCOAT THYER	COATPAOTEIN	TOBACCO MOSAIC VIBIS (STRAIN CH.	3								I
PCOAT THYO	COAT PROTEIN	TOBACCO MOSAJE VIRUS (STRAIN O ALKOVIMI)									
PCOAT THYON	COAT PROTEIN	TOBACCO MOSAIC VIRUS (STRAIN DAI)									
0	COATPROTEIN	TOBACCO MOSAIC VIRUS (STRAIN TONIATOR)	1	Ì			İ	İ	!	- :	
	COAT PROTEIN	100ACCO NECROSIS VIRUS (STRAIN A)					-		j		i
ı	COAT PROTEIN	TOBACCO RATTLE VIRUS (STRAINS P.C P. B.						j			
PCOAT TYBVA	COAT PROTEIN	TOBACCO TELLOW DWALE VIRIS STRAIN ALISTE ALIST					İ				
PCDAT TYMV	COAT PROTEIN	TURKUP YELLOW MOSAIC VIAINS	2				Ì				
PCDAT TYNVA	COAT PROTEIN	TURMIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)					1				
PDWB1 ADE01	EARLY E2A DNA-BINDING PROTEIN	HUMAN ADENOVIRUS TYPE ?				Ī		Ì		j	
POMBI EBV	ALAJOR DNA-DINDING PROTEIN	IN 895.43		170	1	Ì	1	İ		-	_
PDMBI HCMVA	ALAJOR DNA-BINDING PROTEIN	ADIABI	3	201		Ì					
PONDE HIS VSA	MAJOR DNA-BINDING PROTEIN					Ì					
PDMB1 MCAVS	MAJOR DNA-BINDING PROTEIN	NIN SAILTIES							1	1	_
PONIEL POVIC	DNA-BINDONG PROTEIN	POL YOMANTIUS JC			Ī	Ì	1				
PDHBI SCHVC	MAJOR DNA-BRADING PROTEIN	(Z-2)]			Ì					
	DHA LIGASE		Т			Ì		1			
,	DNA LIGASE		Т			Ì	İ	1		1	-
	DNA LIGASE		T	•		1				-	
	DHA POLYGRASE		T			İ	İ	1			
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	DHA POLYMERASE		Ţ.								
	DNA POLYNGRASE	MSARVA CIO ORELLA VIRUS I		Ī	1	1		1			
POPOL FOWPY	DNA POLYMERASIE		Т	717.01			1				
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٦	DNA POLYNERASE			ľ	İ	1	1			<u> </u>	_
	DNA POLYMERASE		Ī	1	İ	İ		1			
	DNA POLYMERASE				Ì	1	1	1			
٦	DNA POLYNERASE			İ	Ì	1	1	1			
PDPOL IDBVP	DNA POLYNEAASE	STRAIN PHILIPPING FF DW 1941		Ì	T	\dagger	1	+	1		
7	DNA FOLYMERASE		443.470	İ	1	1	1	1		1	1
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ī	DNA FOLTBERASE		Т		Ì	İ	1	1	1	+	1
Three Parks	DHA FOLTHERASE		31.53	İ	Ì		1	1	1	+	1
T	DAY FOL THE LASE	EAR POLYMEDROSIS VIRUS	31:18	İ	T	Ť	\dagger	+	\dagger	+	1
Т	DNA POLYNESASE		110-181		İ		\dagger		+	\dagger	Ī
POPOL VARV	DHA POLYAFAKE		710-797					\dagger	-	\dagger	Ī
Ī	DHA POLYMERASE		ž							-	Ī
Ī	DNA POLYNERASE	WOODCHIEF MEANING WILLS OF	213.376						-	-	Τ
PDPOL WITVI	DNA POLYMERASE		٦						-		Ī
T	DNA POLYNEJASE		7	2					_		Ī
ī	DNA POLYMERASE		٦	8.58					-	L	Ī
	DIPHTH TOXIN HOMOL OG CRUZZE PREC		Т	16.00			Н	H			Τ
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	DIPHTHERIA TOXON PRECURSOR	Y	86.	1							
		AIN 1942)		İ	1	1	1				
PDIT ISVSA	DEOXYU S-TRUMOSPH NUCHYDROLASE		1	\dagger	1	1	1	+	1	4	
T	EIB PROTEIN, LANGE T-ANTIGEN		135.13	İ	\dagger	1	1	1	+	7	1
FEIST ADEA	EIS PROTEIN LAUGE I-ANTIGEN		32.30	 	\dagger	$\frac{1}{1}$	+	1	+	+	Ī
7		ILDMAN ADENOVIRUS TYPE 13	3.30	T	\dagger	+	\dagger	$\frac{1}{1}$	1	1	Ī
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THE STATE OF THE S	1107217164	All Viruire (no batteriophages)	Г	ANIA.	77170	ABEAL.	AREA	3000	70720		
TOTAL STATE	MINITORA	XIBUS	111:11				į	!		:	!
LEDGE ANGLE	FIR PROTEIN SMALL T.ANTIGEN	MOUSE ADEMOVIRUS TYPE I				:					
	KADI V FIR 14KD PROTEIN	INDIAN ADEMOVIRUS TYPE ?									
The Appear	EAST VET 14 TED PROTEIN	IRDAAN ADENOVIRUS TYPE ?	T	20,100							1
TELL ANCES	FARI V E1 16 I KD CLYCOPROTER	IRRAN ADENOVIRUS TYPE 3	-								اد
	EAST V PI YOU KIN CALYCOPROTEIN	IKINAM ADEMOVIRUS TYPE 15							į		
100	EAST Y ET 264 KD GLYCOPROTEIN	HUMAN ADENOVIAUS TYPE 15			-	: :	!		<u> </u>		_
ייניי לאנייו	FARLY ET 17 1 KD GLYCOPROTEIN	MOUSE ADENOVIRUS TWY!									į
200	EAST V ANTICEN PROTEIN R	EPSTEIN-DARR VIRIS (STRAIN HALE)	ŀ	10701		!					
EAR CUV	THE RESTREET OF THE PARTY STREET	VARIOLA VIRUS	Т					L			
PETTI VARV	EACH INCOME.	AVIAN RETICULOEMBOTHELIOSIS VIRUS	07-07								L
PENV AVIRE	ENV POLYPROJEIM	ACAN ON CON MECROSIS VIRUS	:	426.474							L
PENV AVISM	ENV POLYPROTEIN	A LEGAL EMPOREMONS VIRUS (STRAIN AIT)	105.452								
PERV BAEVM	ENV POLYPROTEDM	TABLOON CONTROL OF THE LOSS	13.46	\$40.60)	631.695						1
PENT BIVOS	ENV POLYPROTEIN	BOVING INCOMPLETE CONTROL OF STATE AND	7	573-632	660-734						
BENY BIVIT	ENV POLYPROTEIN	BOVINE IMMUNODEFICIENCY VINUS (130LATE 127)	131								
310 10 100	ENV POR YPROTEDN	BOVING LEUKEMIA VIRUS (ANERICAN ISOLATE FLA)						L			
ENV BLVA	STATE OF STA	BOVING LEUKENDA VIRUS (AUSTRALIAN ISOLATE)	3						L		
PENV BLVAU	ENVIOLENT CONTROL	BOYDE LEUKEAUA VIRUS (AMERICAN ISOLATE VDAT)									L
PENV BLVAV	ENV POLITIMO	ROVINS I EURENDA VIRUS (BELGIUM ISOLATE LB185)									L
PERV BLVB1	ENV POLYTHOIEUM	PROVINE I FIREMIA VIRUS (BELGIUM ISOLATE LB19)	104-111								
PENV BLVBS	ENV POLYTRUIEIN	PROGRAM STRING (1APANESE ISOLATE BLV-1)	304-373								L
PENV BLVI	ENV POLYTROTEIN	CAPACITY ANTICONOFPICALITIS VIRUS (STRAIN GAS)	163.192				\downarrow				L
PENV CAEVO	ENV POLYPROTEIN	TALEST THE PARTY AND	668-712							1	1
PENY ELAVI	ENV POLYPROTEIN	EQUINE INTECTIONS AND A VISIT CLONE PL 2.3	649.693								1
PENV ELAV2	ENV POLYPROTEIN	EQUINE RATELINGS ANGRED AND ANGRED OF STATE	1661-312								1
FIN FIAN	ENV POLYPROTEIN	EQUINE INTECTIOUS AMENIA VIAUS (CLONE 17 2.7)	969-677								-
SENT EIAVS	ENV POLYPROTEIN	EQUINE DIFECTIOUS AMENIA VINUS (LLONE 7)	441.312			L				_	
200	ENV POLYPROTEDA	EQUINE INTECTIOUS AMENIA VIAUS (CLONE 1109)						L			
TENY ELAV	MILITARY POR SALE	EQUINE INTECTIOUS AMENIA VIRUS (CLONE CLZZ)	1						L		
PENV ELAVI	TOTAL TOTAL VANCOUR DA	EQUINE DIFECTIOUS AVENUA VIRUS (STRAIN WSUS)				-			L	L	
PENV ELAVW	Table of the second of the sec	FOURE DIFECTIOUS ANEMIA VIRUS (ISOLATE WYOMING)	2							L	L
PENV ELAVY	EAV TOLITICAL STATES	FELTINE ENDOGENOUS VINUS ECE!	99-00			-					
PENV FENVE	CAV CALINOTES	FELTIME BIDAUMODEJICIENCY VIRUS (ISOLATE PETALUMIA)	630.020					1			
PENV FIVE	ENV POLITROISES	FFI THE DOLUMODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	30.00	2				1	1		L
PEN FINED	ENV POLITROIES	FF! THE DOMINODEFICIENCY VIRUS (ISOLATE INU)	640-679					1	1	-	ļ
PENV FINES	ENA POLITACIONA	FEI THE LEINEMAN PROVINCIS (CLONE CFE 4)	509-531				1		-	-	L
PEN FLVCS	ENV POLYPROTEIN	TEL NATIONALIA VARIA (STRAIN AGLASCOW-1)	490-519						1	1	1
PENV FLVGL	ENV POLYPROTEIN	TELLINE TELLISTICS (STRAIN LANDON-BI)	810-338			ļ			1	1	1
PENV FLVLS	ENV POLYPROTEIN	STATE STATES OF THE STRAIN SARMA!	417.516							1	1
PERV ILVSA	ENV POLYPROTEIN	TELEFORMATION CONTRACTOR CONTRACT	77	318-355	166.493						1
PENV FOAMV	ENV POLYPROTEDN	THE PASSONS OF STRAIN CARDINER, ARNSTEIN)	310-319							1	
PENV FSVCA	ENV POLYPROTEIN	THE PARCET STATE AND A PARCET STATE STATE AND A PARCET STATE STATE AND A PARCET STATE STATE STATE STATE AND A PARCET STATE S	680.519								1
PENV FSVCB	ENV POLYPROTEIN	THE INE SAUCOMA VIANS (STRAIN CA)	493-522						4	-	4
PENV FSVSM	ENV POLYPROTEIN	PETINE SANCON VINCE (STORY)	174-103	333.564							1
PENY GALV	ENV POLYPROTEIN	GIBBON APRILEUKEANA VIKUS	342.176	L							4
PENY HILLIA	ENV POLYPROTEIN	HOMEN I CELL LEUKEPUR VINOS I TIE CONTROLEMICOLATE	142.576							-	1
PENY HILLIC	ENV POLYPROTEIN	HUNCA I CELL LEUKENDA VIACO I ITE (COLORE ATE INT.)	102.176							-	4
MI IM	ENV POLYPROTEIN	INDIANT CELL LEUKENDA VIRUS LITE ILISOLATE TITT	114.130								4
IN III N	ENV POLYPROTEDI	INDUAN I CELL LEUKEMIA VIRUS I TTE II	144.463	410.682	20.00	L	L				_
STINE AND	ENV POLYPROTEDY	INDIAN DOWNODE ICIENCY VINUS 177E I (ANY 2011 IOCALE)	444.464		=						
INIT ALL	ENV POLYPROTED ^I	HEALLY BOACHODES ICIENCY VIRUS 1 VPE 1 (BILLIUS DEA)		100	ī						
100	ENV POLYPROTEDA	INMAN DOMINODES ICTENCY VIRUS TYPE I (BITE 190LATE)			Т	678.679	38.5815	Ļ			
200	DO POLYMOITON	INDIAN BOARMODE RCIENCY VIRUS TYPE I IBRAIN ISOLATE)				т	Т		L		
PERV HVIBA	ENV POLYPROTEIN	INDIAN DEANOGE ICIENCY VIRUS TYPE I IBRU ISOLATE)				101.01	1	ļ	Ļ	-	
TEN HAIR	NAME OF STREET	HUMAN BOATHODESICIENCY VIRUS TYPE I (CDC-45) (SOLATI)							-		L
DIA HAIC	EN POLITICAL STATE OF THE PARTY	HUBALAN BEALDMODES ICIENCY VIRUS TYPE I (ELLISOLATE)	2				1	1			
DIA HAID	EAV AND VALUE OF	INDIAN BOADHODE KENCY VIRUS TYPE ! (ILXB) ISOLATE)				1	1		-	-	
PENV HVIR	Con to valoritor	HANDAN DOMINGOEFICIENCY VIRUS TYPE I (IIXB) ISOLATE)			Т	803.63	1	-	-	-	L
PEN HAIR	THE PARTY OF THE P	HEMAN BOARNODESKIEMCY VIRUS SYPE I (MI) ISOLATE)			Т	т	+		ļ	L	-
2											

PCCFNE	167-176-4										
PILENAME	PROTEIN	Mail	-1			Т	7	_	П		
PENV HVIKB	ENV POLYPROTEIN	HUMAN MORINODE PCIENCY VIRILS TYPE I SCIEVING ILL CHIST	430	3	4	J	1	9	A LAZA	ARTAL	AREA
PENV HVIMA	ENV POLYPROTEIN	HUMAN MANUNODEFICIENCY VIRING TAPIT TAKEN TATES	1				İ	-		-	
PENV HVING	ENV POLYPROTEIN	HUMAN BONINGOEFICIENCY VIRUS TYPE I MIE ISOLATE		107.70							
PENV HVINON	ENV POLYPROFEIN	HUMAN BOARNODESICIENCY VIRUS TYPE I AIN ICOLATES	T.				1				
PENY HVINS	ENV POLYPROTEIN	INUMAN BOALMODE/ICIENCY VIRUS TYPE I (NEW YORK -S ISOLATE)	Т						1	1	1
PENV IVIND	ENV POLYPROTEIN	INMAN BOARNODE INCENCY VIRUS TYPE I (NOK ISOLATE)	Т	336 503	62 -673		Ī		İ	†	ļ
PENV HVIOY	ENV POLYPROTEIN	HEMICAN DOMENOCETICAGNOT VIRUS TYPE I (OYI ISOLATE)	T	130.704	785.630				Ť	T	
PENV HVIEV	ENV POLYTROTECN	HUMAN BORUNGGENCIENCY VIRUS TYPE I (PV21 ISOLATE)	145.38	631.68	111.11		Ī		T	\dagger	Ī
PENY AVIET	ENVIOLITIME ENVIOLEN	HUMAN BOATHODERCENCY VIRUS TYPE I (REALIST ISOLATE)	210-307	131.371	554.602	240-029	200-812		t		Ī
PEN HVIST	ENV POLYTEN	HIGHWAY BOARDONE REPART VIRUS TYPE I (SFIRE ISOLATE)	П	136-565	622.674	783.800			İ	f	Ī
PENV HVISC	ENV POLYPROTEIN	HUMAN MACHUMOZI ICIENCIT VIAUS 17PE I (SF)) ISOLATE)	_	633-630	717-115					ŀ	Ī
PENV HVIWI	MATCH AND AND AND AND AND AND AND AND AND AND	HAMAN BEAUMOOFICENCY VIRUS TYPE ((SC (SOLATE)		10.50	134-119					İ	
PENY HVIW?	MATOR VALUE AND THE PARTY AND	MANAGE INCOME TO THE PARTY VIRUS TYPE I (WALL) ISOLATE)		\$45.593	631.683	=======================================		Ī	<u>:</u> 	:	i
T	ENV POLYBORED	MUNICAL DESCRIPTION OF THE PARTY OF THE FOUNTS IS SOLVED.		136-514	613-559	783.604			-		
T	HV POLYPROTEIN	ROMAN MANUNCOLD RELEASE Y VIRUS TYPE ((22/CDC-234 ISO) ATE)		105-205	621.640	30.130					
	ENV POLYPROTEDA	MANAGEMENT OF THE PROPERTY OF	٦						<u> </u>	-	i Į
Ī	ENV POLYPROTEIN	MANAY BORROTERIES VIEW VIEW VARIATION	┑	2	900	2				_	
	ENV POLYPROTEIN	JONIAN BOARDER FIRENCY WELL TORE (C. 14 150 LATE)	╗	20.50	3	37.8.5				<u>-</u>	i
Ī	ENV POLYPROTEIN	INDIAN BARDNOOFFICENCY VIBILS TYPE VICO ATERICS.	2	9	ī						
PEN MACA	ENY POLYPROTEIN	ICHAN BEACACOCICENCY VILLE TOPE THEY ARE THE			Т	5					
PENY HYZDI	ENV POLYPROTEIN	TRACAN BACINOS PICTORY VIEWS 1965 11601 1 P. D. D. D.	314.30	2	52.64						
	ENV POLYPROTEIN	PARLAN BONDO DE PICENCY VILLIS TYPE 3 LICEN ATE CHANGE	Ì		1	7	İ				
1	ENV POLYPROTEEN	HUNKA BOADNOOFFICIENCY VIRIS TYPE PLICOLATERINGS	Ī	7	7	7		-			
	ENV POLYPROTEIN	HUMAN BOILDHODE HORENCY VIRUS TYPE 3 JISON ATE BOOL	1		7	000	65.08	j			
П	ENV POLYPROTEIN	MANAN BONDMOCENCIRENCY VINUS TYPE 3 (150) ATE 51/24 (Ce)	1				İ	<u> </u>		1	· ;
PEN HYSS	ENV POLYPROTEIN	INDIAN BONDWOOD KIENCY VIRUS TYPE I INCHALE SIII ISYI	Ŧ		ī	710	ĺ		-	:	
7	ENV POLYMOTEIN	HUMAN BONUNDOEJICIENCY VIRUS TYPE ZIISOLATE STJ	ī	!	41, 41	-	i	İ	1		
1	ENV FOL YPROTEIN	MANK CELL FOCUS-FORKING ARTINE LEGICEALIA VIRUS	T	ī	7	Ì	İ	†	1	1	Ì
1		MINK CELL FOCUS FORMING MURINE LEUKENIA VIRUS (150LATE CI.1)	400.5115	Ī	Ī	İ	İ	T	İ	 	-
A CONTRACTOR	ENV FOL TPROTEDI	AKY MURDIE LEUKEMIA VIRUS	317.344		Ī	İ	l	\dagger	İ	!	Ī
T		CAS-BR-E MUNDAE LEUXEMIA VIRUS	\$10.539	Ī		T	T	t	1	1	1
T		MEND MUDDE LEUKENIA VIAUS (ISOLATE 57)	113.533				İ	†	1	+	
Ī		FALSEN MURLINE LEUNEAUR VIRUS (ISOLATE FB39)	133-555				T		+	+	Ī
T		HOLD FUNDE LEUKENHA VIRUS (ISOLATE PVC.) ()	83-68				İ		1	\dagger	Ī
T		MONTH MONTH LEUKEMIA VIRUS	\$10.540					T	l	<u> </u>	Ī
Γ		LOS OFFE FORMS FEINERS WINGS	-					\mid	_	l	Ī
Ī		RADIATION BURDA I FIREING VIDIG	20.50	İ					-	H	
		RADIATION MURDRE LEUKENIA VIRUS ISTRAIN KAPI ANI			1						<u> </u>
7		MOUSE MANAKAY TUMOR VIRUS (STRAIN BR6)	2	10.00		1	1	1		+	
7		HOUSE MANMARY TUNIOR VIRUS (STRAIN GR)	Т	100	1	\dagger	+		+	1	Ī
Phy Leves	CAV FOLTEROISE	SPILAN MASON-PFIZER VIRUS	Н		T	l	1	\dagger	+	\dagger	Ī
T		CONTRACTOR CONTRACTOR AND CONTRACTOR CONTRAC	٦					-		-	T
T		A HOUSE LANG CELL PACIE PACIENT	٦	196-223	160-607					ŀ	Ī
Γ		SUCIAN FORLY VEHICLY OF IL	_					-	-	-	Ī
		SDOAN FOART VILUS ITYPE 1/STRAINLEIN	7	104-00	7						<u> </u>
	ENV POL YPROTEIN	SPEAN BORDNOOFFICENCY VIRUS LAGINISS ISON ATES	7	Ŧ	Т	٦	1				<u> </u>
		SPBAN BOACHODE/ICENCY VIRUS (AGM) (SOLATE)	2 2 20 20 2		T	7	2				
		SOCIAN DOCUMODES ICIENCY VIRUS (ISOLATE AGMI/CLONE GIU. 1)	T	T		4.14.708	067-607	+	1	1	1
		SPIGAN DOMINODES ICIENCY VIRUS (TYG-1 ISOLATE)	T	T	Т		+	1		+	Ī
		CHIND ANZ E.E. DONDHODEFICIENCY VIRUS	-	Т	1	T	237.467	+	+	1	1
ENV SIVE		SPEAN BOADHODEFICENCY VIRUS (ISOLATE GB1)	Т	ī	T	Т	+	\dagger		+	Ī
		SINGAM INDIVINOUS (CENCY VIRUS (PONING) ISOLATE)	П	1	T	1	\dagger		$\frac{\perp}{\parallel}$	+	Ī
I	DAY POLYMOTEN	SIMILAN INMANTALICE RESIDENCE STREET PARTY (SOLATE)		277.209				+	+	+	T
Ī		TOTAL CHARLET TINUS (NEW ISOLATE)	153-404			Н				H	Ι
											7

\prod	07217814	AH Vierzes (no hecterophoges)	Г		i	•	۰				
H			I	AREA!	A KAN	- 010	<u> </u>				
١			T		9 845.655	691.718					
	PROTEIN	DLATE	╗	Т	Т	1					
J				554.595		Ì					
			100-463				1	T			
			169-431			j	T	T	Ì		
=			13-62	8	1	Í		T	Ī		•
١		VISMA LENTIVIAUS (STRAIN 1914)	13-43	160.607	1	Ì					
١			11-62	5.100		1					
			100.334						1		
	L		Т	84.69	230-381						
	Т		Т	430.407							
	T	STATE OF IN STRAIN COPENIAGEN	Т	180 483							
T	FABLY TRANS PACTOR 70 KD SUBURIT		╗		1					:	
I				74.210			ĺ		Ī		
1	Г	SINAIN CUTEMINGEN	6.43	174.210	207.30			Ī			
	ŀ		100.119								
	ALLY TRANSCULLION FACTOR	TER VIRUS (STRAIN DUMAS)	116.00								
	LKALINE EXONUCLEASE										
l	AL A ROTED PROTECT	HURAN ADCINO AND	20.210								
Ī	National dates	HUBANA ADDINOVINUS ITTE 41	30-33								
	I o m reconstruction		134.181	446-47)							
	FIREK PROJEIN		771 011	141.441							
Γ	FIREA PROTEIN										
Ī	COLUMN PROTEDI										
T	23.000		175-305	125.352							
May ADEB!	INCH CROSEN	KIOUSE ADENOVIRUS TYPE	138-169								
	FIREM PROTEIN	FAR LAMINE OSTEOSARCONIA VIRUS									
	V-FOS-FOX TILANSFORMENCE AND FACE OF THE PARTY OF THE PAR	A LA A DE TROVELIS NX 24									
Γ	PSS.V.FOS TRANSFORMONO PROTEIN	ANIMA PLANCOS PRODUCE VIRUS									
	SELVEDS TRANSFORMING PROTEIN	B) MUNICIPALITY COLUMN TO THE	230-22						L		
	SALAN VAROTEDA	AVIAN SPLEEN NECKONS TIPOS ATE WYOMING)	144-171								
١	CALCAST CALCAS	EQUINE DO ECTIONS ANEATIN VINUS LISUANIE	621-648								L
١	GAUTOLITAGE	HUNAN SPUNARETROVIRUS	196-442	1171							
>	CAG POLYFAUER	CHANGN APE LEUKENDA VIRUS	911.118								
	GAG POLYPROTEEN	AND AND DANDOEFICIENCY VIRUS TYPE I (ARVEST LIBOLATE)				Ĺ					1
POAD HVIA	GAO POLYTHOJEM	LABLAN MANINODE INCIENCY VIRUS TYPE I (III) ISOLATED			_						1
	GAG POLYPROTED	THE LINE IN THE PRINCE VIRUS TYPE I (MA ISOLATE)									
T	GAG FOL YPROTEIN	HUMAN STATES TO THE STATE BEN									
Ī	A CO VOEDTEDA	INDIAN BEAUTON THE THE STATE AND A TR DIAN	===					1			L
	UAU CALLENS	HABLAN BARLINGE KLENCY VIALS 1775 A 1800 A 18 MIL 31	11:113	L							L
POAD HVIDI	GAG FOLTFRUIELE	IN BLAN BOARWOOES ICENCY VIRUS TYPE 3 (1901-A12 PIN-1)	1								1
POAD HYZNZ	GAG POLYPROTEDI	THE PARTICULAR OF THE STREET STREET STREET					L				1
San Broke		HUMAN WENT AND	100					L	_		
CAC III	SETT OVILLE LELATED GAD FOL YPROTE!	III WILL WINNESS TO THE PROPERTY OF THE PROPER	3	100	200.7		1			L	
AO DHA	THE A PER A TEN GAG POL YPROTE	INOUSE BYTACISTEMAL A-PARTICLE	\$ -130								L
POAD DYA	METHOWAY PRINCIPLE CAS NO VERDITE		1	1.00							1
POAD BYLAE	RETROVEUS-RELATED GAU POLITACIE										4
NAME OF STREET	CAG FOL YPROTEIN		=						L		
	CAST TO VERDITEDA	MOUSE MANAGEM 1	<u>=</u>	36.			1				_
PGAO MONING		WOUSE MANALARY TURIOR VIRUS IS INVIEW OF	333.260	L					1		L
POAG MARTYO	GAU PULTEROISE	ENGAN MASON PIZER VIRUS (NOMV)	107	434.451	L						1
POAG LONOV	GAG FOLYPROTEIN	STOCKE CHARVISIAE VIRUS L.A									4
A SPAN A	MAJOR COAT PROTECT	SACCONE CITY VIBILS (ISOLATE AGN) (CLONE CRU-1)	2		1	1			L		
1	DAG BOX VOED FED	SPAN PARCHODE THE STATE OF A TEN	===				-	-			L
MAG SIVA	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COL	SPAN BOALHOOD FLERE I VACOINE	111.115								1
DAG SIMA	GAUTURO	SOLAN BOACHOOF KIENCY VINUS (SIM ISOLATE)	111								1
PGAO SIVMS	GAG POLYPROTECH	THE HAM PLAN PROPERCIENCY VIRUS (F134/SAITIN ISOLATE)		ļ			_				1
DAD RIVER	GAG POLYPROTEDY	SIMILAR PROPERTIENTY VIRUS (POUDCI) ISOLATE)		1	1		-		L		
80018	GAG POLYPROTEON	SINIVA MENONACIONALIS	397-441			-	+		_	L	
	CAR POLYPROTEDI	STATAN SALUTON TOOL	333-261				1		-		L
CAC SHISA	CATO POL VPROTEDA	SECAN RETROVUOS SKY-1	1184-211	321.348		4	1	1	1	 -	L
POAD SKVI	UAC TOTAL TOTAL	EOUDG HENESVOLUS TYPE I (STRAIN ABA')	11749	_							ļ
HELL HSVED	PROBABLE PELTANASE	LEEPES VIRUS SABADU (STILAIN !!)	111	101.338			L				4
HELL HSVSA	PROBABLE RELICASE	WARITED I A. ZOSTER VIRUS (STRAIN DUNIAS)			-	-	-				4
CA CA 1947			7.02			-	-		-		_
	HENANCELITIDIDI ESTERASE PRECURSO	SOR BOVING CURCHA VIACO (STEAS AND VIAL)	106-141			1	1	-			-
THE CASE	THE PRECURSOR	SE SOVER COLORA VALUE (ST INCAME TO ST)	204-342			-				1	
ATENY CARTA	HONOR OF THE PARTY	EXTENS CORPUS VIBILS (STRAIN NEBUS)									

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1		N. Vinnes fan heeferhaabstert					-	-	-	-	Γ
1000	I		ARFAI	AREAT	AREAD	ARGAG	AREA & AR	AREAG	AREA? AREA!	A O AREA 9	•
PIEMA CVBO	HEMACCLUTININ-ESTERASE PRECURSOR	BOVINE CORONAVIRUS (STRAIN QUEBEC)	206-202						_	Т	1
PIEMA CYNOC	URSOR		101-141								i
PHENA IAAK		HFLUENZA A VIRUS (STRAIN A/AICIIVZ/61)	117.453								
MEMA INDAN		MILUENZA A VIRUS (STRAIN ABANGKOKJIN9)	34.51	111.417						•	1
MEMA INDUD	PRECURSOR	סעועו)	13.13					+	+	+	
HEMA INCAO			9				+	+	1	+	Ţ
PREMA MOTA	INC. LANCOL UT INCH. PRECURSOR	INCLUENCE A VINCE STEAM ACTIVERMENT AND AND THE		113.441	404.438	Ì	1	+	<u> </u> 	1	1
MENT INCH		1,000	76.78			Ì	<u> </u> 		<u> </u>	<u> </u>	1
PHENA IACKY			4		; :	:	:	•	_	•	
MICHAL IACRV		Ī	1	114.441	Ī	İ	1	-	<u> </u>	1	Ī
MENA IANA						T	+	1	+	+	
PIEMA IADAS			18712	490.543						-	I
PHENT IN TANA			117.11			İ			<u> </u>	l	Ī
THE LA LABARA			3.5	418.478		İ	<u> </u>	<u> </u>	!	<u>:</u>	_
PHENT INC.		KIANKI	111.411		:	!	· : i	:	:	:	•
PIEUA JADEI			31:38	407-451	3			1	<u> </u> 	H	Ī
PIENA IABILI		-	111-111						<u> </u>	<u> </u>	
PICEMA IABAS			11.41)			Ī			1	<u>!</u>	
PICEMA IADRU	Ī		111-111						<u> </u>		Ī
PIEMA JADIN	DEMAGGLUTING PRECURSOR		11.43	Ī						<u> </u> 	
PIEMA MADIS		3	10.15	1	!	į į	1	_		_	_
PHEMA IATH			11711			İ		<u> </u> 	<u> </u> 	<u> </u> 	Ī
PIEMA IADRO			111-111			T		-	l		Ī
PIEMA IADOR	HEMAGGE LY DON PRECURSOR		1			T		+	<u> </u>	+	Ī
PIEMA JADAO			×:			T		1			Ī
1			101.453					\mid	l		Ī
L			35.10				- 				
ı		(STRAIN ADUCKNEW YORK/12/11)	25:12							L	
Н	HEMAGGLUT BYTH PAECUASON	1)1/1/6)	101-431					L		-	
П			21-55								
MENA INDU		/63)	3								
- 1		The second secon	٦								
PIEMA MEN			٦		1	1		1	4		
HENA WIT		DATIFICATION A VINUS (SIRVIN ACOME, PLACUE VINUS NO SIUCKOA)		2	1		+	+	1	+	1
PIEMA IAGID	HEMACATTINEN MECIESOR			Ī		1	1	+	+	+	Ī
PIEDA IAGUA			3			+	+	+	+	+	
PIEMA MAL		ER\$/13)	1				-		<u> </u>	-	Ī
HEM MIM										\vdash	
MEMA MICS				194-321	111-457			_			Ī
MEMA MHC		2	1	- X	200						
PITEMA TANDE	HEMANGELO HANN PARCURSON	BET TEXT A VILLE OF TAIN ACCUMENT OF TRUITING		22.4		\dagger	+	+	+	+	T
PIESTA MISO		1076)	-			\dagger	+	$\frac{1}{1}$	+	+	T
PIEMA WICK			100			 		+	<u> </u>	\downarrow	Ī
PHEMA_LANK7			386-452				-				Γ
PHEMA INICE			П	194-221	110-457						Π
HEMA WILD	HEMAGGLUTININ PRECURSOR			194-221	10773				-		Π
HEXA MAG					1	1	+	+	+	1	Ī
HEMA MOSE	HEMAGGLUTDEN PRECURSOR	INTELEGRAL A VIRUS (STRAIN ARQUINGNEW MARKETON)				†	1	+	1	+	Ī
PREMA IMPR				2		1	+	+	+	+	ī
MENA MEN			٥	77.74		\dagger	\dagger	$\frac{1}{1}$	+	+	T
HEM WISA		150	Т	Ī	T	T	+	$\frac{1}{1}$	$\frac{1}{1}$	+	T
PIESTA WISP			Ī	14.221	111-111	†	+	+	+	+	T
PIESAA TAHSW	HEMAGGLUTINGN PRECURSOR	INTLUENZA A YIRUS (STRAIN JAEQUINE/SWITZERLAND/11/17)	2,5	10.15	117		+	+	+	+	T
			1				1			$\left\{ \right.$	7

anauce.	167.17816	AR Viceto (no nativitality)	AREAL	16310	20110	1					
	TO LOCAL	VIEWS						1	1	Ī	١
THE PARTY.	INCHARGE UT BAIN PRECURSOR	DELUENZA A VIRUS (STRAIN ACCUINCITURNESSED AND	36.635					1	1		
THE PART IN THE	THE LANGE OF THE PARTY PARTY IN SOR	POLUENZA A VIRUS (STRAIM ARQUINE) UN 1011	116-452						Ì	ŀ	
2 14 15	INCHESCIPLES PRECIDED	INTELLENZA A VIRUS (STRAIN ARQUINEURUCUATION)	167					1			4
PERO MIN	THE PROPERTY OF	DOLUENZA A VIRUS (STRAIN AUA) ANDOYS I	1	11757							
NEWA WAY	TOTAL PRINTED	INFLUENZA A VIRUS (STRAIN A/KIEVISW79)	T	23.470							İ
A WE	TO SECURITY OF THE PARTY OF THE	INFLUENZA A VIXUS (STRAID) AA ENINGRADUSO!)	97.461								
PENA MEN	TENTA COLUMNIA PRECINSOR	INTLUENCA A VINUS (STRAM) APIALLAND/ASTRAKHAMATORS)	11.43								
NAME OF		INTELLENZA A VIRUS (STRAM AAIALLARD'AS HAKHAMINI)									į
PIEMA IAMAB	HEMACALUINA PACCAROCA	INFILIENZA A VIRUS (STRAIN ARIALL ARDINEW YORKASTUTI)									
PICEMA IAMAO	HEMACCLUTIMA PRECUESOR	INTERIOR A VIRUS (STRAIN ARIENDINS)	2								
PIEMA IAMEI	HEMAGGLUTININ PRECURSOR	CALLEGES A CHIEF ATTAIN ANIENDRISHOUS	19-01								
PIENA IMES	HEMAGGLUTING PRECURSOR	INTUENCY A VINCE TO AND ARTENDATION	14-51	2							
PIESTA TAKES	HEMAGGLUIDIN PRECURSOR	TOLUNCA A UNDER STATE A A LOCK OUT TO A LOCK	11.31	362-441							
	THE MARKET LITTENIN PRECURSOR	INTLUENZA A VINUS ISTRAIN AMILIAS TOTAL	117-453			1		-			
ı	THE STATE OF THE PARTY PORT IN SOR	INFLUENZA A VIRUS (STRAIN ANT MON)	100.000		į						
MENA IAMI	FEMALUS BANK TANGER	MALLENZA A VIRUS (STRAIN AFILL)! WIIAL IJALVINIVI	7,52	1							
	REMACCEUTING PRELONSON	CALLINESS A UTBIS (REPAIN APUERTO RICO/D/14)	29.30								
	HEMAGGLUTININ PRECURSOR	TOTAL TOTAL STATE AND AND WHICH	24-51								
L	HEMAGGLUTOWN PRECURSOR	INTELLEGICA A VIACO (STANCE) A STANCE ON FAIL WILESE YATES)	E Y/47/831 381-451								
l.	CHESTA PART PRECURSOR	DOLUENZA A VIXUS (SI ICAM MACCO) 102010	1111-431								
ı	THE PASSED IN PRINCIPLE SOLD	INTLUENZA A MRUS (STRAIN ASEALMASSACTIONE	27.46	160.187	306-347						
PIEMA MSEZ	TO SECOND	DOLUENZA A VINUS (STRAIN ASHEARWATERVAUSTRALIA 1)									
MEMA MAN	DEMACCIONING FREE COMPON	THE THEN A VIRUS (STRAIN ASTARLINGY ICTORIASTING)	114-110								_
HEM WSTA	INTERPRETATION PRECUESOR	AND THE A CORPER OF PAIN ACT AIN APPLICATION	29.56								L
1	HEMACGLUTING PRECURSOR	THE COLUMN THE PARTY OF THE PAR	415-445								L
L	IN MACCELLITHIN PRECURSOR	INGLUENZA A VIRUS (STRAIM AT LORKE THAT LAND AT LAND	381-451]
•	HELLA COL LITTED PRECURSOR	INTLUENZA A VIRUS (STRAIM ALIOTRE TIPHTAESOLINE	107.134								1
PIEMA INTE	THE PROPERTY OF	INTLUENZA A VIAUS (STRAIN AN URKE YOM (ARIUM)	474.444	911.100							
- 1	TO BE CARRIED THE PARTY OF THE	PULLENZA A VIRUS (STRAIN AN URKEYON (ANDUSTRIAL)	17.00	1	101.432		L				
- 1	PHANCEUL INTERNATIONAL PROPERTY.	THE LENGA A VIRUS ISTRAIN AN URKE YORE GOWILL	20.71								
	HEMACKALUI MAN PRACUASON	THE THEN A VIEUS (STRAIN ATURKE YMISCONSIN 1981)	100-410	2							
L	HENACCE UTDON PLECUASOR	MALTINION A VIBER ASTRADA ACTERIANDSTRALLIAGOC(1)	21-33								
	JEMACCLUTENTN PRECURSOR	CHILDRAL A CARING (CIRAIN ACIDORNIO)/72)	40.67	3							
HENA MUDO	INTERPRETATION PRECURSOR	TOTAL STATE OF THE ANY AND SENSON	29.56	425-478							L
	HEMAGGLUTENEN PRECUISOR	Taring to the life of the ANK TONIA JUST	17:17	311.454							L
	HEMAGGE LITENDA PRECURSOR	INTURACE CONTRACTOR OF PARTY AND AND CONTRACTOR (SALITIVE)	424-477								ļ
	HEMAGGLUTIWIN PRECURSOR	DOLUMEA A TAKUS (STRAIN PORTING FACTORIES)	35.55								
ANA LANA	HEMAGGLUTDEN PRECURSOR	DOLUDIZA A VIRUS IS IRAM A ALIAS COLOS AS A	19-00	187-453							1
	HENAGE UTBON PAECURSOR	Deligion A Value (STRAIR AS WIREA CLOSED SONORIOR)	111-111								1
	AND AND INDIAN PARCIASOR	DELUENZA A YRUS (STRAIN ASWINDING ACIDITIES	617-163				L				
THE MAN LAKEN	THE STATE OF THE S	DOLLENZA A VRUS (STRAIN ASWINERIGING RUNG 12012)	100	175							
PER MAN	TO SECURITION OF THE PARTY OF T	DOLLIEDZA A VINUS (STRAIN ASWINGANDIANA) 726/11)									
MENA MEDI	ROMONE STATES	INCLIENZA A VILUS (SHAIN ASWINEACEW JERSEY) (78)			-						
PIEST NATIO	MEDIA COLUTINON PRECUISOR	THE STATE OF THE STRAIN AS WINEAUXX ELVISA)	317-433								Ļ
HESA WATER	HEMACCLUTOWN PRECURSOR	THE COLUMN OF THE PARTY OF THE COLUMN OF THE	(F-80+	2						1	1
LA BURNE	HEMADOLUTBON PRECURSOR	POLUENCA STATES OF THE PROPERTY.	190-431	419-473	į						1
CHANGE BARRO	HELLAGGE UTDAIN PLECUASOR	INCLUENCE WINDS (STEAM CONTINUED)	390-439	437-481							1
A VICE	LIBERTACE LITERAN PLECUASOR	DALUENZA B VIII O SI PANTI PENANGANI	117-160	429.471						1	1
150	LISTANCE LITTORN PRECURSOR	BUT LENZA BYTHUS (STRAIN BRICKY) ROLL	199-430	431-463							4
1	SELLA COS ITTO ON PRECUESOR	INTEUENZA D VIXUS (STRAIM DULLE PRO)	110.430	478.472			_				4
MENA COLL	STATE OF STREET PRECINGOR	MALUENZA B VIRUS (STRAIN BALAKYLANDYY)	717-101	10.00	1						4
HENA PEND	THE PARTY OF THE P	DELLIENZA B YDUS (STRAIN BAILNONDAMA)	200								
MENA DOME	HENNOCOLUNIA MENDOS	INSTITEMENT BY VINUS (STRAIN BY ONE CONSAU)			-				L		_
HELA POOR	DAME UNING THE COLOR	INSTITUTED A PRUT (STRAIN INSTINGAPORE 221779)	CT-MC							_	
PIEDA DOSS	HEMACCEUTING PRESURSON	MET HENZA B VIRUS (STRAIN BAUSSAVIOURI)		Т		1					L
ICEMA PROS	I DANGE UI BEN PRECURSON	DIFLUENCE & VICUS (STRAIN BYNCTONIAM)	100	7	1	1				L	
EMA POBYI	IEMACALUI MAN PRECUESAM	INSTITUTION DATE (STRAIN EVICTORIAZAT)	100			1				L	L
HEDA INDVA	HEMAGGLUTOWN PRECURSOR	PARTITION A C VIRUS (STRAIN CCALIFORNIA/11)	165-501	1	-	1	1	1			Ļ
PIEMA DICCA	HEMACOL UTHEN PRECURSOR	PART IENTA C VIRUS (STRAIN CENCLANDA) 241)	(0):33		1	1	1	-			L
PIEDA MODI	IEMAGG UTDEN PRECUESOR	RET I BRITA C VIRUS (STRAIN CONEAT LAXE S/1167/54)	401-339		1	\downarrow	1			L	L
HEDA DICCL	HEMAGG UTBON PRECURSOR	KAT I ESCA C VILLE (STRAIN CATOCOVA)	35-136	4	-	1	1		L		L

PCCFNF	10111111	AB Virgin (as hadedashin)						f			F
FILE HAME	PROTEIN	YIRU3	AREAI	AREAI	ARCAL	ARCAS	AREAS	AREAS	AREA? A	AREAB	AREAD
PIEMA DICKY	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CKYOTOVI/II)	412.558				П	1	1	Г	
MEMA BICH!	HEMAGGLUTDAN PRECURSOR	INFLUENZA C VIRUS (STRAIN CAISSISSIPPUIO)	413-536							 	
PHEMA INCHA	HEMAGGLUTININ PRECURSOR	DIFLUENZA C VIRUS (STRAIN CPARANT)	442-558								
MENT DO	HEMAGGLUTINGN PRECURSOR	INFLIENZA C VIRLIS (STRAIN CPICAEIINGIONI)	403-559							-	
MEMA INC.	HEMAGGLUTING PRECURSOR	DELUENZA C VIRUS (STRAIN CPIGNEIIING/IIS/II)	483-559								
MENA INCP.	HEMACCLUTIONIN PRECURSOR	INCLUENCA C VIRUS (STRAIN CPIGMEIIING41941)	413-559								
MENA INCIA	HEMACCLUINAN PRECURSOR	INFLUENCA C VILUS (STEAM CTAYLOR/13)/47)					Ì		1	j	ا
V 100	TECHNOLO I MANTECUASON	THE FORMER OF A PROPERTY OF A PRINCIPLE OF A PRINCI	1							j	
MENA MOVA	TEMACALUI ININ TRUCKAMININASE	NEW CASH LE MARASE VINUS (STRAIN AUSTRALIA-VICTORIA/17)	2.0				1	1	1		
THE PERSON NAMED IN	TENANCE OF THE PROPERTY AND ASSESSED.	NEW CASILE DASEASE VIRUS (SILIAIM BEAUDE) LE CAS)	1					1		1	
WENT TO THE	HEMACALUI MIN PROTAMINIDASE	MEMORALE DISEASE VIRUS (STRAIN DZG76)							1		
PATERIA POPUL	MENACALUI MIN-NEURAMINIDASE	MENTAL MARAGE VICES (STRAIN STRAIN)		İ			Ì	İ	j	i	
THE PARTY	TEMACAL DI MININE DI CAMINIDA SE	NEWCASTLE DESCRIPTION (STRAIN ITALIENAS)	-					İ	1	-	:
PIGMA POVA	HEMACULUI DAN PRUKAMINDA SE	MEWCASTLE DISEASE VIRUS (STRAIN MYADERASI)	2.9								
PIEMA MOVO	HEMAGGLUTIMIN-NEURAMONIDASE	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLANDAS)	3								
PIEMA MOVTO	HEMACKELTI DON-MEUTAMINIDASE	MEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B /41)	2								
PIEMA NOVO	HEMACOLUTING NEURAMINEDASE	NEWCASTLE DISEASE VIAUS (STRAIN ULSTERAS)	2								
PIEMA PHOOV	HEMAGGLUTININ-NEURAMINIDASE	PHOCING DISTEMBER VIRUS	39.66	£-1			ļ				
PIEMA PIIRW	HEMAGGLUTIMIN NEURAMINIDA SE	HUNCAN PARAINFLUENZA I VIRUS (STRAIN WASHINGTOW 1951)	79.110	166-393						<u> </u>	
PIEMA PUB	HEMACCIUTIONN-NEURAMINIDASE	BOVINE PARAINTLUENZA 3 VIAUS	£ 6.								
MENA PUR	HEMACCI UTDON-NEURAMINADASE	HUMAN PARAMFLUENZA 3 VIRUS (STRAIN NIH 47883)	133-41						-		
MEMA PUHA	HEMAGGLUTDAN-NEURANGNEDASE	INDIAN PARADIS LIENZA 3 VIRUS (STRAIN AUS/124854/14)	27-61								
MEMA PUHT	HEMACCEUTING NEURAMINIDASE	INDUCAN PARADAL LIENZA 3 VIRUS (STRAM TEXOSOSMO)	17-76					,			
MEMA PINIU	HEMAGGE UTTHIN NEUTRAMPHIDASE	HOMAN PAKABELUENZA 1 VIRUS (STRAIN TEXPJOSAZ)	23.70						r		Ī
PICEMA PIJHY	IEMAGGLUT DAN WEURAKINIDA SE	MINAM PARANGLUENZA 3 VIRUS (STRAIN TEXIZERIA)	27-61								
HEMA PIIIN	HEMACOLLT INDI-HEURAMINIDASE	HUMAN PARAPELLENZA 3 VIRUS (STRAIN WASHWAITY)	13-41							-	
MEMA PUHX	HEMACCLUTING MELRAMONIDASE	HUMAN PARADILLENZA 1 VIRUS (STRAIN WASIVISIO)	137-61								
PIEMA MACYI	HEMAGOLL/TOWN PRECURSOR	RACCOON FOXYRUS	166.21	256-203							
PIEMA SEXOS	HE MAGGLUT DADANE URANGINIDASE	SENDAL VIRUS (STRAIN Z / HOST MUTANTS)	79-106								
PIEMA SEIO	HEMAGGLUT DADI MEURANGMIDASE	SENDAL VIDUS (STILAIN FUSHING)	¥ 100								
TOTAL STORY	I ENACCEUTION AND ULABORIDASE	SENDAJ VIRUS (STIAM MARCUS)	8				1				
The second	PERMACALUI IPMIN-PELIMANANIANAN	SCHUL VILLE (STILLIN MY)	8	7		1	1				
MENA SEALS	HEALT OF THE STATE OF A PARTIES AND A SECOND OF THE STATE	SENDAL VICTOR (STRAIN 2)	8 :							1	
Т	HEMACO INTERNATION COL	VACCING VINITE OF CORRESPONDED	77	77-16			İ	+	1	1	
PIEMA VACO	HEMADGLUT BON PRECURSOR	VACCEDIA VIRUS (STRADA BID-D)	Т	Т	116.36		T	\dagger	+	\dagger	
Т	PENAGGLUTBEN PRECURSOR	VACCINIA VINUS (STILAIN TIAN TAM)	T	Т	16.36	T	Ť	\dagger	+		Ī
Т	HEMAGGLUTBUN PRECURSOR	VACCINIA VIDUS (STRAIN WR)	Т	13.202	2		T	\dagger	$\frac{1}{1}$	+	Ī
PIEMA VARV	HEMAGGLUTING PRECURSOR	AANOLA VIRUS	- E	117:41	214-244			\mid		-	
PIEXS ADESS	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIALUS TYPE 3	100						ŀ	-	
PHEXB ADEOS	HEXON-ASSOCIATED PROTEIN	ILLEGAN ADEMOVIBLE 1 YPE 5	100-134					-	-		
VIEXO ADEO?	IEXON ASSOCIATED PROTEIN	HUMAN ADENOVALUS TYPES 1 and 7	97:131								
MEX ADEM	HEXON PROTEIN	IRMAN ADENOVICES	-	300	37-480		1	1			
MEY AREA	MENON MOTERA	HIDAAN ANEMOVIE TYPE AN				1	1	1	1	+	
PIEV APER	WANTED THE PARTY OF THE PARTY O	BOUNDE ANEWOODING TOPE 1				1	1	1	1	1	
ACROS STUDIO	IENOR HACE DINICIPAL IS EN PROTEIN		10,50				1	1		1	
PIRO CONOX						1	1	1	+	1	
PILON AGE!	LATE PROTEON 11 MAI	ATBICAN SWINE SEVER VIRILS SCIE AND BASING						1	1	1	1
PIZZE ASFRI	ATE PROTEDUDADA	APPICAN CUMA PRIVE CITIES CONTRACTOR				1	1	+	+	1	1
PINTO CANA	THE PROPERTY PROTEIN	CATE IN OURSE LANGAUT VARIA CATE AND PAR		1		1	1	+	1	+	1
TOTAL CANNO	INC. USION BODY MATRIX PROTEIN	CALE IN OWER LOSSIC VILLE OF TAN DAY				1	1	1		+	
Ţ.	DACLUSION BODY MATRIX PROTEIN	CALL BLOWFA MOSAIC VINUS (STRAIN PVIAT)	917			1	1	+	1	+	T
Т	INCLUSION BODY MATRIX PROTEIN	CALVATION ETCHED RING VIRUS	1			T	1	+		\dagger	Ī
Γ	INCLUSION BODY MATRIX PROTEIN	FIGWORT MOSALC VIRUS (STRAIN DXS)	173-407			Ť	t	+	+	\dagger	Ī
	INCLUSION BOOY MATRIX PROTEIN	SOYBEAN CILCAOTIC MOTTLE VIAUS	Т	331.358		T	\dagger	\dagger	\dagger	\dagger	T
Γ	PROB PROC & TRANSPORT PRO UL 56	HUMAN CYTOMEGALOVIRUS (STRAIN AD149)	Ŀ			T	t	+	+	t	T
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A COL	Ī	ANSACTA MODALI ENTONOPOXVIRUS									
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Ī	THE POLICE IN THE PROPERTY OF		140.00				,		i		٠
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	IN THE PARTY OF TH	S VIRUS (SIRAIN BIRINDE VIBIL			-	1					
KITH ETV	THYMODE KRAN		19:3E								
Ī	CAME 14 PROTEDNIK DVASE	KTALUMU REVERSION	33:-								
Ī,	THE PROPERTY IN THE SECOND COC	VACCOMA VIRUS ISTRAIN COPENITAGEM									
	W. W. Charles and Co. London			I							
	10 KD PROTEIN KINASE POPPOLO	ENIAGEN	143-174				Ī				
PERMIT VACCE	POSSIBLE PROTEDY KINASIL BIZ		147-174	_							
0.000	POATER S PROTEIN KINASE BIS			Ī				(
	CASTALL BANKEN WALKER 18	VACCINIA VIAUS (STRAIN COPENIAGEN)								_	
_	CONTRACT OF THE PARTY OF THE PA										
PERF VALV	POSSIBLE PROTEIN KINASE FIE		===								
	ROS TYROSDIE KINASE TRANSF PROTEIN	AVIAN SALLOMA VIACS (SINALI ONS)	37.48								
T	TYPOGENE FOLKET TRANSF PROTECH RYK	AVIAN RETROVIRUS INC. 10									
I	AN INCHES TO A A A A SECOND TO	A VIAN SARCOMA VIAUS (STRAIN Y?))							L		
PKYES AVISY	200		310-411								
	LATE 100 KD PROTEDY	TOTAL STREET FOR THE PARTY OF T	316-413	`							
	LATE 100 KD PROTECT		167-161								
Ī	ATT 100 KD PROTEIN		116,306								
	SATISFIED BEDIEDA										
ALIM ALEA	LA LE INC. TO SEC. OF	(P)68									L
אנו ישרא	CATERI PENGRACIANI				I						
DI EDVC	LATENT MEMBRANE PROJECT		148-175								
HEAT TANK	LATEST MENGRANE PROTEIN!		28.131								
	l	EPSTEIN-BAUR VIXUS (STRAIM BY)-4)	1	310.314	407.424	632.656					
100	A SAN PANAR I ABLE LIBINA	SHOPE FIDROMA VIRUS (STRAIN KASZA)									
PACEL STVKA	MONA CAPON DO THE LAKE SUBJAN	VALPERIA VILLE (STRAIN COPENIAGEN)		201:-142	160-060						
PACEL VACCE	DON'T CAPPING DIG THE LARGE MISH	10 N		291-318	430-457						
WOLL WACCV	ABOUT CAPPING DIZING, LARGE SUBURG	VALLINIA VALUE (21 MAIL 1974)	11131	391-318	410-457						
VANV PO	LANA CAPPED EXCYME, LANGE SUBURI	_	278.313								
	ACTIVA CAPPOND DICYDOL	ASDICAN SWING PEVER VIXIDS (3) FAMILY BASILY	10.00								
7	TOWN COLUMN TO THE PARTY OF THE	CHICHMER GREEN MOTTLE MOSAIC VIRUS (WATERAILLUM STRAIM W)									
HOVE COLVS	MOVEMENT PROJECT	THE BABER CAPEN MOTTLE MOSAIC VIAUS (WATERAIELON STRAIN SH)	18181							L	
PLOVE COLOW	MOVEMENT PROJECT	DOWNSTONE OF URL BINGSPOT VIRUS	53.60								
MONT ORLS	MOVEMENT PROTECT	TELLIFORNIA VARIA VETRADA I IIA)	3								
MADY TOMVA	MOVEMENT PROTEIN		97-93								
MANY TOLVI	MOVEMENT PROTEIN	TOWN DECEMBER 1	143.170	329-356							
A PERSONAL	LINE TO THE VERTICAL ASE CVIDE	COLORDIA VIND MUIA	15.7	110.173							
	TANKEN ATION NO THANKS CYLAU	PANAMECTUM BURSALIA CHE ORELLA VINUS I	770.01	136.403							
-	AND THE A LICE CONTINUES PROTEON	AVIAN MYELOCYTOWA TOSIS YIRUS CMII		1					L		
MAC AVEC	MISCOS CHANGE OF THE PARTY OF T	AVIAN MYELOCYTOMATOSIS YIAUS MC29								L	L
PACK AVEAC	MIC HAMS COMMON TO SECOND	AVIAN LATEL OCYTOMATOSIS VIRUS HDI	27-102	2						L	
PATIC AVDED	ACYC TRANSFORMEN PROTEIN	ANAL PETROVIEW MODES:	239-268	77.404							
PLYC AVDO	MAYC TRANSFORMENC FRUILLIN	AVIAN BETEOVIEUS OK 10	137.761	10.197						1	1
AYC AVIOR	MYC TRANSFORMENS PROTEIN	A LANGE THE PARTY A CARLLE	393-420								1
PLYC ILV	MYC TRANSFORMONO PROTEIN	FELING LEUKANA VINCE	22755								1
TO IL CAN	LAYE TRANSFORMEND PROTEIN	FELDE LEUKLMA FROVINGS FFF	48.36	179.136		L					
VAR BEV	NACL FOCATS D PROTEDY	BEANG VOLUS									
	MAICH FOCAPSID PROTEDI	BUKYAVBUS LA CROSSE				L	-	L			
	AND DESCRIPTION	BLACKAVIRUS SMOWSHOE HAVE		50.00				L	L		
3											

PCCENE	\$60178s4	All Virgas fas beckriebbeen									
FILERAME	PROTEIN	Mais	AREAI	AREAI	AREAJ	ARFAG	ANFAG	AREAC	1864.9	1000	
PC CO67	MUCLEOCAPSID PROTEIN	CALAREAN-CONGO HEMORRHAGIC FEVER VIRUS (ISOLATE CA1011)	Ē	Ĺ			_	7	Т	Т	
MCA COVO	MUCLEOCAPSID PROTEIN	CANINE DISTEMPER VIRUS (STRAIN OND): RSTEPOORT)	140.176				Ì	İ	İ	1	i
MCS GRA	MUCLEOCAPSID PROTEIN	CHANDIDURA VIRUS (STRAIN 1653) 14)	\$7.90				İ	Ì	İ	İ	
PCA CYCAE	MUCL EOCAPSID PROTEIN	CANINE ENTERIC CORONAVIRUS (STRAIN K.)18)						T	İ		Ī
	7	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN PURD						İ	T		
	1	PORCING RESPIRATORY CORONAVIRUS (STRAIN 84137004 / BRITISH ISOLAT	181.23				İ	İ	\dagger	\dagger	1
PACA DICAV	MUCLEUCATED PROTEIN	PORCINE RESPIRATORY GONONAVIRUS (STRAIN RAIN)	111-111							t	16
700	Water Control of the Control	LICAGE VIALUS	231-365						-	\vdash	
176 17	MUCLEUCAVSID PROJEIN	FELINE IN ECTIOUS PENTONITIS VIRUS (STRAIN 19-1146)	183-209								
	MUCLEUCATSID PROTEIN	HAZAUA VIRUS (ISOLATE PC210)	6.13	114-203						<u> </u>	
102 10 100	NUCLEOLATS DIFFEREN	HAMAN RESPIRATORY STACYTIAL VIRUS (SUBGROUP B / STAKIN 18537)	4.31	74.108	100			Ī		ŀ	Ī
X 22 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	MACHE CASH STATES	HUMAN ALSPUATORY SYNCYTIAL VIRUS (STRAIN A2)	16.4						T	T	Ī
	March Special Property	LASSA VACO (SIRAM WATI)	64.19	147.134			-			-	Ī
200	MUCLEUCAND PROJECT	LASSA VIRUS (STRAIN IOSIAH)	64-79	\$2.5¢					T		
Y	MUCLEUCA'SID PROTEIN	LYMPHOCYTIC CHORIOMENINGITIS VIRUS (STRAIN ARMSTRONG)	16.53			Ī	Ī	Ī	<u> </u>		
200	MUCLEUCA SILD PROTEIN	MAGUAU VIRUS	19-17	192.319			İ				Ī
	MUCLEUCAVSID PROTEIN		2.2								
	MUCLEOCAPSID PROTEIN		137-404	433-412		T		T		\dagger	Ī
	NUCL EOCAPSID PROTEIN	01/1937)	11.404	11777			Ì	T		+	Ī
1	MUCLEOCAPSID PROTEIN	VIRUS (STRATH MIN 14780S	176.40]			Ī	İ	l	T	t	
	NUCL EOCAPSID PROTEIN	PUNTA TORO PIR EDGVIRUS	5.30			Ī		T	1	<u> </u>	ī
THE PURP	NUCL EOCAPSID PROTEIN	PLADMALA VIRUS (STRAIN MALLINAS BI)	<u>₹</u>			Ī	Ì	†	†	+	
PACAP PUDAS	MUCLEOCAPSID PROTEIN	PUDMALA VIRUS (STRAIN SOTRANIO)	2			Ī	Ì	1	\dagger	\dagger	Ī
3	NUCLEOCAPSED PROTEIN	PHELIMONIA VIAUS OF MICE	200			Ì		t		1	
PHCAP BABVA	MUCLEOCANSID PROTEIN		19:10			Ì	t			\dagger	Ī
32	MUCLEOCAPSID PROTEIN					İ	T	1		+	Ī
SAC MAYS	MACLEOCAPSID PROTEIN	PABIES VIRUS (STRAIN SAD BI9)	1916			Ì	\dagger	1	1	+	Ī
9	MUCLEDCAPSID PROTEIN	AIUTANIS	101-101			Ì	t	1	1	+	
30GS 42W	NUCLEOCAPSID PROTEIN	DERS)	107-(9)			Ì	\dagger	\dagger	+	\dagger	Ī
70CX 2007	MUCLEOCAPSID PROTEIN		16).404			İ		$\frac{1}{1}$	+	+	Ī
PACE SES	MUCLEOCAPSID PROTEIN	SICILIAN VIRUS	5			T	T	\dagger	1	+	1
34	MCC EDCAPS ID PROTEIN		¥	Ī		İ	T	1		1	Ī
NCA TACY	NUCLEOCAPSID PROTEIN		2	1		İ	\dagger	\dagger	\dagger	1	Ī
10SV	NUCLEOCAPSID PROTEIN		1				\dagger		1	1	Ī
25 CE	MUCLEOCAPSID PROTEIN		20:10			T	\dagger	1	1	+	
MCA WGW	NUCLEOCAPSID PROTEIN		28.314			T	T	\dagger	\dagger	1	1
THE WISH	NUCLEOCAPSID PROTEIN	Т	Т	384-314	T	T	T	1	\dagger	1	Ī
NS ASMO	NUCLEOCAPSID PROTEIN	_	т	Ī	İ	T	I		Ť	+	Ī
WCA VSVID	MUCLEOCAPSID PROTEIN	RSEY / STRAIN OCIDEN	19:00	36.36		l	t		1	+	1
PHCA VSVS	MUCLEOCAPSID PROTEIN	т	Γ		T	T	+	\dagger	+	$\frac{1}{1}$	Ī
WE HAID	NEGATIVE FACTOR	(ATE)	1				\dagger	\dagger	\dagger	+	1
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MOAN INCAN	NE IN ALTHOUGH OF	INTEREST A VINUS (STRAIN ABLACK DUCKAUSTRALIANOZNE)	9.5					-		-	Ī
PNEAN IACO	METER ALMANDA CIT		٦				-		-	-	1
PATAM JABA	MEI DALDENA CE		٦	2				\vdash	L	H	Ī
PARAM IAISE	MET BANDATO A CE						_				
PNIAM INTW	NELWANDASE	CANE VASIBLE	7	┪						L	Ī
PATAM MICO	NEURALONDASE	(BALLACE)	٦	٦	27:34					\vdash	
PATAM MARK	NEURAMONDASE	MATERIAL A VIEW ACTOR A VIEW ACTOR AND A VIEW AND A VIEW ACTOR AND A VIEW		_						H	[
PATCH INCE	NEURANDADASE		1	9.9	99-400					L	Ī
PRICEM MALEN	NE URANDADASE	25011	2 5	1				1			
PHILAM LANGE!	NEURANDASE		1				1	-			
PROCEED INFAR	HEURANDROASE	DELUENZA A VIAUS (STRAIN APARROTAL STEAT)			1	+	+	+	+	+	Ī
PARAM WAVE	NEURALONDASE		Ī		1	\dagger	+	1	+	+	1
					1	1	1	$\frac{1}{1}$	$\frac{1}{1}$	$\frac{1}{2}$	7

17.000	167217814		٦	1	1		1			-	
1000		VIRUS	19-61			1		-	 	╀	
AM IARUE		MELLENZA A VIRUS (STRAIN ATERNAUSTRALING VOCAS)	12				1	+	-	+	
PHRAM IATRA		INCLUDATE A COMPANIE OF A REMANDALL	2						<u> </u>	-	
MIAM IAUSS		INCLUENCE A VINCE COM AND AND IN THE PAINT IN THE COMMENT OF THE AND AND IN THE PAINT IN THE COMMENT OF THE PAINT IN THE P	19.88				Ī		<u> </u> 	+	
HILAH IAWAN		INTERESTAL VIELE (TEAN ANILSON-SMITIV))	3				Ť		_	-	
PRICEM LAWE		NATIONAL WILLS (STRAIN BALES/40)	Ē							H	1
PNEAN DIBLE	MEURANDRASE	BOACHYX DENSONUCLEGIST VARUS									
PHSI SEDEV	T	OWNERSONALICI EGGIS VIRUS	40-20	Ī							ļ
NS3 SIDEV	Ī	CONTRACTOR OF COOL VIRUS (STRAIN NL-01)		-					<u>i</u> 	i	
PASS BASVA		TO THE STATE OF THE PRAZE IN ISM ATE CENTIME AL		7	1		· !	:		i	
PASS TSWVB	1	CONTRACTOR CONTRACTOR	5.33	İ						+	
MAN TOWN	MON. STRUCTURAL PROTEIN	TONIATO SPOTIED WILL SINGS CONTINUES	10.49					1	1	-	-
VALUE	MICH EOSIDE TRUPHOSPHATASE	AMSACTA MODILE I EMILIANO MINOS	13:166	147.174	524-551			+	1	t	1
	LANCE ENRING TRIPHOSPILATASE I	CHORISTONE URA BIEJONIS EN IUMOPONATINO	16:53	194.421	\$14.547				1	†	
אונו כפני	THE PARTY TO SHAPE AS INCOME.	VACCINIA VIRUS (STRAIN COPEMIALEM)	Γ	194.421	\$14-517					t	
PHIP! VACCC	THE PROPERTY OF THE PARTY AND	VACCOGA VIRUS (STRAIN WR)	Ţ,	130.413	483.403					1	
PHITP I VACCV	AUCTEDAME INCHES	VARIOR A VIRUS	Т			114.613				_	
PATEL VARV	PRICE EOSIDE TRUMOSMINITASE	PERFECTION EX VIELS (TYPE 6/ STRAIN UGANDA-1102)	B							r	
PPIGO HSV&U	MAJOR ANTIGENIC STRUCTL PROTEIN	TEN CO JUNE 14 COMPANY OF NAME	81.13							 	
אינער	POLY(A) POL CATALYTIC SUBURIT	VACCINIA VIAUS (SOLATION COLOTION)	111:11						<u> </u>	Ì	l
	THE SUBURE	VACCINIA VIRUS (STRAIN WA)						1	1	t	١
PANI VACEV	THE PARTY OF THE PRINCIPLE	VARIOLA VIRUS	1					-		1	ļ
PI VARV	POLICY COLOR STATE	CAPILIPOXVIAUS (STRAIN KS-!)									
FI CAPAK	POLY(A) POL REU SUBURIL	SOUTH ON VIRING									
VOND CAMPV	POLY(A) POL REG SUBUNUT	TOWELOW THE STATE OF THE POLYHEDROSS VIRUS	61-105					+		İ	ļ
100	13 1 KIN PROTEIN IN PE STECTION	AUTOGRAPIA CALIFORNICA NOCESTA SIEGNATIC VIBILE	61.95					1	1	Ì	١
I'S PAT	THE PROPERTY IN PAR STREETION	OAGYIA PSEUDOISUGATA MULTILAZBID POLITICARDIS	104.348					-	1	Ì	١
PPELL NOVO	TO NO THE PARTY OF THE IN	AUTOGRAPIA CALIFORNICA NUCLEAR POLYTICOROSIS VIALS		1		_				1	
PPEJE NOVAC	MAJON IMPREMATE BASE OF THE PASSAGE	ALITOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS									
PPEAS MPVAC	48 3 KD IN PE-P28 IN ERICENIC ACOUST	CAN APPROVING GALIDISTRAIN SAJ)			17.5				-	_	
PEN ADEGX	PENTON PROTEIN	TAVEN SELL OF LEGENIC VIRUS (GERALAN ISOLATE)	113:01		_						
A DAYNO	GENOME POLYPROTECH I	PANES TELEFORM AND A PANESE STRAIN II-1)	1774-1801	1134-226				\dagger		T	
I VAN	CENOMIS POLYPROTEIN I	BALLET TELLOW MUSAC VINOS MOCALO VINIS	481.500	1404-1441						T	١
200	RMAI POLYPROTED	HUNGALIAN GRATEVINE CINCINE MOSKIC	136.193	119-919	\$36-956	1161-1193		1	1	T	ļ
	PUAL POR VPROTEDA	GRAPEVINE FAMILIA VINUS	1096-1123						1	1	
2	AND VODO TENA	TOWATO BLACK RING VIRUS (STIVAIN 3)	100.000	101.123						1	1
TOTAL TRANS	MAN TOUR OF STREET	BALLEY YELLOW MOSAIC VIRUS (GERMAN ISOLATE)	176 971	101.00							ļ
POLT BAYNO	CENTRE POST POST POST	MARI EY YELLOW MOSALC VIRUS (IAPANESE STRAIN II-I)									
POLY BATH	GENOME FOLYTHUISIN 1	LEGICANTAN CHAPTER CHACKLE MOSAIC VIRUS	=				Ţ				l
700 FO	KNA3 POLYPROTEIN	TOTAL STATE OF STATE	349-376							T	١
VIOLS GILV	INNAS POLYPROTEDN	COOK BY THE TANK THE TANK BEER YOU	983-1009		_					T	١
With the	INVA POLYPROTEDN	TOWATO REMANDI WAS USOCALE STA	1744	1010-1053						T	
2	CENTAL POLYPROTEDI	BOYDUE ENTEROVIRUS (STRAIN VC 3-27)	639-660	1012-1112	_	-	_	1609-2616	201-1042	1	1
TOTAL CONTEX	THE PART OF THE PARTY OF THE PA	BOVINE VILLE DIABINEA VINUS (ISOLATE MADL.)	1	÷	1	6 2803-2829	9 333-3550		_		
FOLD BYDYN	CENOME FOLIT POLICE	BOVING VITAL DIABLICEA VITUS (STRAIN SD-1)				_		-			
PPOLO BYDYS	CENORG POLYPROTEUR	SEAN VEH TOWN MORAIC VIAUS	2			1					
POLO BYLY	GENOME POLYPROTEIN	CONTRICTION OF A 11 VETT A DM COE	1-34	1	╗	-					١
POTA C COYAL	GENOME POLYPROTED	CONTACE LAND AND AND AND AND AND AND AND AND AND	1040-1036							T	
STATE OF THE	CENTALE POLYPROTEDI	COXSACREVILLO AT (31 MOST COCCS)	11959		1021-1057	-				Ť	
	CELINAM BOLIVARDIED	COXIACKEVEUSEI	1624-1060	1881-1901	-		_			1	
3	THE PERSON NAMED IN COLUMN NAM	COXSACKLE VIDIUS B 3	167.77	1033,104		-	L	_			
00000	CENCHE POLITICAL	COXSACXIEVIRUS D4		-		1					İ
FOCO COOL	GENORG FOLTFRUIEN	TOVE APPROPRIATE TO SERVICE THE PROPERTY OF TH	701		-		-				
SOCO COOS	CENONG POLYPROTEIN		120-134		-						
AND U PAR	GENOME POLYPROTEIN	CLOVEA TELLOW VENT TITLE AND ENCAPORE (1) (A0)	1836-1683	280-2915	-	_	_		+	I	l
1172	CENTRAL PROTEDI	DENGLE YELUS 177E I (31FAIR 31FOC.	1804-1531		_	_		_			
	CESSONAL BOX VPROTEIN	DENCIA VAUS TYTE 2 (STIAIN THE !)	1504-153	1030-1005	3 248-2319	4 2404-2935		113.7			1
1	Charles for valoritin	DENGUE VALUS TYPE 2 (STRAIN 1991) FUR. 21)	1564.1571	1155.1105	3 1401-1015	15 3117-31-01					
200	CENTRAL SECTION SECTIO	DENGLE VINUS TYPE 3 (STRAIN JANIAICA)			-	13 2979.1013		1141.1170			
FOLG DENEU	GENONE FOLTITUDIEUR	PASSACIAL VIREIN TYPE 2 ISTRAIN PRISOS!			-		-	-			
POLO DEDEU	GENORE FOLTPROTEEN	POLICIE CONTIC TYPE 3 (STRAIN TONGA 1914)	1174-1161		= 1			100 101 111 1111 1111			
PENED DENIE	GENOME FOL YPROTEIN	CONTRACTOR AND	137-064			1404-23					
OCA DIVE	CENDAGE FOL YPROTEIN	DEPART VALUE I TIE A	2115-1930	0 7977-3011	11 1142-1360			1	+	Ī	
							_	-			J
	CANADIST NAMED IN THE PARTY NAME		~		_					l	

PCGENE	167117814	All Virues (se breceriophages)							t	ŀ	ſ
A POST OF PARTY	CENTRAL BY VERNITOR	YARUS	AREAI	4864	4364	ARFA 4	AREAS	AREAG	AREA? A	AREAS	AREA 9
POLG EMCYB	GENOME POLYPROTEIN	FINCE PALA PAYOR ARMITIC VIOLES (1975)	8	186.15							
POLO EMCYD	GENORAL POLICES	ENCENATIONAL OCCUPATION (STRAIN ENC. B NORDIALE TOGENIC)	2	120	_						
Proto Eleaco	GENOAGE POLYPROTEIN	LIGHTO BACEPITAL ONLY OF A STATE VILLE STEELS IN THE	10.97	1416-1520	1524-1565						
	GENOME POLYPROTEIN	NENGO ENCEPTAL ONIYOCARDITIS VIRILS	3				1				-!
	GENOME POLYTROTEIN	FUOT. AND MOUTH DISEASE VIRUS (STRAIN A 10-A 11	101.130	171					1	1	5
	GENONG POLYPROTEIN	FOOT-AND-MOUTH DISEASE WRUS (STRAIN ATT)	301.338	9			Ì	1	1	+	-
٠l	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIBES)	1119.1146					Ī	1	†	-
اج	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRATM CI-SANTA PAU (C.SI))	101-138				Ī	T	Ť	†	
1	GENOMA POLYPROTEIN	IEPATITIS C VIRUS (ISOCATE 1)	101.179				Ī	1	\dagger	T	
	GENOME FOLYPROTEIN	HOG CHOLEAN YTHUS (STRAIN ALFORT)	64.73	1103-1232	1303-1333	14)4.146	1001.1001	1404.3440		1	
- 1	GENOME FOLVTROTEIN	HOG CHOLLEA WAUS (STRAIN BRESCIA)	645.73	1165-1333	1064-1015		-			\dagger	
-1	CENCHAI POLYPROTEIN	MEPATITIS C VIRUS (1504 ATE RK)	20.13	1049-1033			İ	į	-	!	:
THE PERSON		MERATORIS C VIRING (INCH. A DE 11)	77.72	1011.1011				_			_
AND INCOME	DEPONIE POLYPRUTEIN	INCRAFILIS C VIRUS (1919.A.) III : F.	174.401	3089.2116					•		_
١	CENCINE FOLYPROTEIN	IEPATITIS C VIRUS (ISOLATE INC. II)	1049-1836	3069.3116		!		İ	1	i	-
1	CENTRE FOLTFIOLEIN	MEPAITIS C VILUS (ISOLATE JAPANESE)	336-405	201.126	1013:101				\dagger	T	Ī
l,	CENTRAL FOR THE DESIGN	HEZATITIS C VIXUS (ISOLATE HC.IT)	303-726	1043-1072			ĺ			+	
. 1	CENCINE FOL TPRIOTEIN	HEPATITIS C MAUS (ISOCATE TAIWAN)	201.126	100.50			İ		1	Ť	i
TOTAL PAYS	CENCINE POLYFIOTEIN	HEPATITIS A VIRUS (STRAIM 20A)	201-217	1021-104	117.1149	135.131	İ	<u> </u>	<u> </u>	+	:
From IPAVA	GENGAGE FOL TPROTEIN	MEPABITIS A VIAUS (STRAIN JC)	201.117	1021.104	3	36.12	İ	T	t	İ	
PROLID HPAY	GENOME POLYPROTEIN	HEPATHIS A VIRUS (STRAIN 165)	201.21	1071.104	117.1149		Ī	1	İ	1	ļ
Proto HPAVC	GENOME POLYPROTEIN	PEPATITIS A VIAUS (STRAIN CRUZE)	100	ĺ			Ì	İ	1	-	İ
	GENOME POLYPROTEIN	INEPATITIS A VARUS (STRAIN GA76)	7	Ī	Ī	Ì	j		1	-	-
1	GENORAL POLYPROTEIN	INEPATITIS A VIRUS (STRAIN (DI. 175)	-	100	971	Ì	Ì	1		-	
PROLO HOAM	GENOME FOLYPROTEIN	HEPATITIS A VIRUS (STRAIN CA)	-	_			1		1		
	GENOME FOLYPROTEIN	HEPATITIS A VIRUS (SITAIN ABB)	T			Ì		j	1	1	
ı	GENOME POLYPROTEIN	SOCIAN HEPATITIS A VIRUS (STRAIN AGAL. 17)	Т	1034.1043		Ì	Ì	\dagger	1	1	
-1	GENOME POLYPROTEIN	SOUTH HEPATITIS A VIAUS (STRAIN CY-145)	t			İ	1	†	1	1	Ī
TOLO MAY	GENORG POLYPROTEIN	HUMAN ANIMOVIAUS 14	1	330.516	611.670	13:18	İ	\dagger		*	1
STATE OF THE PARTY	CENCHA POLYFROTEIN	HUNGAN PURNOVIRUS IB	1133-1159	100	÷	İ	T	1		1	Ī
Τ.	CENCING FOLVEROTEIN	HEMAN REGNOVIRUS 3	15	1331:131	Ī	İ	T	T	+	\dagger	Ī
	CENCINE FOLYTROTED	HERLAN RUMOVIAUS 19	98:38	-	1366-1607	162.1889		l	+	\dagger	
T	CENCONAL POLYTROTEIN			-	-			\dagger	\dagger	\dagger	Ī
Т	STRUCTURAL POSTERS	RAIN OH)				İ			+	t	
PHOLD TARVE	COUNTY BOX NO CHEST	IN ACTOR ENCLOSION VIRUS (STRAIN SALIA)			1796-2811				-	+	Ī
Τ	GOOME POLYPROTEIN			_	1796-2833					$\frac{1}{1}$	
Γ	GENOME POLYPROTEIN	APANESE DICEPHALITIC VIEW (CITATA DAY AVAILA)	1	اه	2786-283						
Γ	GENOME POLYPROTEIN					1					
	CENORG POLYPROTEIN		1	1777		1					
	GENOME POLYPROTEIN	LAIN YELAMISEV)	T		T	1	1	1	1	1	1
70.0	GENOME POLYPROTEIN		100	T	T	t	\dagger	1	+	+	Ī
Ţ	GENORA POLITICITED	126)			T		t	\dagger	+	+	Ī
A STATE OF THE STA	CENCINE FOLYTHUIEIN	HOSQUITO CELL FUSING AGENT	671-696	1054-3083	0000	T	\mid	\dagger	ł	+	
T	CENCING FOLTEROISED				-	T	t	+	+	+	Ī
	GENOME FOLITHUISIN	SVIRUS	313-256	İ	T		\dagger	I		+	T
PROTO DESCOR	GENOME FOLTTRUIEIN				Т	T	\dagger	+	+	+	Ī
T	CENCINE FOLTFRUIEIN	PEPPER MOTILE VIRUS (CALIFORNIA ISOLATE)	-	<u>e</u>	3.5	126-006	1167-1201	415.15.17	1707-1814 243	2431-2464	1
Τ	GENOME FOR VEHICLEIN		R			1	-			+	Ī
T	CENOME FOR VARIOTED			_	1903-1933	H	l	H	-	+	Ī
Ţ	CENTAGE FOR VORDIEDA		į	161-191				-	L		l
Τ	GENOME POLYTROTEIN			161.101							
1	GENOME POLYPROTEIN	COUNTY AND PIG COUNTY STATES		96				H			
Γ	GENOME FOLYTROTEEN	CONTRACTOR (AND INC.)	-	0(61-004							
PPOLO PPVEA	GENOME POLYPROTEIN	PLUM FOX POTYVIRUS (STRAIN FLAMAR)		2	2771-2798	1				H	
				1	1	1	1	1	1	-	Π

2000	1102:178:4	An Virtual (no perinting project)	Г	_	_	ARFA	AREA S	AREAS	AREA?		
100	PEDITE		000	100	200	Т	1	Т	Г		
10000	CENTRAL POLYPROTEIN		Т	- 1	100.00				1	:	!
THE PARK	CONTRACT OF VALUE IN		N. C.				i		į	:	:
5	CONTRACTOR STATES		200-223							ľ	
POLO PESMI	GENOME FOLVENO	\$: £	391-416								İ
PIOLO PRIVA	GENOME POLYTROTEIN		419.916								1
POLO PLISTA	CENORAL POLYTROTEIN	A DV DPD11	311.115	1132-1177	1310-1337						
POLO PEBATY	GENORGE POLYPROTEIN		Г	201-735						ļ	۲
PROLID PYYC	GENOME POLYPROTEIN	POTATO VIDUS T (SIRAM ULITAT)	٢	433.460	201.335	(16-131)	1111.1111				
SANAN SANAN	CENDACE FOR VPROTEIN		1	116 146	İ		İ		: !	٠.	
ļ	CALLAL MEN COMPANY		ı					!	:	:	:
١	CENTRAL FOLDER		13-460	701-755							
POLO PVYO	GENOME FOLVEROTEIN	TOTAL TOTAL STATE OF THE PUBLIC AND A TEN DESTINATION OF THE PUBLI	1124-1151	2707.2734							
POLD PYFVI	CENONE POLYPROTEIN	PALSHIP YELLOW PLEAK VINUS (1901A) E C'141)	10.13								
Ļ	CENCIAL POLYPROTEDI	SUGARCANE MOSAIC VIRUS (STRAIM RU)	970								
L	CENTRAL POLYPROTEIN	SWINE VESICULAR DISEASE VIRUS (STRAIN IV) 10)									L
	CELTA AL PARTIENT	1024-1040			1		-				_
Ţ		TICK. BORNE ENCIPHIALITIS VIRUS (STRAIN SOLVIN)	17-131	336-277	1633-1661		1000				
1	CENCHE POLITICIEM	POSITE PARTY TOTAL VIRIAL VIEW SAID LYPE)	1632-1659								1
ž	GENOME POLYPROTEIN		145.072	1148-1175	1416-1443	1773-1800					
	CENDINE POLYPROTEIN	TOWACCO ELCO VINOS	1 ×	100.001							
T-GV	CENDAG POLYPROTEIN	THE LEAS MOUNT ENCEPHAL UNITELLIES VINUS (SIRVING)	1	111							
ON DE	CENOME FOLYPROTEIN	THE LEAS MEDIC ENCEPHALONIYELITIS VIRUS IS HALL ON		100							
DAMA D PLANT	CAMPAGE POLYPROTEIN	THE ILEA'S MUNDAL ENCETIAL CHATELITIS VIRUS (STRAIN COVIN)		140							
	COLUMN OF BOTH VINE ATTENN	TURNIP MOSAIC VIRUS	2	3							
	CONTRACTOR OF CHANGE	TOBACCO VEIN MOTTLING VIRUS		20.00	2						L
POLO TYMY	Comme route and a second	WAYERLOST ON MOSAIC VIRUS II	201.170								
POLO WANZ	GENOME FOR TITUDIEIN		110-134	1185-3412							
PIOLG WITY	CENONCE POLYPROTEIN	WEST FALLS WAS A STATE OF THE PARTY OF THE P	436.463								
	CENONE POLYPROTEIN	TELLOW FEVER VIACO (STRONG PORT)	136-46)								
	GENOME FOLYPROTEIN	YELLOW FEVER VIAUS (STRAIM PASTEUR TOTAL)	40.04								
l	CENDAGE POLYPROTEIN	SUCCHINI YELLOW MOSAIC VIRUS	10111101	1601.1031							
MI NOT IN	GENOME FOLYPROTEIN	POLIOVIRUS TYPE I (STRAIM MIAJIONE T)	1403 1447	1604.1931							L
T HE WATER	MONETHE SCHURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STANIN TRINIDAD DONNET)									L
	ACCOUNTS OF THE PARTY PROTEON	FELDIE CALICIVALUS (STRAIN CFUSE FIV)	7777								L
200	COLUMN STATE THE ALL POLYPROTEIN	I ELINE CALICIVIALIS (STRAIN F9)	on afoi								
10 P. V.	MANAGEMENT OF THE AMERICAN	INEPATIBLE EVINUS (STRAIN BUTNIA)	***	9							
200.00	MATCHE AT THE AT WAS DEEN	INEPATITIS E VIXUS (STRAIN MEXICO)	219.246	2							
OF REAL	THE PERSON OF TH	INDIATIFIED VIBUS (STEATH MYANDIAL)	219-346	100							
DEN HEVAT	HOUR LOCAL POST CONTRACTOR OF THE PARTY OF T	LEBA PHILE VIELS (STRAIN PAKISTAN)	110-245	346-375							
POLY HEWA	NON-STRUCTURAL POLITICAL	LANGE BIRTH VIBILE	155-942								
OLY MODOV	NONSTRUCTURAL POLITRUIES	CANNON NY MAIN STREAM GIRLD	2453-2480								
POLH CHENNO	NOWSTRUCTURAL POLYFRUIEIN	A LEGISTIANT PACE ACE VIEW	113.347	1657-1684							
NOTH INDA	NON-STRUCTURAL POLYTROTED	KABIII MANONINA MANASA	1037.1084	1637.150	3410.2445						
POLN RAVN	NOWSTRUCTURAL POLYTROTEIN	ROSS RIVER VIXUS (31 PALM PERMY)	161.44	1017.1114	÷				L		
POLY LEVE	HONSTRUCTURAL POLYPROTERY	ROSS RIVER VOUS (STRAIN TO)	100								L
TABLE NO	NOWSTRUCTURAL POLYPROTEDY	RUBELLA VIXUS (STRAIN THERIEM)									L
A 100	NONSTRUCTURAL POLYPROTEIN	SEMALIKI FOREST VINUS							L		L
CHICAGO TO SERVICE STATE OF THE PERSON SERVICE STATE SERVI	INCASTRIBETION POLYPROTEDI	SINDBIS VIXUS (SUBTYPE OCKELBO / STRAIN EDSOYN 12:3)	2								L
	NOW THE PURAL POLYPROTED!	WESTERN EQUAE ENCEPHALITIS VINUS									L
100	CHEST OF ALL BOX VPROTEDA	AVIAN DIFECTIOUS BLASAL DISEASE VIRUS (STRAIN 52/10)	200								ļ
TOLS BOYS	STRUCTURE TO CONTROL	AVIAN DEFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRALIAN 001-73)	231-258								1
YACE BOX	SIRULIUM IN THE STATE OF	AMAN DESCRIPCING BURSAL DISEASE MAUS (STRAIN CU-1)	131-138								1
PPOLS INDIVI	STRUCTURAL POLITROILE	STATE OF PRINCIPAL PARENCE VARIES (STRAIN E)	331-350								
POLS BOVE	STRUCTURAL POLYTROTEIN	AVIAN DA EL INCO DOTA DI CARE VIDIR (CTRAIN PRO-91)	111.139								
POLS BIDY	STRUCTURAL POLYPROTEIN	AVIAN BEECHOUS BURSAL DISCASE VIROS (STRAIN STC)	1						L		
SACIA S INDAS	STRUCTURAL POLYPROTERY	AVIAN DATECTIONS BUILDING MINUS (3) POINT 31-1)								L	L
OL L CHONG	STRUCTURAL POLYPROTERY	DYYCHICHTONG VIXUS (STRAIM COLU)	100								L
PROFE BRAN	STRUCTURAL FOLYPROTEIN	ROSS RIVER VILLS (STILATIN MEXOT)							L		
POLE LEVI	STRUCTURAL FOLYPROTEIN	ROSS ALVEA VIRUS (STRAIN 141)			-			<u> </u>			L
OCOUR S INVA	STRUCTURAL POLYPROTEIN	SINDELS VINUS (SUBTYPE OCCRELED) STRAIN EUSUTIN 12:3)									L
VOIG SPOV	STRUCTURAL POLYPROTEIN	SINDELS VIDES (STILADAS HASP AND HOLLY)			1						L
VIIIV S PACE	Service to the Control of the Control	INTERTION EQUIPMENT DISCONDENIES VIRUS						-			ļ
			745 747	1916.343			-	_	_	_	_

Profesion	71472416.4	Value Carte Cartes de la Carte								f	f
THE HAME	PROTEIN	VIRUS	ANTAI	AHEAL	ARIAS	AHEAS	AREAS	ARTAL	AKEA?	AREAL	AREA 9
MOL CLEVC	POL POLYPROTEIN	CAPRONE ARTHOUGIS ENCEPHALITIS VIRUS (STRAIN CORK)	104-924			_					
mar comy	PUTATIVE POLYPROTEIN	COMMELINA YELLOW MOTTLE VIRUS	33	2	1075-1102	ê			1	1	
LIVE TAN	POL FOLTED	EQUING DA ECTIONS APENTA VIRUS (CLONE 1941)	60.						1	1	
PROFESSION OF THE PROPERTY OF	POLITICAL INTERPRETATION	FOURSE BY ELITORS ANEALD VINOS (LLONE LLZZ)	200.77	100.10		T		Ī	1	+	Ţ
PIOL FENVI	POL POLYPROTEIN	SELINE EMPORENCIES VILLE FLE	Т	137.463	Ì	T	T			t	1
PROL PINE	POL POLYPROTEIN	FELINE BOUNDE HOUNGY VIRUS (ISOLATE PETALUAIA)	Т				T				
POL DAYD	ENZYMATIC POLYPROTEIN	FIGWORT MESAIC VIRUS (STAAIN DXS)	Т								1
POL OALV	POL POLYPROTEIN	GIBBON APELEUKEMBA VIRUS	28:55	676-703			Ī	:		-	:
POL HTLIA	POL POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (STRAIN ATK)	111:313								
POC HTLIC	POL POLYPROTEIN	HUMAN FCELL LEUKEMIA VIRUS TYPE I (CARIBUEAN ISOLATE)	634.311								
PPOL_HVIA1	POL POLYPROTEIN	HUMAN BOAUNODEFICIENCY VIRUS 1976 I (ARVINSF21SOLATE)	Г	130-461							
PPOL HVIB!	POL POLYPROTEIN	HUMAN BEAUDIODEFICIENCY VIAUS TYPE I (DIIIO ISOLATE)	130-257	437-473							
PPOL HVIBS	POL POLYPROTERY	INMAN INMUNODERICIENCY VIRUS TYPE I (1111) ISOLATE)	_	(1)-(1)						!	
PPOL HVIBE	POL POLYPROTEIN	INMAN MANDODEFICIENCY VIRUS TYPE I (IIRU ISULATE)	230.257	631.673			i				·
POL HVIEL	POL POLYPROTEIN	HOMAN DAMINODEFICIENCY VIRUS TYPE I (ELI ISOLATE)		624-660							
POC FYIND	POL POLYPROTEIN	HUMAN BOADWODEFICIENCY VIRUS TYPE I (HXB2 ISOLATE)	П	130.00	- F						
POL HVIR	POL POLYTROTEIN	HEMAN MORENOETICIENCY VIRUS TYPE I (IRCSF ISOLATE)		624.445							
PPOL HVIMA	POL POLYPROTEIN	INCHAN LAMINODEFICIENCY VIRUS TYPE I (MAL ISOLATE)	313-344	476-510	099-619						
PPOL HVINA	POL POLYPROTEIN	HIGHAN INDAINODEFICIENCY VIRUS TYPE I (MN ISOLATE)		633-464							
POL SVINS	POL POLYPROTEIN			625-661							
POL HVIND	POL POLYPROTERN	,	П	624-460							
Prof. HVIDY	POL POLYPROTÉIN			620-661							
POL HVIPV	POL POLYPROTEIN		130-257	611-673							
PPOL HVIRH	POL POLYPAGIEM			619-460							
PPOL HVICA	POL POLYPROTEIN	SOLATEU		313-540	099-619						
PPOL HVIZI	POL POLYPROTEIN	OLATE)		099-619							
PPOL HV2BE	POL POLYPROTEIN		2 2 2					Ì			
POL HVICA	POL POLYPROTEIN	1	3								
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LUA DRECTED NAY POL 15.0 P) LUA DRECTED NAY POL 15.0 P) LUA DRECTED NAY POL TWE KASE NAM DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA DRECTED NAY POL TWE KASE LUA POL TWE KA	INT LUENZA C VIÁUS (STRATIN CREALINUMS)	Т	 -	1	1		$\frac{1}{1}$	\dagger	
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ANA DOLECTED BAY POLYMEASSE ANA DOLECTED BAY POLYMEASSE ANA DOLECTED BAY POLYMEASSE ANA DOLECTED BAY POLYMEASSE ANA DOLECTED BAY POLYMEASSE ANA DOLECTED BAY POLYMEASSE ANA DOLECTED BAY POLYMEASSE ANA P	THOCOTO VIXUS	336.385	=	_				\dagger	
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ANA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA DOLETTE NA POLYBEASE NA POLYBEASE BETA SUBUNIT NA POLYBE	MURINE CORONAVIRUS ABIV (SIRAIN JIB.)	П	_		ŀ				
INA DESCRIPTION FOLVERASE INA DESCRIPTION FOLVERASE INA DESCRIPTION FOLVERASE INA DESCRIPTION FOLVERASE INA DESCRIPTION FOLVERASE INA FOLVERAS	DEKAR VAUS	╛	1043.984						
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INA DRECTED NA POLYNGASSE INA DRECTED NA POLYNGASSE INA DRECTED NA POLYNGASSE INA DRECTED NA POLYNGASSE INA POL	PORCINE TRANSPESSIBLE GASTROENTERUTIS CORONAVIRUS (STRAIN 1577)	- [114.419	1			+	\dagger	1
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HAY DOLECTED HAY POLYMERASE H	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN KD1121)							-	
HAY POLYPEAGE BETA SUBUNIT HAY POLYPEAGE HAY POLYPEAGE HAY POLYPEAGE HAY DOUGHAGE HAY DOUGHAGE HAY DOUGHAGE HAY DOUGHAGE HAY POLYPEAGE HAY POLYPEAGE HAY POLYPEAGE HAY POLYPEAGE HAY POLYPEAGE HAY DOUGHAGE HAY DOUG	BELLETONOUR VIRUS (SCHOTTE 1971SOLATE USA)	\$							
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A NAA-DOBLITIO NAA POLYDEAASE NAA-DOBLITIO NAA POLYDEAASE ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA POLYDEAASE BETA SUBUNT ANA BOBLETTED BANA POLYDEAASE ANA BOBLETTED BANA POLYDEAASE ANA BOBLETTED BANA POLYDEAASE	HUMAN RESPONTORY STACYTIAL VIRUS (STRAIN A1)	1	Ť	Т	100)-1014		1453-1480 177	1776-1803 206	2062-2089
ANA PORCEDO NA POUTREASSE ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA POUTREASSE BETA SIBINIT ANA BOUGETTED ANA POUTREASSE ANA BOUGETTED ANA POUTREASSE ANA BOUGETTED ANA POUTREASSE	MARBURG VRUS (STRADI MUSOKE)	_		34 1811-1831		2316-2366		-	
ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBLINE ANA POLYMERASE BETA SUBLINE ANA POLYMERASE BETA SUBLINE INA BOLYMERASE BETA SUBLINE INA BOLYMERASE BETA SUBLINE INA POLYMERASE BETA SUBLINE INA BOLYMERASE BETA SUBLINE INA BOLYMERASE BETA SUBLINE INA BOLYMERASE BETA SUBLINE INA BOLGETED BUA POLYMERASE INA BOLGETED BUA POLYMERASE INA BOLGETED BUA POLYMERASE	MARBURIO VIRUS (STIAM POPP)			19				-	
ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLYMERASE BETA SUBMIT ANA POLEMESTED BANA POLYMERASE ANA ADGESTED BANA POLYMERASE ANA ADGESTED BANA POLYMERASE	MEASULES VIRUS (STRAIN EDMONSTON)		-	=					
ANA POLYPEAALS BETA SUBLINE ANA POLYPEAALS BETA SUBLINE ANA POLYPEAALS BETA SUBLINE ANA POLYPEAALS BETA SUBLINE ANA POLYPEAALS BETA SUBLINE ANA POLYPEAAS BETA SUBLINE ANA POLEFED BANA POLYPEAAS ANA BOLEFED BANA POLYPERAS	MUMP'S VIRUS (STRAIN MOYAHALA VACCINE)	╗	П	2				L	
NA POLYTECH SET SUBLINI NA POLYTECH DAY POLYTECHS NA POLYTECHS BETS SUBLINI NA POLYTECHS BETS SUBLINI NA POLYTECHS BETS SUBLINI NA BOLETED NA POLYTECHS NA BOLETED NA POLYTECHS	MEMORALE MARASE VIRUS (STILVIN BEAUTETTE CAS)	┪	7	=					
I NA DOECTED NA POLYDERASE ANA POLYDERASE BETA SIGNIMI ANA POLYDERASE BETA SIGNIMI ANA DOECTED RAN POLYDERASE ANA DOECTED RAN POLYDERASE ANA DOECTED RAN POLYDERASE	T		-	_	_				
INA POLYNERASE BETA SUBLINIT INA POLYNERASE BETA SUBUNIT INA DOLETED RAY POLYNERASE RAY DOLETED RAY POLYNERASE RAY DOLETED RAY POLYNERASE	PURMALA VIRUS (STRAIN HALLMAS BI)	T			107-141	7017-6117		1	1
INA POLYMERASE BETA SUBUNIT RNA DIGECTED RNA POLYMERASE RNA DIGECTED RNA POLYMERASE	INCREES VIRUS (STRAIN PV)	Т	T	is		+	1	\dagger	
RNA-DOLECTED RNA POLYNGRASE RNA-DOLECTED RNA POLYNGRASE	AABIES VINUS (STRAIN SAD BIP)	Т	1	: =	1		1	\dagger	Ī
RMA-DOLECTED RNA POLYMERASE	AKCE DWARJ VINUS		 -				-	+	Ī
	E RIFT VALLEY FEVEA VIRUS (STRAIN 211-549 MI2)	-	100						1
PART, SENS LAN POLYMENAL BETA SUBURIT SENSOAL VALUE (STANDE Z.) HOST MUTANTS)	SENDAL VICUS (STRAIN Z / HOST MUTANTS)		1116 1729-1754	34 2145-2130	9				
KNA POLTMEKASE BEIA SUBUNIT		901-616	- 1	36 1965-2000			-	Н	

PCCTNT.	1107817814	All Viruses (no bacteriophoges)	AREA! A	EA1	ARGAZ	1	2				
TANK THE	PEDITIN		1	1063-1116	119-1756	2145.2160					1
1000	TANA BOY VAVERASS BETA SUBUNIT		١		131.751	\$65.93					
TUNE SEALOR	ALL PARE PARE BAY BOT VASS ASE		Τ:	12	410.1310	1170.3147			L		
UN. SEOGN	MA DUEL IED MAN I DE 1 PROPE		ন				1016 0104				L
PREM. SVSWR	KNA POLTPEAASS BEIN SUBJECT		7	1				1416.1443	1631.1698	1157-1674	0112 1 902 1
REPL STATE	ANA POLTIFICASE DE LA SUSCILI	TOWATO SPOTTED WILT VIRUS BRAZILIAN ISOLATE CPMII/BR-01)	Ž.		2				-	-	
PREAL TOWNS	KNA-DUECTED KINA POLTMEDASE		ΞÌ	-						L	•
			-+	-							L
PRUPE SUK	INA POLTMENANE	-		6			1			1	Ļ
ALPL VSVIH	ANA POLYMENASE BETA SUBURIT	_								1	ļ
PAUL VSVIO	ANA POLYNGRASE BETA SUBURGE	TOTAL AND AND AND AND AND INC.	1540-1567	1764-1791						1	1
ALM. VSVS	ANA POLYMERASE BETA SUBLIMIT	-	118-364	25.32							1
VALUE ACLEV	ENA-DURECTED BNA POLYNERASE	11 14 25	136-363								4
WWW CHIEF	MITATIVE BUA-DIR BUA POL		131.300								4
TOWN COMMO	MITATIVE BNA-DER RINA POL		985					L			_
2	STATE OF THE BUY POR										_
- 1	PULLING BAN-TAK BAN BAN	,	Ï	٦	1						L
PRINO BYDYR	PUIATIVE ECA-DAR ANA POL	╗	Ť		5		1	1			
- 1	PUTATIVE RMA-DIA RAA POL	_	=	00			ļ				Ļ
ı	PUTATIVE MA-DIR RAA PA	AVIAN PARCTINAS BURSAL DISEASE VIRUS (STRAIN 3270)	٦				1	1	1	1	-
ł	PUTATIVE MAA-DIR KWA MA		991.68	2						1	-
PRAPO BOVA	PUTATIVE RMA-DIR RMA POL		99.						1		1
PERSON INVITATIONS	PUTATIVE KNA-DOR KNA PUL		333.800						1	-	+
PREMO DYNYS	PUTATIVE RNA-DIR RNA POL	RONG	31.0%	1052-1019					1	1	+
PILLIPO LYCVA	RNA POLYNGAASE		403-439	109.736	1073-1079		_				\downarrow
PREPO PPARVS	PUTATIVE RNA-DIR RNA POL		10.10							1	4
PRINO REDVO	ANA-DIRECTED ANA POLYMERASE		1							_	+
PRING REDAL	NAA DIAECTED ANA POLYMERASE		T	310-245	31.01						4
PRINCE POTRE	RNA-DIR RNA POL SUBUNET VPI		Ţ	211.245	100	935.1002		L			4
Control of Control	BMA.DIE BNA POL SUBURIT VPI		Ī		141.390	50.55				L	
THE POLICE	RNA DIE ENA POL SUBLINGT VP!	OWDEN)	1		20.101	973.1002					H
20100	RNA DIR BKA POL SUBURIT UP!	MED	T		475.1003			L	L		
PARTO BOTS	ANA DOR RNA POL SUBLANT VPI		L				L	L			
A MOS CHAR	INA. DOLECTED RNA POLYMENASE	S CENEVISIAE VIAUS L'A	Ţ	241.231	1103.1134	1918.200	_	L			_
PAT O TACV	RNA POLYNGRASE		Т	1114.1343	1307.1424			L			4
Washington of the Control	PUTATIVE RIVA-DOR RIVA POL		Т				-		L		
100 mm	THAT POLYNGERASE ALPIN SUBUNIT	BOVDAE RESPUENTORY SYNCYTIAL VIRUS (STRAIN ASTROL)					L			L	_
CACO PARE	ANA FOL PACRASE ALPHA SUBURIT	CANNE DISTEMPER VIXUS (STRAIN ONDERSTENDORT)					L	L			
200	BNA POLYMERASE ALPHA SUBURUT	HUMAN RESPONSORY SYNCYTIAL VIRUS					1	L	L	L	
101 41	INVA POLYMORASE ALPHA SUBUNIT	HUMAN RESPONSORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIM 1937)					1	-	L	-	ŀ
THE PARTY	BNA PCT WAS LASE ALPHA SUBURIT	HIDLAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN AZ)								 -	H
1500	BINA POLYNGRASE ALPHA SUBUNIT	FIGHTAN RESPONATORY SYNCYTIAL VINUS (SUBGROUP A) STRAIN LONG!	5			1	L		L	L	-
20 100 100	RNA POLYMERASE ALPHA SUBURNI	ACASLES VIRUS (STRADY EDMONSTON)				-			L		H
100	ANA POLYMERASE ALPHA SUBUNIT	PEASTES VIRUS (STRAIN D-)-CA)									
VALUE OF THE PARTY	RNA POLYNGRASE ALPHA SUBURIT	MEAST ES VIRUS (STRAIN YANIAGATA-!)		314.261	175.416	ļ	L		L		
Wille 44144	ANA POLYNGRASE ALPHA SUBURIE	HEBLAN PARADATURACA I VICIOS (SIRAIM C.3.)	17.0	234.261	23.416		1			Ц	
PLLY MINC	ANA POLYNGRASE ALPHA SUBUM!	HOMAN PAIADGLENZA I VIKUS (2) KAIR C37)	1	131.161	33:416						4
CHIEF PAIR	ANA POLYNGRASH ALMIA SUBURIT	HEMAN PALABOLUERA I VIRUS (3) PAUL (1) (1)	14.111	346.271	33:48	L					
DIM MAIN	INA POLYNERASE ALPHA SUBURIT	HEALAN PARADIELUENZA I VIRUS (STRAIM CLITAR)	731.181	20.000		L		L		L	Н
1110 0000	RNA POLYMERASE ALPHA SUBURIT	INDIAN PARADOLLENZA I VIRUS							_		
PARTY PLANT	RNA POLYNGRASE ALPHA SUBUNIT	HUMAN PARADIT UENZA 2 VIRUS (STRAIM TOSTIBA)		11.31	100		-				Ц
BIN SHE	LINA POLYNGRASE ALPHA SUBURIT	BOYDG PARADGLUDIZA 3 VIXUS	77171	260.290		L					
HILL GALLS	ANA POLYNGJASE ALPIN SUBUNIT	HOLGAN PARAMOLUEIGA 3 VIRUS (STRAIN MON 4782)				1	L		Ц	Ц	\dashv
Philips Pickly	KNA POLYNGRASE ALPHA SUBURIT	HUMAN PARANGLIENZA 4A VIKUS (SI KAIN 103146A)	1111						L		_
WIN LAIV	RINA POLYNGRASE ALPHA SUBUNIT	LABES VILUS (STRAM PV)	130-157	119-410							-
OG MIN	KNA POLYMERASE ALPHA SUBURIT	SENDAI VIRUS (STACIN 27 PROST PROTACTS)	130.359	379-420				_			-
PREP SENDS	ANA POLYMERASE ALPHA SUBURIT	SENDAL VIRUS (STUAM 674)	30.33	379.10		L					┧
PLUE SECO	RHA FOLYMERASE ALPHA SUBUMI	SECOND VIRUS (STICKET TO STATE)	336.33	33.430	L	L	L			4	$\frac{1}{1}$
1000 see	RNA POLYNERASE ALPHA SUBCRET	SENDAL VIALIS (STANA PASA)	1	378.430		-	L	-	_		_
						_	_	_	-)

PCGENE	107117014					П	П	П	П	П	\prod
THE RAME	THOUSAND STATES AND BUT CITALISME	CINTAN VIBIR SISTEAN WILL	97.50			1	7	4	70740	0700	2000
PLODE VACEV	SUPEROXIDE DISMUTASE LIKE PROTEIN	VACCINIA VIXIIS (STRAIN WR)	72.99						-	-	Ī
PSODE VARV	SUPEROXIDE DISMUTASE LIKE PROTEIN	VARIOLA VIRUS	11.99						_		
PEMIR AMERY	SPHEROIDIN	\$	91.118	140-167	227-261	161.190				-	
PSPII MYXYIL	SERPOVI	SANNE)	36-33					1	1	1	4
PSPI2 VACCV	SEADUE PROTEINASE INGUITOR 3	VACCINA VIRUS (STRAIN WIL)	20.00					1	1	1	
PEC CINE	SEATHER THUS EASE INSTITUTION OF STATES OF STA	PARAMECHIA BURKABIA CILORETTA VIRING						T		<u> </u>	4
PTAA2 VACCV	TRANS-ACTIVATOR PROTEIN AS		97.133				:	: :	;		-
PTAGE FOWPY	TRANS-ACTIVATOR PROTEIN PPO	FOWLPOX VIAUS	15.								
PTAGE VACCV	HANS-ACTIVATOR PROTEDY CK1	VACCINIA VIRUS	8.								
PTAGE VARV	TRANS ACTIVATOR PROTEIN CK1	VAUOLA VIRUS	3.30								
PTALA BFDV	LANGE T ANTIGEN	BUDGERGAR FLEDGLING DISEASE VIRUS	31:31				Ĭ	Ì		1	1
TALA POVBO	LARGE T ANTIGEN	BOVING POLYGMAVIRUS	2	-		•	-		•		_
TALA POMIA	LARGE T ANTIGEN	IIAAGTER POLTOMAVIRUS	307-63				1	1	1	\dagger	
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	LAKUB I ANI KOEN			****					\dagger	\dagger	T
PTAIA POWA	R ARGE T ANTIGEN	MOUSE FOLYOMAVILUS (STRAIN A)	11:31					T		+	Ī
PTALA POWAC	LANGE T ANTIGEN	AWFORD SMALL-PLAQUE)	\$01.335					T	\vdash		Ī
PTATE NOVAC	TRANS-ACT TRANS REG PROTEIN	DROSIS VIRUS	407-434	489.523	\$12.559					H	
PTATA MPVBM	TRANS.ACT TRANS REG PROTEIN		42.439	494-528	337.564					1	
PTATE NEVOP	THAMS ACT TRANS REG PROTEIN	PSID POLYNEDROSIS VIRUS	25.2							1	1
PTECU EBV	LAKCE TECHNONT PROTEIN	EPSTEIN-BAUR VINUS (STRAIN PP)-1)	143-172	1215-1242	174-1971	1876-1903		1	\dagger	\dagger	Ī
FIELD BENEVA			17.57	1471.117				1	-	\dagger	
PIEGO MANIE	LARCE TECHNONI PROTEIN		103.130	231.243	112.(1)	1003.000	1001.1101	1461-1488	1107-1011	\dagger	
PTEGU HSVED	LARCE TECHNENT PROTEIN		336.355	266.303	1305-1333				+	$\frac{1}{1}$	l
PTEOU HSVSA	PROBABLE LARGE TECUMENT PROTEIN		334-403	\$72-700		146.898	949.676	101.00	1467-1497 210	1102.2115	
PTEGU VZVD	LAIGE TEOUNENT PROTEIN	VANCELLA ZOSTER VIRUS (STRAIN DURIAS)	131-1131	1979.1609							
PTEAM ADEO?	DNA TERMINAL PROTEIN		117-561								
TIMA AVISA	TRANSFORMING PROTEIN MAS	AVIAM PROSCULOACIMENTO IN PIBROSANCONIA VIRUS ASA		,,,,			1		1	+	1
PIOPI SPORA	DNA TOPOSONEJASE I			791119				1	+	\dagger	
PIGPI VARV	DHA TOPOISOME BASE I		1				T	1	+	+	T
HOM ASTALL		PEVER VIRUS (ISOLATE MALAWI LIL 2011)	102.936			1		T		+	I
PTYSY HSVAT			116-143							\vdash	
FTYSY HSVSA	THYMEDYLATE SYNTHASE		130-149								
PULOS EBV	VILON PROTEIN BEILT	ESTERN-GAURY VINUS (STRAIN BYS-1)		97.740	22.300		1	1		+	
HAD HAVE	VILLON CENT SA PROTEIN		10.66		Ī			1		1	<u> </u>
PULOS HS VSA	VOLON GENE 43 PROTEIN		27.	302.338	207-191				\mid		
PULGE HONVA	HYPOTHETICAL PROTEIN U.S.	4 ADI69)	Î								
ruti EBV	HYPOTHETICAL PROTEIN BBLF!		2							\dashv	
PULIT HONYA	INTRO THE TICAL PROTEIN ULT	HUMAN CT LONG CALLUVIAUS (STRAIN ALVIEV)	11.71	T	T		1	\dagger		+	1
0 ZA 7 JU	LAYPOTHETICAL CENTE 44 PROTEIN		9	Ī		T	T	\dagger		1	Ī
PULIS HONA	HYPOTHETICAL PROTEIN ULIS		2111				T	T		+	Ī
PULSO HONVA	HYPOTH PRO ULZO PRECURSOR		19-97						<u> </u> 		1
PULLI HISVED	GENE 40 PROTEIN		14-71							<u> </u>	
ונטון אנט	CENE 38 PROTEIN	N DUN(AS)	10-60								
PULL HSVEA	VIDON GENE 19 PROTEIN	HELVES VICOS SABARU (STRANTI)			25.318		Ì	1	1	$\frac{1}{1}$	
PULLI HOAVA	MYTOTAL PROJECT OCT IN THE TAXABLE IN THE		┰		T			1	+	+	1
PUC 18VII	VINON PROTEIN ULIA	E I / STRAIN 17)	613				Ï	T	ł	+	
PULM HBVSA	GENE 67 PROTEIN		204.335					İ	\mid		Τ
מאצא אכווא	VIDLON CEDIE 24 PROTEIN	IN DUMAS)	113-139							-	
MILIS HOWA	INPOTIGETICAL PROTEIN ULIS (135-363							Н	Π

PCGENE FILE HAME	10/11/010			7	AHLAJ	1	4				L
	7111	YIRUS	16.00	Т							
	CKULL	HERVES SEARLEX VIRUS (TYPE 1/STRAIN 17)	T.	11017							
	PROTEIN ULD?	FOUNDE HEADES VIA US TYPE I (STRAIN ABAP)	7								
PULST HEVED	CENE 2) PROTEIN	CREAT CANDING STRAIN !!)	Т		3116.346	1001-100					
PLESS HISVEA	CDG 01 PROTEIN	VANCENT A POSTSE VIEWS (STRAIN DUNIAS)	Т								
HUJ VAVD	GENE 11 PROTED	CONTINUE VALUE (STRAIN DUNIAS)	*								
HLLI VAVO	HOST SHATTOFF VISION PRUIESA	THE LES HAM BY WATER TAYED I / STRAIN 17)	7								•
FULLI HSVII	DALA-BINDENO PROTEIN ULA	WAS LEST A SPREED WILLS BETAAIN DUAIAS)	7	2		15	İ	:	i	: i_	_
HEAS VEVD	GENE IS LENGTANE PROTEIN	TANAMAN AND AND AND AND AND AND AND AND AND A		21712							
WILLIAM INCOME	PROTEIN ULA?	INDIAN CTIOMEDALO VANOS (STRAIN)	416-315								ļ
	Control profit the (B.A.)	HEAPES SOUTEX VINUS (TVPE I / 3 HAVIN I /)	211:313								1
12V	VIALOR FROITERS OF	HERFES SPOLEX VIALIS (TYPE 1/STRAIN!)				L					
PULLS HSVIF	WINDS FIGURE USA	ECONOMISTACE AND STATE 4						L			
PLAN HSVEA	TANS PRODUMO PROTEI	CONTRACTOR OF CATERAIN AD169)	7								
AVACA AT 114	PROTEIN U.SO	HUMAN CT TOWNS OF THE PARTY OF	165.213	787-014		i	!	!	İ	:	:
	PROPERTY BEN ICATION PROTEIN BSLF1	EPSTERMENT VILLES (31 AAI'N DVI'S)	Π	943.970							1
100	THE PARTY OF A TANK BE OF THE PARTY OF THE P	EQUING HELDES VIAUS TYPE I (STRAIN ABOT)	Т			L					1
PULLY HSVED	DNA KEALKAI KAN PROJEK GAS	LIFE BOY EVALUATE (STRAIN !!)						L			
HESS HSVSA	PROB DRIA REP CENE SA PROJECIN	TATALET A SACTED VININ MITRAIN DUMAS)	1							L	
HE IS VZVD	PROB DNA REP GENES & PROTEIN	THE THE PARTY I SUMMY CONTAIN ADIMS	74-101				-			L	L
AVA COLOR	HYPOTHETICAL PROTEIN ULSP	HUMAN CT CORECTED TO THE ACT AND LAND	65-93							L	L
W C 2	PACE DAY LEP PROTECT UL?	HOMAN CTIONS CALLUTANCE OF TAXABLE TO SELECT	5.3							ļ	L
V/2007	In the year often Precursok	KIDKAN CYTOMEGALUTAGOS (STRAIN POSTES)	77.6								ļ
	LINGS THE ALL GENES SO PROTEDI	HEAPESVEUS SAMON (STICUM II)	43.79							1	1
	LANGUAGE THE AL PROTEDNUL 74	MUNICAL CALLONG CALLONIANS (STRAIN AD 187)	408-434							-	1
PULTA HOAVA	THE STATE SECOND PROPERTY INC. INC.	EPSTEIN BALL VIALIS (STRAIN BONS)	(15.41)	729.764						1	1
ATT I	HITCHES AND AND AND AND AND AND AND AND AND AND	HEADES SOUTEX VIRUS (TYPE 6/ STRAIN UGANDA-1102)	2077 0.01			L	L	·			4
PULLEY HSV&U	HYPOTHER PART THOUSEN	NEADERVELIS SABORI (STRADY 11)		791 071		ļ	-	L			
PULLI HSVSA	HYPOTHETICAL CENE 24 TROITER	CASTERNITY (STRAIN 89% 8)		2						_	
PULM EDV	HYPOTHETICAL PROTESP BULLY	THE PART OF TAXABLE STRAIN	12.0			1			L	L	L
PUR DE MSVSA	HYPOTHETICAL GENE 31 PROTEIN	THE TANK OF THE PARTY (STEATH AD109)	2				+			L	L
PLE 93 HOAVA	PROTEIN (ILS)	TOTAL STATE OF STRAIN AD (49)	7.2			1	1				L
AVACH HE BIG	HYPOTHETICAL PROTEIN UL'S	HOMEN CT TO CHAIR CHOSE A / CTRAIN LICANDA-1102)	37-100	105-174			1	-			L
PIE OF HEVEL	HATTOTHE (ICAL PROTEIN 13R	HELVES SUCCESS VINCOLOUSE OF STREET	4-31	443-411		_			-	1	1
AVACAM AVAIL	VILLON PROTEIN UT. 104	HUMAN CTTOME DALIO VINOS (STRAIN AD 148)	33.31				-		1	1	1
AVAIL DE LANGE	HYPOTHETICAL PROTEIN ULI 19	HOMAN CYTCH CALCULATION COLOR	90-134					1		1	1
127	INVESTIGATION PROTEDIUM 130	HUBACH CYTOMEGALOVIUS (STRAIN ACTOR)	135.1%						1	1	1
Taring many	IRACE DIA GETCOSTILASE	HEAPESVINUS SADADU (STRAIN 11)	11:118				-	1	1	1	1
	I I ACH JAMA CA YCOSYLASE	SHOPE FIBROALA VIXUS (STRAIN RAZLA)		20.42	L					1	+
AND DAKE	THE PAIN OF VICTORY ASS	VACCIDIA VILUS (STRAIN COPENNAGEN)	1	2012	L	L				1	4
PUND VACE	THE PART OF WORLD ASS	VACCORIA VINUS (STRAIN WR.)			L	L	-				4
PUNO VACEV	ULACITA OF SPORT ASI	VARIOLA VILUS					-				4
PUND VALV	UMACLUMA ULTUS ILASS	HISTAN CHTOME GALOVOUS (STRAIN AD169)	1		1	-	-		L		
PUSON HONVA	HIPOTHETICAL PROTEIN PALS	LA FLAN PYTON GOLD OVINUS (STRAIN AD149)	5		ļ	1		-	L	_	
ANCH HISTORY	HYPOTHETICAL PROJECT RALL	WALLE POPULATION (STRAIN AD109)				1			-		_
PUSIE HOUVE	MENDALANG PROTEIN HWLL'S	TOTAL FUNCE BEVTE VALUE (STRAIN USS?)	2			1	+	-	L	-	L
DVIII ASPLS	115 131-1 PROTEDY	CALLED TO STATE OF THE ATTENDED AND A STATE LEIDEN)	703-729			1	1	-	ļ	ļ	
PVIST AVMLE	113 KD PROTEDN	ALVALA PLANCE CANAGE CONTRACTOR A DA (1555)	1:39			1	4		-	+	-
S TO S TIME	LIS 137 PROTEDA	AFUCAN SWIPS SEVEN VINCE OF SEVEN SEED	39.48			4	-	1	1	1	+
100	14 KD PROTEIN	TORKED FOR THE VACOR OF THE BANK WAR DRONG VIRUS	25.45	945-972				1	1		1
200	HE ICACE	AUTOGRAPHA CALIFORNIA PROCESSA POLITICAL	2012						1	1	+
200	IAND MOTEDA	TOBACCO MATTLE VILLE (STRAIN 190)	Z.	110-131	190-040				4	1	+
TVIK LAVIS	A SOCIETY	BROAD BEAN MOTTLE VIRUS		177	3	192.919			4	4	1
PVIA BBMV	IAPRUIENT	BRONE MOSAIC VIRUS	210		1	Т	L	H	L		4
PVIA BMV	IA PROTER	CONFEA GROADITC MOTTLE VINUS		\downarrow	1	-	ļ	-	L		Ц
PVIA COAV	IA MOTER	CITIZENES MOSAIC VIRUS (STRAIN FINT)			1	$\frac{1}{1}$	$\frac{1}{1}$	$\frac{1}{1}$	L	-	H
PVIA OAVE	IA PROTEDI	THE TOTAL VALIS (STIAN)	2	2	4	+	+	 	-	-	L
PVIA CACVO	IAPROTED	CUCUMER MOCKAC VIII'S (STRAIN 9)	11:34		4	+	$\frac{1}{1}$	+	\downarrow	ļ	H
2	IA PROTED	CUCUMER MOSAN VANDA VINE	€ :3	373-399		7	1	+	1	+	+
	14 PROTEIN	PEANUT STURY VILLE (STANDARY)	15:11	111-291	176.403	157-114		$\frac{1}{1}$	-	+	+
ALV VIA	A PROTEST	TOWATO ASPERMY VILUS	3	L	L				-	+	+
AVI YIA	STATE OF THE PARTY	AUTOGRAPHA CALIFORNICA MUCLEAN POLITICOROSIS VINCE	219	L		L			4	4	+
PYZSK NOVAC	Market Co.	PEA EAST Y BLOWNEND VINUS	13.4		L	-	L	Н	\dashv	4	4
PVZW PEBV	De La Parista	TANK A TANK TO THE VIEW		۱	۱		l				

PV29K_TRVTC		All Viruses (no bacteriophages)						j	-		
PV29K_TRVTC	PROTEIN		AKEAI	AREAI	AREAZ	1	AKEA S.	SEA SEA	AKEA1 A	ANIAL	AHLAS
	29 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCM)	5		i		: 1				
PV2A BBMV	2A PROTEIN	BAGAD BEAN MOTTLE VILLS	, io	:	:	-	:		-	;	
PV2A COMV	2A PROTEIN	COWPEA CHLOROTIC MOTTLI; VIRUS	78.70					1		1	
PV2A_CMVFN	1A PROTEIN	(IN FNY)	32.819				-		1]
PVZA PSVI	2A PROTEIN	KAIN J)	2 2 2 2 3 3 3 3	2.7.				1		1	4
PV2A TAV	2A PROTEIN		33.340	22.78				1	1	1	
PVJOK HOLVE	130 KD MAJOR EARLY PROTEIN	HUMAN CYTOMEGALOWRUS (STRAIN EISENIARDT)	27.55				+	+	†	+	-
PVJOK TRVIC	79.1 KD PROTEIN	TOBACCO KATILE VINOS (STRAIN II AT)	8 :	i	!	!	-	•	:	•	
LAND VIDE	33 KD MOSMOMOTEIN	IIIUMAN AUCHOVIRUS 117'E 41	2					†	1	1	
PV362 ASTB?	K'342 PROTEIN	AFINCAN SWINE FEVER VIRUS (STRAIN BATIN)	22.62					1		1	
PV36) ASFB?	D'363 PROTEIN	AFICAN SWINE PEVER VIRUS (STRAIN BAZIN)	2	72.199				†	1	1	
LANK BACA	JA PROTEIN	BROWE MOSAL VICES					+	\dagger	T	\dagger	
PVJA CAMPIA	JA PROTEIN	CUCUPIBLE MODAL, VIRUS (STRAIN PAY)	777				1	1	†	İ	
MA CAM	3A PROTEIN	CUCUPIBER MOSAR, VIRUS (STRAIN NI)	76.17			İ	1	j		+	1
PVJA CANO	JA PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	22:32		Ĭ		+	1	1	+	
VJA CARY	3A PROTEIN	CUCUMBER MOSAUC VIRUS (STRAIN Y)	200				+	1	1	1	
PAD VCA	IA TROILIN	AVIAN INTECHAND BRUNCHILIS VINUS (STRAIN BEACH): ILL.	i i				†	†	1	\dagger	T
COARD WAY	IN TACIENT	A CANA WERE THOSE SECTIONS CHAIR SECTIONS OF THE TAIL SECTIONS OF THE TA						Ť	1	\dagger	
EAR TRAIN	STACLES.	A VIOLENCE DE CONTRACTOR DE CO				Ī	+		1	†	ĺ
VXX BYDY	NA KUTAULEM	BALLET IELLOW DWANG VINUS HOUNE FAND	2				+		†		!
TANK BULAN	SI KUTAOLEM	BEEL WESTERN TELECONS VINUS (INCLASE TOP)							1	Ť	
PASSE BATAC	S AUTOLEUM	POCE WESTERN TELEVISORISMENT IN						1	1		T
	W COLUMN	POTATO LEGISTE VIETE SET ALL CACETAINS					1	†	†	İ	
	W THOIEN	POINT OF CHAPTER AND STRAIN AND CHAPTER AN					+	t	1	Ť	Ī
A STATE OF THE PERSON NAMED IN COLUMN 1	SE NO PROTEIN	BACKET STATE MOSAN, VINOS		\downarrow			1	1	1	\dagger	Ī
AND 88 AND	Matter Care and	POTATO L'ESTROLL VIBILA CATRAIN MAGENINGENI	1.0.146				+	1		\dagger	
PAGE ALVALE	SOKO PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 435 / ISOCATE LEIDEN)	107.134					1		T	
PVADE VAPOR	PROTEIN A4	VACCINIA VILUS (STRAIN COPENHAGEN)	157.216	280.233	283-310	3	+		T		
VALUE VALUE	PROTEIN A6	VACCINIA VIRUS (STRAIN WR)	\$6.2 56.2 56.2	249.276	282.300	2		T	t		
PVA06 VARV	PROTEIN A6	VARIOLA YIRUS	157.216	250-277	213-310	314-355			T	l	
PVADS VACCC	PROTEIN AS	VACCINIA VIXUS (STRAIN COPENHAGEN)	176-206				-				
PVACE VARV	PROTEIN AS	VARIOLA VIRUS	176-206								
PVAOP VARV	PROTEIN AS	VARIOLA VIRUS	60.93								
PVAII VACCC	PROTECHALI	VACCINIA VIRUS (STRAIN COPEMIAGEN)	219-283								
PVAII VARV	PROTEIN AIL	VARIOLA VIRUS	220-284								
PVAIS VARV	SEKD ABOATIVE LATE PROTEIN	VANOLA VIRUS	19079						1	Ì	
PVAJO VACCC	PROTEIN A20	VACCINIA VIRUS (STRAIN COPENHAGEN)	29	30-33			1	1	1	1	
VAZO VAKV	PROTEIN AZO	VAUCLA VIALIS AND PORCHAINCEIN		1000				1		Ì	
PVAD VACC	PROTED! AZZ	VACUNA VINOS (STRAIN COPENHAGEN)						1	1	1	
PVAZ VAKV	PROTEIN ASS	VACCING VINIS (STRAIN COPENHAGEN)	95.144				1	\dagger	t		I
2000	Partition A21	VARIOUA VIRUS	25.44					T	t	†	
PVA28 VACCV	PROTEIN A28	VACCINIA VIRUS (STRAIN WR)	17-49				\mid	t		t	
PVAZE VARV	PROTEIN A28	VANIOLA VIRUS	22-49								
PVANO VACCV	PROTEIN A30	VACCINIA VIRUS (STRAIN WR)	12-55	Ц							
PVA31 VACCC	PROTEIN A31	VACCINIA VIRUS (STRAIN COPENHAGEN)	8-1:3								
אאי ואיי	PROTEDY ASI	VARIOLA VIRUS	22					1	1		
PVAJ4 VACCC	PROTEIN A34	VACCINIA VILUS (STRAIN COPENHAGEN)	2					1	1	1	
PVAJ4 VACCV	PROTEIN AJ4	VACCINIA VIKUS (STRAIN W.R.)	-						+	1	
PVAJA VARV	PROTEIN AD4	VARIOLA VIXUS					+	1	1	†	Ī
PVA36 VACCV	PROTEIN AND PRECURSOR	VACCIMIA VIXUS (STRAIN WR)					1	†	-	+	
PVAJ6 VARV	PROTEIN AJ6 PRECURSOR	VAUDLA VIKUS	× .				1	†	+	1	
PYAJE VACC	MOTEUN AN	VACCIMIA VINUS (STRAIN COPENHACEN)						+	1	+	T
WASH WACEV	MOIEM AN	VARIOUA VIRIS	1				+	†		1	1
WAN WAC	PROTEIN AND	S (STRAIN COPENHAGEN)	17:71	155-182	\int	I	+	t	f	\dagger	T
יייייייייייייייייייייייייייייייייייייי	I'MOLES SOL							1]

FILE RAME 1 VAND VACCO 1 VAN	PROTEIN	YIRUS VACCDUA VIRUS (STRAIN WR)	П.	193-220			-		1	
		AALLINA HEGS STILL			-	-		-	-	
	TACIENT CO.	THE PROPERTY OF THE PARTY OF TH	143-172	j	1		1			
	PROTEIN A43	VALCINA VINOS (STATIS CO. T.	143-172				-			
П	PAOTEIN A43	VACUALA VIROS (SIRVINA TR.)	146-173						· -	1
	PROTEIN A43	VARUELA VIRUS	143.184				+			i
	PROTEIN A47	A COUNTY OF IN CITE AND WELL	143.114			1	+		-	ľ
П	PROTECH A47	VACUAL VINOS (SI COLO SI COLO	143.114			1		+	-	1
Ī	PROTEIN A47	VI CHAIR WEIT (STRAIN CHENNIAGEN)	16-19							:
PVA® VACCC	PROTEIN A49	VACCINIA VIRUS (STRAIN WR)	16-19			1		-	-	1
7	PROTEIN A49	CABINA VIEW	16-19	_					+	
٦	PROTEIN A49	UAPCINIA VIETE (STRAIN COPENIAGEN)	55-62	126-156	435-462	1	+	1	+	
	PROTEIN ASS	A ANNA AMERICAN AND WAS	28-82		435-462		1		$\frac{1}{1}$	
>	PROTEIN AJS	AACERA VANO (SINGER SIN	13-49				-			1
	ALI PROTEIN	BEEL COLL TOT VINOS	39.106						$\frac{1}{1}$	
	ALJ PROTEIN	CASSAVA LATERI VIROS (STRAIN WEST MENTALLY)	79.106							
Γ	ALS PROTEIN	CASSAVA LATERI VIROS (STRAIN PROCESSA)	101-128]
Γ	ALJ PROTEIN	SQUASH LEAF CURL VIAUS	79.129							
	ALS PROTEIN	TOWATO TELLOW LEAV CORE VINOS	Γ	93.129					1	
Г	APIED TRANSMISSION PROTEIN	CAULTOWER MOSAIC AND CITE OF THE CAULTON	23:30						-	
	APHID TRANSMISSION PROTEIN	LAULT COMES ACCESS COMES STATES TO BRITE STATE	12.70	93.129						1
П	APHED TRANSMISSION PROTEIN	CAULTION FOR MODING COMMAND AND COMMAN	22.70	93-129			1			1
	APHID TRANSMISSION PROTEIN	CAULTOWER WAS IN CORP. (STRAIN PAIR)	22.70	93-129	H					1
PVATCUM	APPED TRANSMISSION PROTEIN	CAULTONICA HOSTIC SINCE	32-70	011-16			1		1	1
	APHED TRANSMISSION PROTEIN	THE COMES MORALE VIRIS (STRAIN W260)	υ - π				1	1		1
	APPED TRANSMISSION PROTEIN	CAULTOWER MUSIC VISION WILL	102-138						$\frac{1}{1}$	1
Г	APHOD TRANSAGSSION PROTEIN	CAUNTIUM BICMED MING VINCE	33.43	103-130	<u></u>				-	1
	APHID TRANSMISSION PROTEIN	PROPERTY AND A COLUMN TO THE PARTY OF THE PA	104-135							4
PVB03 VACCV	PROTEIN B3	VACCIPILA VIRUS (81 PALIN WA)	93-123	183-211	286-313	134-361				4
PVBON VACCC	PROTEIN BA	VACUALA VINCE (STANDA OF UNE)	93-133	112-211	116-313	124.361		1		1
PUBOL VACCV	PROTEIN BA	VACCIAL VACCO (STRONG TA)	189-129	103-211	116-313	124-361		+		1
П	PROTEIN B4	VACCES VIEWS (STRAIN LCIGNIO)	154-284				1		+	1
	PLAQUESIZE / HOS I PLACE 7 NO FACE	VACCINIA VINUS (STILAIN COPENHAGEN)	234-284				1	1		1
١	PLACOSIZE / POST PLACE PRO PRE	VACCINIA VIALIS (STRAIN LISTER)	294.284				1			\downarrow
	PLAQUESIZE / POST RANGE TRO PREC	VACCIONA VIRUS (STRAIN WR)	154-284				1	1		1
	PLAQUE-SIZE / HOST INVOICE THO THE	VACCEDIA VIRIS (STRAIN WR)	28-62					1		1
PUROT VACEV	PROTEIN BY PRECURSOR	VACCINIA VIRUS (STRAIN COPEMIAGEN)	26-53				1	1	\ 	ļ
PVBOR VACCC	PROTEIN BY PAEL UNDUR	VACCEDIA VIRIIS (STRAIN WR)	26-53				1	1		╀
PVBOR VACEV	PROTEIN BE PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	21.54				\dagger			1
PVB11 VACCC	PROTEST	VACCINIA VIRUS (STRAIN W.R.)	5:31				+	+		1
PVB11 VACCV	PROTEIN BILL	COWPOX VINUS	113-140				†		+	\downarrow
PVB16 CDWFX	AND TAN PARTICION	VACCENTA VIRUS (STRAIN COPENHAGEN)	231-313				1		-	1
TANK (IRA)	PROTECTION BLA	VACCINIA VIRUS (STRAIN WR)	135-203				1	-		L
MARIA AVCTA	TRUING ST	VACCIPILA VIRUS (STRAIN COPENHAGEN)	21.700				+			1
Well Water	TAU I LANDING	VACCIMIA VIRUS (STRAIN WR.)	27.70				+			-
WBIE WALLY	TRUITS BIS	VAUGLA VIBUS	37.7.1				1	1	-	-
PVBIS VAKY	COMPANY AND CONTROL OF THE CURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	112:213				1	+	-	╀
LANG AVECT	SON THE ACTUAL OF CHILDSON	VACCONIA VIRUS (STRAIN DADLEN I)	012-031					+		L
AND VACED	SULL AND	180-210				1		-	+	
PVB19 VACEV	SUPPLY AND INTERNATIONAL PROPERTY OF THE CORP.	VANOLA VRUS	180-210						+	1
PVB19 VARV	SULPACE AN INCHAS OF PRESENCE	VACCINIA VINUS (STRAIN COPENHAGEN)	40-03				†	$\frac{1}{1}$	+	ļ
WESS VACE	PROTECTION INC.	VACCINIA VIXUS (STRAIN WR)	64-9				1			-
PVB2! VACLV	PAULE NO.	BEAN GOLDEN MOSAIC VIRUS	120-147	248-273						1
PVBLI BGIV	BLI MOLEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	118-145							╀
PVBLI CLVK	BLI PROTEIN	CASSAVA LATENT VIXUS (STRAIN NIGERIAN)	111-145					1	1	+
ואשרו מיא	BLI MOTEIN	POTATO YELLOW MOSAUC VIRUS (ISOLATE VENEZUELA)	120-141				1	+	1	1
PVBLI PYNVV	BL! PROTEIN	VAPCHINA VIBINS (STRAIN COPENHAGEN)	405-432	Ц					+	1
PVCE VACCC	PROTEINCE	VANCANTA VIBILE (CTR AIN WILL)	11-11	405-432						4

PCGENE	107117014	All Vienses (ne batteriophages)			П	_	П	П	-Т	П
FILENAME	PROTEIN	YIRUS	VEV.	4	485	1	<u>र्या</u>	ARIA AREAZ	AZ AREA	SALES.
PVCM SFVKA	PROTEIN CA	SHOPE PIBROMA VIRUS (STRAIN KASZA)	209-236	25.313		1	1	+		
PVCS4 VACCC	PROTEDICA	VACCINIA VIRUS (STIAIN COPENHAGEN)	77				1			
PVCD4 VACCV	PROTEDICA	VACCINIA VIRUS (STILAIN WIL)	3778			1	1	1		
PVCON VARV	MOTEDIC	VARIOLA VIDUS	12-46			1				-
PVCBS SEVICA	HYPOTHETICAL PROTEIN CS	SHOPE FEBROMA VIRUS (STRAIN KASZA)	15:123	152.179		1	1			4
TVOS VACCC	PROTEDICS	VACCINIA VIRUS (STRAIN COPENHAGEN)	6			1	†	1	+	ļ
WOS VACTV	MOTERICS	VACCINIA VINUS (STIAME WA)	3				\dagger	+	+	+
PACES VACES	PROTEIN	VACCINA VIBIR (STRAIN WE)	10.11			T	İ	<u> </u>	<u> </u> 	-
THE PARTY OF THE P	TRUISING.	A CALLER A CALLER	1			T			 	-
PUCTO VANCO	PROJECT CA	IVACCIONA VIBIIS (TITA A IN POPENNA CIENA	03.60	2.116	178.205	252.279	289-325 57	\$75-603		
TO ALL	Section 2	VACCIDIA MEN CONTRACTOR	89	12.116	74-70\$	Т	Т	\$75.605		-
PWC10 VACCE	PROTECNICIO	VACCOUR VINUS (STRAIN COPENHAGEN)	136-180			Т	T			L
PVC10 VACCV	PROTEIN CIO	VACCINIA VIRUS (STRAIN WR)	136-163			Ì				-
PVC16 VARV	PROTEIN CIO	VANIOLA VIRUS	136-163	•	:	•	!	•	:	
PVCI3 SPVKA	PROTEIN CIS	SHOPE FIBROMA VIRUS (STRAIN KASZA)	3.30	39-66	137.182	206-240		-		
PVCI7 VACCC	PROTEIN C17/823	VACCINIA VIRUS (STRAIN COPENHAGEN)	111-152							
PVCIS VACCC	PROTEIN CIMBIA	VACCINIA VIAUS (STRAIN COPENHAGEN)	40-74							
PVC19 SFVKA	PROTEIN CI9	SHOPE FIBROMA VIRUS (STRAIN KASZA)	26-97							
PVC26 VACCC	PROTEIN C30/B36	VACCINIA VIRUS (STRAIN COPENIIAGEN)	73-99							
PVC22 VARV	PROTEIN C12/B18 HOMOLOG	VANUOLA VIRUS	299-326							
PVCA EDV	MAJOR CAPSID PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 895.8)	847-874							L
PVCAP_HSV6U	MAJOR CAPSID PROTEIN	HERPES SOUPLEX VIAUS (TYPE 6 / STRAIN UGANDA-1102)	136-170	355-382						
PVCAP HSVSA	MAJOR CAPSID PROTEIN	HENVESVIRUS SAIMIN (STRAIN !!)	169-199							
PVC03 NPVAC	DNA-BRIDING PROTEIN	AUTOCRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	133.165	199.248						
PVCOM ADEM	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE 2	E-E-							
PVCOM ADEOS	MINOR CORE PROTEIN	KUMAN ADENOVIRUS TYPE S	17-114							
PVDOS FOWPI	92.6 KD PROTEIN	FOWLPOX VIRUS (STRAIN FP.1)	6-3	184-21	321-348				1	
LADOS VACCC	PROTEIN DS	VACCINIA VIRUS (STAAIN COPENHAGEN)	240-267	333-360			1			\downarrow
PVD09 VACCV	PROTEIN DS	VACCINIA VIXUS (STINAIN WX)	140.767			T	\dagger	+	1	\downarrow
PATON VACO	SPOTEN DA	VACCIDIA VIBIR PETRAIN COPENHAGENI	31.15			T	\dagger		 	
TATO VACE	PROJECT DA	VACCINIA VINE (ATEAN WE)	3.5		1	1	T			
PUTOR VARV	PACIFICACION DA	VALIDIA VIRUS	23.160		Ī	T	\dagger		-	\downarrow
PVD10 SEVEA	PROTEIN DIO	SHOPE FIBROMA VIRUS (STRAIN KASZA)	11-53							
PVDBP CERV	DNA-BINDING PROTEIN	CARNATION ETCHED RING VIRUS	25.5				T	-	-	
PVECT VARV	PROTEIN E2	VAUOLA VIRUS	262-532						_	
PVEDS VACCC	PROTEIN E6	VACCINIA VIRUS (STRAIN COPENHAGEN)	911-68	437-464						
PVED6 VACCV	PROTEIN EA	VACCINIA VINUS (STRAIN WR)	25-116	437-464						
PVED6 VARV	PROTEIN E6	VAUOLA VIRUS	9	367-394	437-464		1			
PVEI HPV18	EI PROTEIN	HUMAN PAPILIDIANTIUS LYPE IS	2		1	1	1			
FVEL HPVZA	EL PROTEIN	TOWAY PALLEMAN THOU I THE SA	100.00			1	1	+	+	\downarrow
PVEL LOVID	EI PROTEIN	HIDAAN PARI I MAAVILUS TYPE 19	103-130			T	1	+		1
PVE1 HPV41	EI PROTEIN	HUNAN PAPELLONAVIRUS TYPE 41	55.89			Ī	T			L
PVEI HPV42	EI PROTEIN	HEDALAH PAPELLOMAVIRUS TYPE 42	25-59							
PVEI HPV47	EI PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47	146-173							
PVEL HPVS7	EI PROTEIN	HUMAN PAPILLOMAVIAUS TYPE S7	21-48							
PVE26 NPVAC	EARLY 35.9 KD PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	3							
PVE2 CRPVK	PROBABLE E2 PROTEIN	COTTONTAIL RABBIT (SHOPE) PAPILLOMAYIRUS (STRAIN KANSAS)	ž					-		
PVE2 HPV0S	PROBABLE E2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE S	2.5							
PVE2 HPV13	E2 PROTEIN	HUMAN PARLLOMANIAUS ITPE 13	27.	106-30			1	+	-	
PVEZ HPVIO	E2 MOIEIN	NUMBER OF THE PARTY OF THE PART	91.11	200216		İ	+	-	+	-
PVEZ HEVIB	EJ PROJEIN	MOMENT PARTY IN THE IS IN THE IS	150.186				\dagger	1	1	1
PVES HOUSE	ES PROTEIN	HOMAN PAPEL CHAVITUS TYPE 2A	159-193				\dagger	1	+	\downarrow
TANK TANK	ET PROTEIN	RIMAN PAPELLONAVIRUS TYPE 33	20.50		T		t	-	+	\downarrow
***							1			

Ш				A SEA	V CANED	1					
П	MILL CALL			327-354							
T			Т	121-157							
			Ī	T.	176-303						
1			1	Т							
		DALLAN BARN I OLIA WRITS TYPE SI	201-162								
VEZ HPVSI		TANKS DANIELIS TYPE ST	٤								Ĺ
VE2 HPVS7		TOWAY CALL CASE OF THE PARTY OF	2.36	309-336							•
		UNANT AN ILLUMANT TO SEE A	13.51								
	E2 PROTEIN		32-150								
			Г	127.361							
I		VIRUS TYPE I	Т								
1			27.72								
			11.10								L
		HUMAN TATLESTAN TANGET IN	66-93								
		FORTH PAPELLONA VINOS 117E 19	39.86								
Ī		ASMAN PAPELOMAVIAUS I TPE I	20132					1			
		HOMAN PAPILLOMAVIRUS TYPE 31					L		_		_;
		HENDAN PAPILLOMAVIRUS TYPE 41	16:40								:
WEA HOVA!		STATE OF A VISIT TYPE SE	202-220								L
WEA HOVER			9-00								1
	2	HUMAN PAPILLONAVIRUS 177E 11	20.65						:		_
10 VC		HUMAN PAPILLONIAVIRUS TYPE 611			:	:					_
VESA MOVES		IN MAN PAPILL OMAVIRUS 1 VM: CC	2		!						
VESA HPV6C		THE AND A PAIL OWANIEUS TYPE 15	37.54			1					L
ES HOVES		MUMANT ACCOUNT OF THE CO.	11-41						Ì		i :
ALVE & LYBOVER		HUMAN PATILLUMATING 1115.78	13.62								1
		PYCMY CHIMPANZEE PAPILLCHIAVIRUS ITTE	16.10								_
VES POVI		HINDIAN PAPILLOMAVIRUS TYPE 18				1		L	L		
WES HOVIS		THE AND A PART I CAMA VIRUS TYPE 31	69.90			1			-		_
WES HOVE		CANAL DAVA VIEWS TYPE 39	71-102			\downarrow	1				L
PVEA HOVOS		TARREST OF TARREST TAREST	19-146								-
VES HOVE	EA PROTEIN	HUMAN FA LACORD STATE STATE AND AS	75-102								ļ
VEA NEVAL		KUNAN PATILLOMAN MAGA 1 1 1 2 2	72.00		! 						1
AND AND AND	FA PROTEDI	HUMAN PARLUMAVIANS 117E 31	11.102		_						-
		HUMAN PAPILLOMAVIRUS TYPE PIETE	430.447			L					4
200	L	AUTOGRAPHA CALIFORNICA MUCLEAR POLITICIANOSIS VIROS	411.411			L					
- L	WEAT ENMANCEMENT PACTOR	TRICHOPLUSIA MI GRAMULOSIS VIAUS	118.164								
N CALM	PASSES OF VENERAL PRECURSOR	DHON VIXUS (STILADA INDIANI) 1.341)						L			
WENT DRIVE	TAL AND A WANTED PROTECTION	EQUINE ARTERITIS VIRUS	177.51			1					
VEN EAV	THE STATE OF THE S	THOGOTO VALUS			1	-	-		L	-	_
VENV THOOV	ENTELOPE OLYCOPROJEM PRESONO	VACCIONA VIBILIO (STRAIN COPENHAGEN)	31:00					-	-	-	L
VF03 VACCC		The state of the second	11:10	22.5						 	ļ
VADV WAVE	-1	VACLIMIA VICTORIA POR	13-60								1
	A NEXBELANE PRO PRECURSO	VACCINIA VILUS (STIXAIR L-147)	33.60		L	_					4
1 S	\sim	VACCINIA VIRUS (STIAIN WR)	150		-	-					4
VPO VALLY	ı	VAUOLA VIRUS			+	-		-		_	
MISS VARV	MOIEM	VACCIMIA VIBLIS (STRAIN COPENHAGEN)	176-9/2			-				-	L
PVF11 VACCC	PROTEDIFIE	VACCIMIA VIRUS (STRAIN L-1VP)	270-21-2		1	1	-		-		L
WELL VACO	PROTEDN FILE		274.321			4	-		-		+
VALUE VARV	PROTEIN F11	VAUUA YUWA	10-37	113.140	1354-581	_					1
	SECURITY BIS	VACCINIA VIXUS (STRAIN COFFINANCIA)	10.51	113-140	354-581	_					4
AND AND	CANADA PIS	VACCINIA VIXUS (STRAIN L-IVF)		1	τ	-	-	-	L		
VEIN VACO	TAULENTIA	VARIOLA VIRUS			7	+	+	-		-	L
VF12 VARV	PROTEINFIZ	VACCINIA VIRUS (STIVAIN COPENHAGEN)	262	22.		1	1	-	1	-	-
VF16 VACCC	PROTEDY FIG	VACCINA VIRILE (STRAIN L. IVP.)	35-62	22.5	-						-
VEIL VACO	PROTEDN F16	WOLLD'S WAS LONG TO SEE THE SE	35-62	149-179			4				$\frac{1}{1}$
VALL VALV	PROTEIN FIG	VAUGA VIAUS	146-173	L	_				-	4	1
2000	PROTEIN PP4	FOWLYOX VIKUS	29:16			-					-
	I A W DE INSTRUMENTAL PROTEIN	ONE VIRUS (STRAID NZZ)	77.51					_			4
14300	Catholic and Catho	VACCINIA VIRUS (STRAIN COPENHAGEN)			-	-			L	L	•
PVFUS VACCC	IA KU PUSANT PROJECT	VACCINTA VIDUS (STRAIN WR)	6/6		1	+			-	-	L
PVFUS VACCY	KD FUSION PROTEIN	VALITHIA VIRUS (STRAIN COPENHAGEN)	225-252	2		1	+	1	1	-	-
PVCBI VACCC	PROTEING	VACCING MINISTRAIN WRY	164-191	240-274		4		4	1	1	+
VACCV	PROTEIN GI	AACUAN ANGELES	225-252	301-335				-		$\frac{1}{1}$	+
VANV VANV	PROTEDIO	VARUAL VALUE	96-123	L					4	+	\downarrow
	ICATINE ATSC DEP PROTEIN	VACCINIA VIXUS (STRAIN W.K.)	1 26-123	L	-	L					4
1	THE PROPERTY	VAUOLA VIRUS									

PCCENE	1107117214	[All Virgins for begrerfenberen)						ľ	-	ľ	{
FILE HANG	PROTEIN	YIRUS	AREA	AHEA 2	AWKAR	AUVA	1.17	4 4.7.4.4			
PVC03 HSVES	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE: I (STRAIN ABAP)	100					•	-		֭֭֭֝֟֝֝֟֝֟֝֝֟֝֓֓֓֓֓֓֓֓֓֓֓֓
PVG03 IISVEK	GENE J PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN KINTUCKY A)	146-176	!	:	!	:	:	:	:	:
PVG65 VACCC	PROTEIN GS	VACCIMÍA VIRUS (STRAÍN COPENÍTAGEN)	48.75	131-161	225-289	355.389			Ī		
1 V COS VALV	MOTENGS	VANOLA YIRUS	48-73	191-921	155-219	355.319				-	
PVCO PSVI	HYPOTH GENE 7 MEMB PRO	ICTALUNID HEAVESVIRUS 1	11-98								-
מינים מינים	TACIENT	VACCIMA VIAUS (STRAIN COPEMIAGEN)	301.338								
PACON VALL	PEOTENE	VACCINIA VIKUS (STRAIN WR)	271-301			1		:	<u> </u>		
PVOL2 COVIR	CENE 13 PEOTEIN	CANDON VINOS	201.3			j	1				
PVGIT HSVII	HYPOTHETICAL CENE 12 PROTEIN	Interior Medicality	ŝ				1	1	1	1	
PVOIL HSVII	HYPOTHETICAL GENE 10 PROTEIN	ICTALIND WEIDESVIKUS I	5 7			1		1	1	1	
PVGI SPVIR	CAPSID PROTEIN	SPIROPLASMA VIRUS SPVI-RSAZ B	340.383			1	1	T	1	1	
PVGI SPV4	CAPSID PROTEIN	SPIROPLASMA VIRUS 4	711.02	017.111		Ì	İ				-
PVG22 HSVII	HYPOTHETICAL GENE 12 PROTEIN	ICTALUND HEAPESVIRUS I	131.400	667 153	306 377	76.37	1	1	1	İ	
PVG24 HSVII	HYPOTHETICAL GENE 24 PROTEIN	ICTALUND HENDESVIRUS I	5.5				1	T	1	1	Ī
PVG28 HSVII	HYPOTHETICAL GENE 24 PROTEIN	ICTALUND HEAVES VIRUS I	233.380	497.528		T	İ	1	T	Ì	
PVGIR ANGEN	HYPOTHETICAL G2R PROTEIN	AMSACTA MOOREI ENTOMOPOXVIRUS	Г	811-16				T	T	\dagger	T
PVG2 SPVIR	GENE 2 PROTEIN	SPIROPLASMA VIRUS SPVI-REAZ B	Ļ				T	Ì		t	I
PVG2 SPV4	GENE 1 PROTEIN	SPIROPLASMA VIRUS 4	Т	175.205	262-310	Ī		T	T	\dagger	Ì
PVGM HSVI	HYPOTHETICAL GENE 34 PROTEIN	ICTALURID HENDESVIRUS I	95-122					T	T		T
PVCD7 HSVI	HYPOTHETICAL GENE 37 PROTEIN	ICTALUND MERPESYIRUS I	443-469						T	 	
PVG19 MSV1	HYPOTHETICAL GENE 39 PROTEIN	ICTALURID HEAPESVIRUS I	651-678	1041-1115					T	\mid	
PVG3L AME.PV	HYPOTHETICAL GIL PROTEIN	AMSACTA MOOREI ENTOMOPOXVIRUS	2.29								T
PVG3 STVIR	GENES PROTEIN	SPIROPLASMA VIRUS SPVI-RBA2 D	15-49				İ		İ	ļ	ĺ
MCD STAN	GENE 3 PROTEIN	SPIROPLASMA VIRUS 4	18-52	87.148					l		
AND HOUSE	HTTO HELL GENE 45 PROTEIN	HEAVESVIAUS SABAIRU (STRAIN II)									
PUCKE LICKER	INCOMPLE MACON COLYCOPROJEIN	ICIALUMO MELANSVIRUS I		346-373	103.034	473-1007					
VENTA ALTON	GAR BEOTHER	ALVELOPA MODELLE ENTONIONISTI	260.38								
PVO SVIE	GENE A PROTEIN	SPIROPLASIAA VIRITE SPVI. BBA3 II	3								
PVOSI HSVII	HYPOTH GENE SI MEMBRANE PROTEIN	ICTALINE MENESYALUS 1	Т	11.11	1	1	†	1		1	
PVG52 HEVSA	HYPOTHETICAL GENES 52 PROTEIN	HERPESVILUS SABARU (STRAIN 11)	Τ		Ī	1	1	1	1	1	
PVGS6 HSVII	HYPOTHETICAL GENE SO PROTEIN	ICTALURD HEIDESVIRUS I	\$82-609				\dagger	T	\dagger	†	
PVOS SPVIR	GENE S PROTEIN	SPIROPLASMA VIXUS SPV1-REAZ B	65-92					T		\dagger	
PVGS SPV4	GENE 5 PROTEIN	SPIROPLASMA VIXUS 4	26.8 3					T		+	T
PVG65 HSVII		KCTALURD NEAPESVIXUS I	550-584				l	İ	l	T	
TVCA HSVII		ACTALURED NEIVESVIRUS	47.50							l	Γ
PVCAL LEVIL	INVESTIGATION OF ALL PROTEIN	CTALLIN WEB PERVIS	213-123								
PVQ67 HSVII		KTALUED SERVESTI	307-700		1		1				
PVG64 HSVII		CTALUND HELPESVIRUS 1	361.38	T		1	1	1		1	ĺ
PVG72 HSVII	HYPOTHETICAL GENEE 72 PROTEIN		177.77			1		†	1	1	
PV075 HSVII			277116				I	\dagger	\dagger	\dagger	T
PVG76 HSVII	CENE 76 PROTEIN	KTALUNIO HELVESVIRUS I	700-127				t	I	t	\dagger	T
PVG7 SFV4	TED	SPIROPLASMA VIRUS 4	7			l	l	\dagger	t	t	T
PVGF! BV8		AVAN INTECTIOUS BRONCHITIS VIAUS	2	2408-2435				l		\mid	T
rwar cwar)		642-676	1022-1044	1274-1305			-		
PVG2 CVBL9	EZ GL. YCCPROTEEN PRECURSOR	BOVING CONCINAVIALIS (STIMAIN LY)		П	1022-1084	1278-1305				H	Γ
PVGL CVBLT			Т	975-676	1023-1084	1378-1305					
			٦	62.6% 62.6%	1022-1084	1278-1305			ŀ	_	Γ
200			Т	62.676	1022-1064 1271-1309	271-1305					
			Т	642.676	_	1378-1305					
WG 2 CWA		Wit O TVPE A	1	600-600	2	1	1				
Т				201-001	078 1040	1	+	1	1	+	
Γ			1,	16	3	1	1	\dagger	1	+	
П		MURDIE CORONAVILUS MAIV (STRAIN JPM)	Ť	189-931	T	†	\dagger	\dagger	\dagger	\dagger	T
			1		1		1	1	1	1	7

П	107617864	ser (se bacteriophige)	AREAL	Ū	TVINO	2854	SATA SATA	AREA	4		
П	PROTEIN	PARTIES TRANSMISSIBLE CASTROENTENTIS CORONAVIRUS (STRAIN FS772/69	Ī	7	1072-1145						1
PVQ1 CVWS	ET CLYCUTROTEIN PRECURSOR	PORCONE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN MILLESS-110	Т	7		1131-151					1
T	St. C. LOCKED TENT PERCENTAGE	PORCINE TRANSMISSIBLE GASTROENTENTIS CORONAVIRUS (STRAIN PURA)	T	1	100						
T	S CLICATOR DE CHIEFUR CON	PORCINE TRANSMISSIBLE GASTROENTIAITIS CORONAVIRUS (STRAIN PURI) 69-107	Ì	7							
T	S. S. VOORD TEN PERCINCAL	PORCINE RESPIRATORY CORONAVIRUS (STRAIN IN 177004 / BRITISH ISOLAT 44	J	†	6011-671					-	
T	ES OF VOORDITRIN PERCITATOR	POICTHE RESPIRATORY CORONAVIRUS (STRAIM RAIA)	J	1	1147-1103	111.111				-	
200	PARTY OF THE PARTY		T								
2	AND THE LANGE AND CO VOCABOTEIN		7	Т		17,1					!
T	ESTA VANDA OTT IN PRECIDENCE	TUS (STRAIN 79-1146)	ī	_	100.00						
100	STOCKED STOCKED BOTTON		╗	10.40	1001-7401		ļ				ļ
1	EL LETCOTRO LEIN FRENCHENS		╗	23.83	10%-1000		\downarrow		1	1	1
١	E G. YOUROI EM PRELORSON			176-903	1037-1091				1	\downarrow	1
۱.	ET CL YCUPIOTEDA PILELUASON	13)		115-902	1056-1090					\downarrow	\downarrow
	E2 GLYCOPROTEDY PRECURSOR		808-835	173-902	0601-9501						1
PAGE BAN	E2 GLYCOPROTEIN PRECURSOR		95-122	631-658							4
	GLYCOPROTEIN GP110 PRECURSOR	401401	23-61	197.424	440-467	1131-178					-
ž	GLYCOPROTEIN B PRECURSOR	HOLLAN CTIONECALUTING STRAIN ADVISED	Γ	397.424	435.462	82-879					4
	CLYCOPROTEIN B PRECURSOR		Ţ,	Т		L	L	L			
SAN S FLAG	GI VCOPROTED/ I PLECURSOR									_	_
	OF VOICE OFFICE BUT PRECIETOR		T				-	1	-		L
	CLUCK CHEN IN PRECITE COL	15A)	٦	24.4			1	1	-		-
VG.B HSVEI	CONTROLL BUTCHEST BOOK		7	0.000			1	1	1	-	+
1	OLI COLLOS DE LA PROPERTIDADA	(STRAIN ABI)	╗	34.90			1	-	1	1	+
	G. YCOTROJEM B PRECORSON			934-961				1	+	-	+
	CLYCOPROTEIN B PRELUASOR	UCKY D)	443-470	133-960						1	+
	CLYCOPROTEIN B MECURSON		021.66	352-379					-	4	+
	GLYCOPROTEIN II PAECURSUA		_	41.475	,			4	1	+	+
	GLYCOPROTEIN B PRECURSOR		469-510							$\frac{1}{1}$	+
П	GLYCOPROTEIN C PRECURSOR	15	686.510				Ц		4	4	+
PVGCC HSVIK	GLYCOPIOTEDI C PRECURSOR		124-151						4	4	-
PVGLC HSVED	GLYCOPROTEIN C PRECURSOR	EQUIND HELCES TAKES I THE AND MINISTERS AND	295-322		L					4	-
Г	GLYCOPROTEIN GPV		195.322		L						$\frac{1}{1}$
Γ	GLYCOPROTEIN GPV		111-148								4
PVGLE HSV1	CLYCOPROTEIN E PRÉCURSOR	HELDER SDOTLEY VACO (1 176 4)	200	24:202	216-243	442-469	416-531				1
	FUSION OLYCOPROTEDN PRECURSOR	HACEN	365	154-202	216-24)	177	488-533	L			-
WOLF BRSWC	FUSION OF YCOPROTEIN PRECURSOR		11.65	154-202	216-243	444.471	48.533	_	_		
VGJ BASVA	FUSION CLYCOPROTEIN PRECURSOR		٦	340.367			-		_		Н
OAU A	FISION GLYCOPROTEIN PRECURSOR	T	T	164.301	42.43	461.515		L	-	L	
IAS OF TONE	FISION OF YCOPROTEIN PRECURSOR	BY STANIN 18331)		54.30	13.34	115-117	-	L	L	-	L
AVAIL TOV	FIRM OF YCOPROTEIN PRECURSOR	T	Τ	1		1	481.515	-	L	-	-
N. 10.	FIREM OF YOOM OF END PRECURSOR	STRAIN LONG)	T			15	15.11	-	-	L	H
	THE HOLD VOICE OF THE PLECTREOR	(2-5)	7					1	-	-	ŀ
VOL. PUSYA	TOSHOW OF VOODE OFFICE PARCHINGS		707-977			\downarrow	1	1	1	+	+
Val. MeAse	TOTAL CHANGE OF THE PRECITE OF		271-205			1	1	1	-	\downarrow	+
TVCT MEAN	TOSKIN CONTRACTOR SEECTING	STRAIN YAMAGATA-I)	20.52			1	1	1	1	-	+
VGC NEAST	POSICON CELECON STATE IN PRECISEOR	MUMOS VIXUS (STRAIN SBL-1)	٦	77.70			1	1	+	1	+
Vol.	STATES OF VANDE OF THE PRECIES OF	MUNDS VINUS (STRADN MOYAHARA VACCINE)	Ī	2		\downarrow	1	\downarrow	+	+	+
PVGL MUMPH	STRICT OF VINE OFFICE PRECURSOR	MUMPS VIRUS (STRAIN RW)	ž	447-486		1	\downarrow	1	1	+	╀
VGL MUMUK	TOSION OF VONSONTEN PRECIPIOR	MUNGS VIDUS (STRAIN SBL.)	Т	420-31		-	1	1	1	1	+
PVGLF MUMO'S	THE PERSON OF THE PERSON	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA)2)	7	426-512		4	\downarrow	1	1	+	+
VOL NOVA	POSICIONAL CONTROL PRECIDENT	NEWCASTLE DISEASE VIXUS (STIVAIN BEAUDETTE C/45)	7	476-512		\downarrow		1	+	-	+
VOL NOVS	FUNDING TOO ACTION TO BE STITLE OF	NEWCASTI E DISEASE VIXUS (STRAIN HEIVI)	121-12	2 2 2 2 2 3 2 3		4		4	+	+	+
VOL NOWU	POSICIONE OF LOCATION PRECIBION	NEWCASTLE DISEASE VIRUS (STRAIN BI-HOTCHDREMAT)	151-178	426-312			1	1	\downarrow	+	+
VOL KOVA	PUSHON OF THE PUBLICATION	NEWCASTLE DISEASE VIXUS (STRAIN IT ALIENVS)	21.73	426-512			1	1	+	1	+
VOL. NOV	FUSION CLICOTROLEGY PRECIDENCE	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46)	151.17	192-219	<u> </u>		4	+	1	1	+
PVGL NOV.	FUSION OF TOWN DEED PRECINGOR	NEWCASTLE DISEASE VIRUS (STRAIN MOYADERANSI)	131-178	27.512		1	+	-	1	1	+
NO.	ETRION OF VONEDITEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLAND/96)	21:12			1	+	+	\downarrow	1	╀
NOT TON	THE PRECINSOR	NEWCASTLE DISEASE VIDUS (STRAIN TEXAS)	21-151			1	+	1	+	+	+

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TURNOG GLYCOPOGINE MELCOLOGY SHAWN MAJOR STRANK UPIN STRANK UPIN STRANK SHAWN STRANK SHAWN STRANK SHAWN STRANK SHAWN STRANK SHAWN STRANK SHAWN STRANK SHAWN SHAW	AGE PRODY	FUSION GLYCOPROTEIN PRECURSOR	MIOCINE DISTEMPER VIRUS	ž	207-122	36.55		i		:	<u>:</u>	•
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PURDING CATOOMOTER PRECAUGAS RESOLUTION SERVICE AND ATTACK STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND STAND ATTACK STAND ATTACK STAND ATTACK STAND ATTACK STAND ATTACK STAND ATTACK STAND ATTACK STAND STAND ATTACK ST	IVG.	FUSION CLYCOPROTEIN PRECURSOR	AINDEAPEST VIRUS (STRAIN L.)	224-265	458-506	L					\mid	Ī
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STREET OF CONTOURNEY PRECURSOR VARIETINA STREET	Die Control	CHANT OF OCCUPANT AS PARTY AS PARTY	EQUING RELUCES VICUS 1 TPE (STRAIN ABAP)	313-410						-	-	
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GLYCOPROTEIN H PRECURSOR HERPESVIRUS \$LAMIN (\$TRAIN !!) 111-1135	PVGLH HSV60	GLYCOPROTEDN H PRECURSOR	HEAPES STADLEX VIRUS CHYPE & / STRAIN CO.		.07				1			
E. GLYOPROTEIN PALCUASOR INDAVIA CYTÓNEGALOVIRUS (STRÁIN AD169) (7-11) M. PÓLYROTEIN PALCUASOR BUNYA YRUS (STRÁIN AD169) (7-11) M. PÓLYROTEIN PALCUASOR BUNYA YRUS (STRÁIN BALL) (91-54) (91-54) M. PÓLYROTEIN PALCUASOR BUNYA YRUS (STRÁIN BALL) (91-54) (91-54) M. PÓLYROTEIN PALCUASOR BUNYA YRUS (STRÁIN BALL) (91-54) (91-54) M. PÓLYROTEIN PALCUASOR BUNYA YRUS (STRÁIN BALL) (91-54) (91-75) M. PÓLYROTEIN PALCUASOR HANTÁAN YRUS (STRÁIN BALL) (91-70) (91-75) M. PÓLYROTEIN PALCUASOR HANTÁAN YRUS (STRÁIN BALL) (91-70) (91-70) M. PÓLYROTEIN PALCUASOR HANTÁAN YRUS (STRÁIN BALL) (91-70) (91-70) M. PÓLYROTEIN PALCUASOR PRÓPÉCT HALL YRUS (91-70) (91-70) M. PÓLYROTEIN PALCUASOR PRÓPÉCT HALL YRUS (STRÁIN BALL) (91-70) (91-71) M. PÓLYROTEIN PALCUASOR PRÓPÉCT HALL YRUS (STRÁIN BALL) (91-71) (91-71) M. PÓLYROTEIN PALCUASOR SEOLL YRUS (STRÁIN BALL) (91-71) (91-71) M. PÓLYROTEIN PALCUASOR SEOLL YRUS (STRÁIN BALL)	PVOLH HSVSA	GLYCOPROTEIN H PRECURSOR	HEAVESVIRUS SAUMIN (STRAIN II)		100-401				+	1	-	
M POLYPROTEIN PRECINSOR BINYAVEUS GERGITON 911-939	PVOLI HOAVA	IE GLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD189)					1	+	1	+	
M POLYROTEN PRECINSOR BUNY AVRUS IA GROSSE (ISOLATE L'14) 911-940 91	PYCHA BUNCE	M FOLYPROTEIN PRECURSOR	BUNYAYIRUS GERMOSTON	L	014.041	1178.1355		1		1	+	
M POLYMOTEN PLECURSOR BUNYAANEA VRUS 511.709	PVOLM BUNE?	M POLYPROTEIN PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L'14)	L				1	†	+	+	Ī
M POLYTROTEN PLECUSOR DUCASE VARIO	PVGLM BUNNY	M POLYPROTEIN PRECURSOR	BUNYAMWERA VIRUS	340-374	304.535	601.709		T	-	1	+	T
M POLYMOTERN PAECINSOR MANTANY VRUS (STAIN HED) 15-102 15-	PVCLM DOGBV	M POLYPROTEIN PRECURSOR	DUGBE VIXUS	945-972					T	ŀ	+	T
M POLYROTEN PLECUSOR MATANA VILLS (STAAN PAUL) 15-102 15-1	DATE IN FINA	IN THE TREE LINE SECTIONS	MANIAAN VIKUS (SI KAIN B-1)	77-100	693-720						ŀ	Γ
M POLYMOTERN PRECUSOR MAYTAN VEUS STANK LEIS 75-102	ENVI A COM	M POLITIKO I EUN PRECUNSOR	HAN I AAN VILLE (STRAIN HOJO)	75-102						-	-	
M POLYMOTER PRECINGOR PAPATERS RECORD STAND	AND IN TAKE	W BOX VOECTIVE BEET IN COR	MANIFORM VINUS (STRAIN LEE)	25.102				-		_		
M POLYMOTERN PRECURSOR PROSPECT HELL VINUE PROSPECT HERT VINUE PROSPECT HELL VINUE PROSPECT HELL VINUE PROSPECT HELL VINUE PROSPECT HERT VINUE PROSPECT HELL VINUE PROSPECT HERT VINUE PROSPECT HELL VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VINUE PROSPECT HERT VIN	AND IN DICK	W POW VPROTEIN PRECINCOL	MANATON MEDICAL SECTION	75-102								Γ
MPOLYPRÓTER PLECURSOR PUDALLA VRUE (STRAN HALLNAS B1) 73-110	AND PARTY	M POR VPROTEIN PRECISE OR	PACKET IN VIEW	628-635	1069-1101							
M POLYPROTEIN PEECINSOR FULDAGLA VRUE (STRAIN SOTRANO) 77-110 77-11	PVOLM PUTTON	M POLYPROTEDY PRECURSOR	PUTMALA VIRUS (STRAIN HALL NAS RIL	8.5							-	
M POLYPROTEIN PRECINSOR SEOUL VIRUS (STRAIN 80-39) 113-540	PYCLM PUDAS	M POLYPROTED PRECURSOR	PUDMALA VIRUS (STRAIN SOTKANO)								-	
M POLYPROTEIN PLECURSOR SEOUL VIRUS (STRAIN ALT) 73-100 313-340 644-721	PVCLM SEOUS	M POLYPROTEIN PRECURSOR	SEOUL VIRUS (STRAIN 10-19)	Т	200					-	+	
M POLYPROTEIN PAECUISOR SEOUL VILUS (STRAIN SR.11) 71-100	PVGLM SEOUR	M POLYPROTEIN PRECURSOR	SEOUL VIRUS (STRAIN R22)	Т	077-170	100 404		1	+		1	
NOWSTRUCT GLYCOPRO GAS PLECUTSON BOVINE EPIEMGRALI FEVER VIRUS 513-544 115-1179 116-1171	PVOLIM SEOUS	M POLYPROTEIN PRECURSOR	SEOUL VIRUS (STRAIN SR-II)	Т	200	77-160		1	+		+	
PEPLOMER GLYCOPROTEIN PAECUASOR BELNE VINUS GLYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPROTEIN POLYTROTEIN PAECUAS GAYCOPR	PVGLM BEFV	MONSTRUCT GLYCOPRO GNS PRECURSOR	BOVINE EPHEMERAL FEVER VIRUS	Т		7/:-			1	1	+	
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GLYCOPROTEIN POLYROTEIN PAECUNS (LASSA VRUS (STRAIN GAJ9)) 66-113 GLYCOPROTEIN POLYROTEIN PAECUNS (MEGRA VRUS GLYCOPROTEIN POLYROTEIN PRECUNS (MEGRA VRUS GLYCOPROTEIN POLYROTEIN PRECUNS (MEGRA VRUS GLYCOPROTEIN POLYROTEIN PRECUNS (MEGRA VRUS GLYCOPROTEIN POLYROTEIN PRECUNS (MEGRA VRUS GLYCOPROTEIN POLYROTEIN PRECUNS (MEGRA VRUS (STRAIN VS)) 105-138	PVCLY JUNDA	GLYCOPROTEIN FOLYPROTEIN PRECURSO	JUNIN ARENAVIRUS			*	700-000	1		+	+	Ī
GLYCOPROTEIN POLYPROTEIN PRECUNS GMOPEIA VRUS GLYCOPROTEIN POLYPROTEIN PRECUNS (314-373 GLYCOPROTEIN POLYPROTEIN PRECUNS TACARIBE VIRUS GLYCOPROTEIN POLYPROTEIN PRECUNS GTACARIBE VIRUS GLYCOPROTEIN POLYPROTEIN PRECUNS GTACARIBE VIRUS (317A/N V.) 100-338	PVGLY LASSO	GLYCOPROTEIN POLYPROTEIN PRECURSO	LASSA VIRUS (STRAIN GA191)	19				†	+	1	+	1
GLYCOPROTEIN POLYTKOTEIN PECUNSCHICHINDE ALENAVIRUS GLYCOPROTEIN POLYTKOTEIN PECUNSCHICHING STRAIN VI) GLYCOPROTEIN POLYTKOTEIN PECUNSCHICHING STRAIN VI) 100-131	PVGLY MOPES	GLYCOPROTEIN POLYPROTEIN PRECURSO	MOPELA VIRUS	19	316-346			İ	\dagger	+	$\frac{1}{1}$	Ī
GLYCOROTEIN POLYROTEIN PRECUSSY ACADES VRUS GLYCOROTEIN POLYROTEIN PRECUSSY ACADES VRUS (STAIN VS)	PVGLY PIARV	GLYCOPROTEIN POLYPROTEIN PRECURSO	MCHINDE ARENAVIRUS					\dagger	+	+	$\frac{1}{1}$	Ī
OCIOCATO I SINCE I PACITACI EN PRECIONA I I ACADOBE VINOS (SI IXAIN V.S.)	PVGLY TACV	GLYCOPROTEIN POLYPROTEIN PRECURSO	TACARDE VIRUS		115-350				l	\mid		T
	river Invit	GUICOTAVIENT FOR TOWNSHINT FELORAL	I ACANDE VIKUS (STRAIM VS)	103-331					F		F	Γ

PCCENE	107217824	All Virenzs (no bacterfophages)	AREAL	ABEAL	AREA? A	1	24310	4			
TILE HAME	-1	VARUA	302-337			1					
PVOLY TACY	GLYCOPIOTEIN FOLYPROTEIN PRECURSO	TACALIBE VIXUS (STEAM TO)	303-338								
NA TACKT	CLYCOPIOTEIN POLYPROTEIN PRECURSO	TACAUSE VILUS (STIVAM IRVL 11378)	152:231		İ						
VALUE CONTRACTOR	CENCHAE POLYPROTEDY M	COWPEA SEVERE MOSAIC VIRUS (STRAIN US)	104-148		-						1
VAN FRV	PROBABILE MEMORANE ANTIGEN GP15	EPSTEIN-BARR VIXUS (STRAIN BY)-1)	280-314								1
VOS FROV	STRUCTURAL CLYCOPROTEIN PRECURSO	EBOLA VINUS	Т	919-619							
WCP MARVA		ALARBURG VIRUS (STRAIN MUSCINE)	Т	919-619							1
PUZS MARVE		MARBURG VIRUS (STRAIN POPT)	Т								
AND VAPOR		VACCINIA VIRUS (STRAIN COPENIAGEN)	1			Γ					
A CONTRACTOR		VACCINIA VIAUS (STRAIN WR)	1	130-184							_
7000		VALIOLA VIRUS	5								
VIEW VARY	AN ICASE	LELY SYNATONG ESS VIRUS	3		T	Ī					
A TOWN		VACCIDIA VIAUS (STILAIN COPENHAGEN)		Ī							L
WOW VACE		VACCINIA VIRUS (STRAIN WR)	1		†					L	
WHEN WACEV		VACTIMIA VIEUS (STRAIN COPENHAGEN)	1	2		T					ļ
VIOI VACCC		VARIA A VIRIA		2	1						-
VIOI VARV		VACCINIA VIRIIS (STRAIN COPENHAGEN)	80.09							ļ	ļ
VIDI VACCC		VACCINIA VIRIJS (STRAIN WR)	160-190		1						1
VIDI VACCV		VANIA A VINIS	160-190								1
VXD3 VARV		VACCINIA VIBILICATE AIN COPENHAGEN)	290-313	28.57	593-612					\downarrow	ļ
VIOL VACCC	PUTATIVE KNA HELICASE IN	VACCIDITA VIRING (STRAIN WR.)	190-317	£6.573	593-632					\downarrow	1
VIDE VACCV	PUTATIVE RNA HELICASE IS	Victor A Vietre	290-317	\$48-575	593-612				1		\downarrow
VIOS VARV	PUTATIVE RNA HELICASE II	CALLE ACTIVATION OF STRAIN SMITH	161-211							1	1
VIET MONNS	DOMEDIATE-EASLY PROTEIN I	CONTINUE CT I CONTINUE TO THE ACTUAL THE APPLICATION FOLLY WEDROSIS VINUS	155-345						1	\downarrow	1
VIET NAVOP	DOGDÍATE EALLY PROTEIN IS-2	THE SECTION OF THE PARTY FAR POLYHEDROSIS VIRUS	217-325	343~400						1	+
VIEW NOVAC	IE REG PROTEIN IE-N	AUTOMORIA CALLO CALLO TARRESTANDE I (REMAT ISOLATE)	62-29							1	\downarrow
VIF HVIRH	VIDION DEFCTIVITY FACTOR	THUMAN LINEAUTONIC COLORS (1801 ATE AGM / CLONE GRU-1)	2-36							\downarrow	1
VIE SIVA	VIXION DIFECTIVITY FACTOR	SIMILAR CHANGE CONTRACT (STRAIN ABAP)	147-174							1	1
VIDE HSVEB	PROB INTEGRAL MENDRANG PROTEIN	THE PERVISITE SALVEN (STAAN II)	80-107						\downarrow	1	+
VDAP HSVSA	INTEGRAL MEMBRANE PROTEIN	SER FOLDMIS VINUS-LIKE PARTICLE SSVI	13-100						1		+
עואר נואנו	PROBABLE INTELMANS	VACCINIA VILLIS (STRAÎN COPENHACEN)	22:36						1	-	ļ
VIDI VACCC	PROTEIN	VACY DRUS (STRAIN WR)	87.72						-	-	-
VIDI VACEV	PROTEIN	VARIOLA VIRUS	×2.2							-	-
VIOI VARV	PROTEIN JE	COTTONTAL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	231-313						L	-	-
VLI CUVK	TOURANT OF THE PROPERTY	AVIAN PAPILLOMAVIRUS PPV-L	G .							L	ŀ
YLI FPYL	TORVELLE IN SECTION	HEDMAN PAPELLOMAVIRUS TYPE	24.74				1			L	ŀ
VL. HOVOE	TACHARIA LI PROTEIN	HUMAN PAPELOMA VIRUS TYPE IS	017:01						ļ		-
V.I POVIE	TACOMAN E I S DO TEN	HUMAN PAPELOMAVIRUS TYPE 11	9							L	ŀ
VLI REVIS	PRODUCE I PROTEIN	HUMAN PAPILLOMANDUS TYPE 41	77.00						L	-	L
VLI PEVAL	PRODUCE IL I PROTECIA	HUMAN PARLOMAYBUS TYPE SI				١				L	\vdash
VLI HEVSI	SOCIAL WILLIAM	HUMAN PAPELOMAYTRUS TYPE SE	27.50								-
W. Person	BECORAGE I S PROTEIN	HUMAN PAPELOMAYBUS TYPE IA							_		L
WIT HAVIA	PROPERTY OF PROPERTY	HUMAN PAPEL COMAVORUS TYPE 41								_	L
10 A 10 A 10	VITATOR CORR PROTEIN LANGEDA 3	REOVENIS (TYPE 1/STRAIN DEALING)	1000								L
STATE OF THE STATE	KINDS CORE PROTEIN LANGEDA 3	REOVINIS (TYPE 1/ STRAIN LANG)	146.180	635.65			L		L		
ALL MEDAL	S S S S S S S S S S S S S S S S S S S	TIPULA INDESCENT VIRUS	200	100							L
VLW IKVI	LANDS VIRION STRINCTURAL PROTEIN ME	-	117002						1		ŀ
PVMI JEUVIL	WAS WEIGHT STRUC PROTEIN MILIME	•	708-070						-	1	ŀ
PWG! NEOVO	MACH VIEW STRIK PROTEIN MILION	•	624-661						-	1	H
PWC1 KEOVO	MAJOR VIDOR STRUCT ROTTED MILITARI	-	934-661				1		1	\downarrow	╀
PVAC REOVI	MAJOR VILLON STANCE PROTECTION VALLE	1	159-186	E C	20.483	2		1	-	1	╀
WAD REOVE	MAJOR HOPS I AUCTIONAL PROTEIN	+-	124-152					1	1	\downarrow	+
PVALLE BRSVA	MATRIX GLYCOPKO LEIN MG	HINAN RESPIRATORY SYNCYTIAL VOLUS (STRAIN A2)	124-151				\downarrow		1	1	+
PVMA2 HDLSVA	MATHER GLYCOPRUIE IN PAC	MOUNTE BECPTE A TORY SYNCYTIAL VIRUS (STUAIN AS1903)	219-246							4	+
PVMAT BRSVA	MATRIX PROTEIN	HIDAAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	219-246						4	1	\downarrow
PVALAT HOLSVA	MATRIX PROTEIN	INSTITUTAÇÃO VIRUS (STRÁIN CIIVSO)	131-185						1	+	+
PWAT INCLI	MATTUX (M) PROTEIN	MEWCASTI & DISSASS VIRUS (STRAIN AUSTRALIA-VICTORIAA)	247-274						\downarrow	+	+
					_						

FILE RAME			1	1	7	т		Ī	ľ	۰	
SOWAT MIR	PROTEIN	YIRUS	J	TOTAL	77:37	AREA	ANEAS	AREA	ABEA 2	S S S S S S S S S S S S S S S S S S S	ARIA
1 1 1 1 1 1 1 1 1 1 1 1	MATRLX PROTEIN	BOYING PARAINPLUENZA 3 VIRUS	102-102					1	1	1	1
PWAT PUH	MATRIX PROTEIN	HUMLAN PALAINPLUENZA J VIRUS (STRAIN MILL 47115)	167-107					1	†	†	
PWAT SV41	MATRIX PROTEIN	SDAGAN VIRUS 41	200					1	1	İ	
PYMEI CYBM	EI GLYCOPROTEIN	BOVINE CORONAVIRUS (STRAIN MEBUS)	M2:5/E					İ			
PYAEL CYTKE		TURKEY ENTERIC CORONAVIRUS	175-209					1			1
PVACE DIVE	EI CLYCOPROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN 642)	37-12	164-218				1		1	
PVACE) CBVB	EI OLYCOPROTEIN	AVIAN INTECTIOUS BRONCHITIS VIRUS (STRAIN REAUTHETE.)	1						1	1	4
PVACE IBVB2		AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE NIE)	7	212-51				1		1	
PVACE DIVE	EI OLYCOPROTEIN	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN KIRKS))	184-218					İ		j	
PWO CLANC	MOVEMENT PROTEIN	CAULBLOWER MOSAIC VIRUS (STRAIN CIL. 1841)	220-254	273.324		•	:	_		_	
PWP CANO	MOVEMENT PROTEIN		3.62	120-254	273-124						
PYLO CALVE	MOVEMENT PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN BBC)	117-254	\$11.11							
WALL CALVA	LACVELIENT PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN NYSISS)	2:0-334	273.334					-	<u> </u>	
200	WOOD TO SECURE	CAIR IN OWER MOSAIC VIRUS (STRAIN STRASHOVIRG)	T	273.324		İ				<u> </u>	
	Constitution before	CALE IT NOTE MOTAN VIRING (STRAIN WALD)	T	271.174				ľ		T	
	LOUGHT PROTEIN	CARMATION STORED BING VIRIA	T	100.127			İ	:	!	<u>:</u> -	
	MOVEMENT FROIEIN	Course to the Carte Course				1	İ	!	İ	!	: :
PVID SOCIAL	MOVEMENT PROTEIN	SOTECAN CALCACOTIC MICH. STATUS	-					1			
PVMSA HOBKE	NAJOR SURFACE ANTIGEN PRECURSOR	HEACH HEPATITIS B VIRUS	_			j		:	-	-: :	:
PWG! DW!	MATRUX PROTEIN I	DHORI VIRUS (STRAIN INDIAN/1)13/61)		237-264							
PVACTE MOXVIL	Г	MYXOMA VIRUS (STRAIN LAUSANNE)	163-190								
PWITE WOOM	Т	MYXOMA VIRUS (STRAIN LAUSANNE)	465-492								
PATA BOTT	Т	PORCINE ROTAVIRUS (GROUP C./ STRAIN COWDEN)							<u> </u>	-	
	T	BOWNER BAR WOVERING	140.176								
NOW PANE	PROBABLE MOMEANSID PROTEIN NET	BOVING CANADA INC.							1		
PYNCE ABVG	NONCAPSID PROTEIN NS-1	ALEUIAM MINA DISEASE PARVUVIAUS (STRAIM U)							1	Ì	
PVACS AEDEV	MONCAPSID PROTEIN NS-1	AEDES DENSCRUCLEUSIS VIRUS (STRAIM UK V 002 002)	T	Т	100	70.62					
PVNCS MAINING	NONCAPSID PROTEDNINS-1	MURLINE MINUTE VIRUS (STRAIN MANIT)	1	487-707							
PYNCS MUMBY	NONCAPSED PROTEIN NS-1	MUNICHE MONUTE VIRUS	٦	262-289						1	
PVACS PAVID	NONCAPSID PROTEDNINS-1	HUMAN PARVOYIRUS BI9	236-270							1	
PANCS PAVIOR	NONCAPSID PROTEIN NS-1	HAMSTER PARVOVIRUS HI									
PVACE PAVPA	NONCAPSID PROTEIN NS-1	PORCINE PALVOVIRUS (STRAIN NADL-2)	24.55	169.196	116-346						
PVNSI BOVI	MONSTRUCTURAL PROTEIN NSI	EPIZOOTIC HEMOREHAGIC DISEASE VIRUS (SEROTYPE 1/STAAIN ALBERTA			,						
PVNSI LAALA	MONSTRUCTURAL PROTEIN NSI	INFLUENCA A VIRUS (STRAIN AVALASKANGT)	171-196								
PVASI LANN	NONSTRUCTURAL PROTEIN NSI	INSTITEMEN A VIRUS (STRAIN MANN ALBORAGO)	171-196								
PWS! IACID	NONSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN A/CHILE/1/8))	171-196								
PVISI IACKO	NONSTRUCTURAL PROTEIN NSI	DALLENZA A VIRUS (STRAIN ACHICKENGERMANYAN49)	131-198								
PVNS1 IACKU	NONSTRUCTURAL PROTEIN NSI	DFLUENZA A VIRUS (STIVAIN ACHICKEN/JAPANZA)	164-195								
PVNS1 IADA2	HORSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN ADUCKVALBERTA/6076)	171-191								
PVNSI IATOM	HONSTRUCTURAL PROTECN NSI	INTLUENZA A VIRUS (STRAÎN A/FORT MONMOUTH/1/47)	171-196								-
PVMS1 IAFOW	HONSTRUCTURAL PROTEIN NSI	INTLUENCA A YIRUS (STRAIN A/FORT WARREN/1/50)	171-191						1		
PYNSI MEI	HONSTRUCTURAL PROTEIN HS!	DIFLUENZA A VOLUS (STRAIN ALENINGRAD/134/57)	171-198								
PVNSI JAHA6	NONSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN AMALLARDIALBERTAINTIG)	171-198								
PVKSI LAPII	NORSTRUCTURAL PROTEIN MSI	INTLUENZA A VIXUS (STRAIN APINTAIL/ALBERTA/131/79)	171-191								
PWSI LATO	NONSTRUCTURAL PROTEIN HS!	INFLUENZA A VIXUS (STRAIN APINTALLALBERTANSU19)	171-194								
PWS1 LATES	NONSTRUCTURAL PROTEDNINSI	INTLUENZA A VIRUS (STRAIN A/TURKEY/BETHLEHEM-GLILIT/1492-B/12)	171-191								
PWS1 LATEC	INDIVITABLE PROTEDINS	INFLUENZA A VIXUS (STRAIN A/TURKEY/CANADA/61)	171-198								
PVNSI JATRI	NONSTRUCTURAL PROTEDY NSI	DEFLIENZA A VIDUS (STILAID A/TERM/TURKAGMIA/11/72)	171-198								
PWS MOO	HOWSTRUCTURAL PROTEIN NSI	INTLIERZA A VIKUS (STRAIN AUDORNYOTTZ)	171-198								
PWKI IAIBS	NONSTRUCTURAL PROTEDNINS	INFLUENZA A VIAUS (STRAIN AUSSRI9077)	171-198						-		
PVNSI DOBPA	NONSTRUCTURAL PROTEIN NS!	DIFLUENCA B VIRUS (STRAIN BPATP)	171-198			L			\mid	T	
PVNS IATER	NONSTRUCTURAL PROTEDNINGS	DOTLUENZA A VILUS (STIVAIN ATURKEY/OREGON7!)	17.114						ŀ		
PANS DOLL	NOWSTRUCTURAL PROTEIN NS2	DELUENZA & VIXUS (STIAIN BALEE/40)	11.71							r	
PONCS DONA	MONSTRUCTURAL PROTEIN NS2	INTLUENCA B VIDUS (STRAIN BY AMAGATAVIRI)	\$1.78							l	
PACES PACES	MONSTRUCTURAL PROTEDNINS	DIFLUENCA C VIRUS (STRAIN C/11/50)						T		T	
SALVE STATE	MONSTRUCTURAL PROTEDY 3-1	PORCEME TRANSMESSIBLE GASTROENTERLTIS CORONAVIRUS (STRAIN FS772	729.36							T	
TOWN CANE	MONSTRUCTURAL PROTEIN 4	HUMAN CORONAVIRUS (STRAIN 229E)	9.76							T	
PVNS+ NSV	HOMSTRUCTURAL PROTEDI NSA	RICE STREE VILUS	9						H	Ī	
PVNS) CVCAE	HONSTRUCTURAL PROTEIN?	CANTHE ENTERUC CORONAVIRUS (STRAIN K111)	11-45								
TANS C. S.											

PCCENE	107117514	All Viruns (no besterlaphages)	ANYAL ANYAL	AMMA	1	3				
FILERAME	PROTEIN	FEI INE ENTERIC CORONAVIRUS (STRAIN 79-1681)	7							
PVNS) CVTEJ	MONSTRUCTURAL PROJECT	PORCHE TRANSMISSIBLE GASTAGENTERITIS CORONAVIRUS (STRAIN FS772	14-61			İ	-			
PVNS) CVPFS	MONSTRUCTURAL PROTEIN ?	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN FURI)			:					•
PVNS) CVPTO	SOUSTINE THE AL PROTEIN?	PORCINE RESPURATORY CORUNAVIALIS			-	•	:	į		
NO.	MONETHER PROTEIN?	FELING INFECTIOUS PERITONITIS VIRUS (STRAIN 79-1146)								
1110	MONSTRUCTURAL PROTEIN C	HUMAN PARAMFLUENZA I VIRUS (STRAIN CI-1413)	86.89							-
ALTINE POLITICAL	NOWSTRUCTURAL PROTEIN C	HUMAN PALAMALUENZA 3 YIKUS (STILATIN MIN 41843)	262.296		L					
PVNEM INSV	HONSTRUCTURAL PROTEIN NS-M	DAPATIENS NECROTIC SPOT VIRUS	57.44	_		j	: :			:
PVMST BUNDLE	NONSTRUCTURAL PROTEIN NS-S	CROSSE	146.180							
PVNST TOSV	NONSTRUCTURAL PROTEIN MS-S	TOSCANA VIKUS	311.369							
PVALC EDOV	MUCLEOPROTEIN	CHULA VIRUS	378-405							
PVMIC LANA	MUCLEOPROTEIN	INFLUENZA A VIKUS (31 KAII) MARKAS ACCIONING	378-405							
PVSAT LAANN	MUCLEOPROTEIN	INTELIENCA A VIRUS (STRAIN AARPA ALGONOSO)	378-405							
ALEX LABA	MUCLEOPROTEIN	INCLUENCA A VIRUS (STRAIN AUGASIO) (170)	378-405							
PVALC IABID	MUCLEOPROTEIN	PATLIENZA A VIKUS (3 IIVAIN MBULDOLMONIO)	378-405				1			:
PANE IACAL	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIM AN ALIFORNIA IN 19)	378-405							
SWAY IACKG	NUCL EOPROTEIN	INFLUENZA A VIRUS (STRAIN ACTIIC REPORTATIONS)	338.405							
A PARTY OF THE PAR	NAMES FOR ROTEIN	INFLUENZA A VIRUS (STRAIN ACHILLE MENTENNS I CAMINA	378.405							
1000	MICH BOPROTEDY	INFLUENZA A VIRUS (STRAIM ADUCENAUS INCLINES)	338.405		L					
2000	MICH ECPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKOEIJING 17.1)	331.405	-		L				
PARIS MARK	ANICH ENPROTEIN	BREUENZA A YRUS (STRAIN ADUCINCZECHOSLUYANIAN)	176-401	-						
1 M	A CORPORATION	INFLUENZA A VIXUS (STRAIN ADUCKENGLAMDVI)	307 84							
NAC.	SOMEON STATE OF THE PARTY OF TH	INSTUENZA A VIRUS (STRAIN ADUCE/CENGLAND/1/62)	307		-					
PYNIC MDE2	MOLEUROIEM	INGLUENZA A VIRUS (STRAIN ADUCKANONG KONG/1/1/3)	205-816	1		1				
PVAUC INDIK	MOCEURICIEM	INGLIENZA A VIRUS (STRAIN ANNCKAREADHISM18714)	278-603	1				L		
PVNC INDIA	MOCLEUM	INTELLENZA A VIAUS (STRAIN ADUCKAIAMITOBA1/33)	600-116		1			L		L
PVNUC INDIAN	MUCLEOFIUM	INFITENZA A VIAUS (STRAIN ADUCKNEW ZEALAND/)1/76)	278-405		1	\downarrow	-			
PVNUC INDIKE	INCLEORAGIEM	INFLUENCA A VIRUS (STRAIN ADDICKARRAINE/2460)	331-403		1	ļ				
PVACC IADOS	NUCLEURAUTEN	INVESTIENZA A VIRUS (STRAIN AENGLANDVIWSS)	376-403							
PVNUC INENS	MUCEOTION	INSTITEMENT A VIRUS (STRAIN AFORT MONTHOUTHINGS)	378-405	1	1	1				
PVNC INFOM	MUCLEOTICIEM	INFLIBITA A VIRUS (STRAIN AFORT WARREN'I/30)	378-403		1	1				
PVNC MOV	MUCLEOFKOIEIR	INCLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSDOBSON/DUTCHTT)	378-403	+	1	1				L
PWCC WPD	MCLEUTAVIEUR	INFLUENZA A YIRUS (STRAIN AFOWL PLAGUE VIRUSTIOSTOCK))4)	378-403	1	-					
PVNC WIR	MCCACTACION	INFLUENZA A VIRUS (STRAIN ACREY TEAL/AUSTRALIAUM)	2100		1	1				L
PVNUC LAGRE	MOLEUROIEM	THEI TENZA A VIAUS (STRAIN AGULLA IARY LANDISM?)	376.403		1		\downarrow	L	-	
PYRUC [AGUI	MUCLEOFICIE	INFILIFICA A VIRUS (STRAIN ACULL/MARYLAND/19477)	378-403		1	-				
PVMC MOST	NUCLEURIUM BUN	DIFLUENZA A VIXUS (STIVAIN AGULLAKANYLAND/182478)	(OF 1)		1	-	-			
PVNC MOU	NUCLEUR POPERTY IN	INFLUENZA A VIXUS (STRAIN AGULLMARYLANDVII 1579)	207 817		1					
PYACE INC.	T	DIFLUENZA A VIRUS (STIAIN AGULLASTIAKHANZZZZZ)	107.0%		1	-			L	
PVACE INCOM	7	DATUENZA A VIXUS (STRAIN AGULLMASSACHUSETTS/26/10)	216.403		1	-	-			
PVRIC IAGOR	7	INFLUENZA A VIXUS (STRAIN A/GULL/AIRNNESOTA/9/10)	20,000		+	1	1			L
A STATE OF THE STA	T	DOTLUDIZA A VIRUS (STRAIN AMICKOX/40)	207.15	1	-		-			
200	MINI FORMOTEDA	DATUENZA A VINUS (STRAIN A EQUINE/ILLININA)	378-405	-	-		L			
PARTY INTO	T	DOLLODOZA A VILUS (STRAIN ARCHUMELUMENT)	378-405	-						\rfloor
DALL TARK	T	INTLUENZA A VINUS (STRAIN ALCHUMOMINAMINA)	178-405		_	_				
COLA PARA	T	INTLUENZA A VIRUS (STRAIN APROPIL ROPO 1789)	13.40		 -					
1000	MACH FORIOTEIN	DOLLIESZA A VIRUS (STRAIN AMONU KUMOZO)	171.40\$		-		L			
200	WHICH ROPROTEDA	DATUE CA A VILLE (STRAIN ARCOUNTINGUE)	171.401				L	L	_	
3	CALC BORROTED	INFLUENCE A VIRUS (STRAIN ARQUINETENNESSEED) 400	307 26.5		-				Ŀ	
WACC WHILE	NOTICE EDEBOTEDA	DOLUENZA A VIRÚS (STRAIN ARLEVISATY)	- W	+	\downarrow	+	L	L	L	
PYRIC IACE	NULEUTAOLIEM	INSTITENZA A VIRUS (STRAIN AAENINGRAD/SWI)	207-107		-	1	1	ļ	L	L
PWC MEN	NO. LOS POSSONES	DIFLUENZA A VIRUS (STRAIN AMALLAIDVASTRAKHANZ44TZ)	201		-	-	-	L	L	
PYNUC IMMA	NUCLEURING	INFLLIENZA A VIRUS (STRAIN AMALLARDNEW YORK/675071)	178-403		\downarrow	1		-		
PVAUC INVA	NOC FOR STEEN	INTLUENZA A VIRUS (STIVAIN AMENIKASWEDENDA)	371-403	+	+	1	-	-		
PVNUC INCH	NUCLEURING EAR	DOTLUENZA A VIRUS (STRAIN ANEW JEASEYANS)	378-405		1	1	1	1	-	
PVNC INE	1	INTLUENZA A VIXUS (STRAIN ANTROKS)	37170	1	-	+	+	-	-	
PVNC INTE	NOC EUROIEM	INFLUENZA A VIRUS (STRAIN AOHIO/463)	1711-405			$\frac{1}{1}$				
PVNUC LAOPE										

	PCCENE	107217814	All Viruses (no bacteriophages)	7	П	┱	Т	т	т		
	FILENAME	PROTEIN	WRUS	Т	т	т	TA AREA?	2000	4	4	1
NUTLEMPTOTES SPILESTA NUTS GIALNA MALLANGINAN 174-00 174-0	PVNUC LAPAR	NUCLEUPIOTEIN	INCLUENCE A VINUE (STRAIN APPLIERTO RICOADA)	9			-	+	-		
NETERPOTES SPILESLA NULL GIALNA ASPERANCIA AND 114-40	PVNIK IAND	NICIEOPROTEIN	INTLIEUZA A VIAUS (STRAIN ARUDDY TURNSTONENEW JERSEYA7/15)	171.405			+	-		L	
NETERFOTES NETERFOTES NETERFOLA VERIS STATUM AND STATEM AND	PVARIC IASED	MICH EDPLOTEIN	DISTLIENZA A VIRUS (STRAIN ASEALMIASSACHUSETTS/1/10)	178-405		-	-		L	L	
NICEDENOTION NICEDENOTION 1714-05 1714	PVNUC 1ASH2	MUCL EOPROTEIN	INSTLUENZA A VIRUS (STRAIN ASHEARWATER/AUSTRALIA72)	178-405							
MICLEGROFTH MILLURAL A VILLE STRAIN ACTUAL STRAIN 171-421	PVNCC IASIN	MICL EDPROTEIN	INFLUENZA A VIRUS (STRAIN ASINGAPORE/1/57)	374-405	-						
NUCLEARDER NOTIVE A. VIRIS STRAIN ATURKSTONTAND 1714-05 17	PYNUC LATEL	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAM ATEALACELANDASMO)	378-405							٠
	PVNUC LATKN	NUCLEOPROTEIN	DIFLUENZA A VIALIS (STRAIN A/TURKEYA/INNESOTA/1661/11)	378-405	-						
NUCLEGROTH NUCLEGROA VARIES (STAIN ATRIBACINICALINATION) 151-405 151	PWILE LATIKO	NUCLEOPROTEIN	INFLUENZA A VIALIS (STRAIN A/TURK EY/ONT ANIOM?) 2/46)	378-405			L				
RACEDEROFIER INCLUDEAL A VINES (TRAIN ATINATIVE) 1/14-05 RACEDEROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDEROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDEROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDEROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVE) 1/14-05 RACEDROFIER FINELIDEZA A VINES (TRAIN ATINATIVA) 1/14-05	Pyruc LATRS	NUCL EDINOTEIN	INFLUENZA A VIRUS (STRAIN ACTION/SOUTII AFRICABI)	178-405		L	H			L	Ĺ
WICLEPROFIES WILLIPEZA A VRIUS (\$TRAN ACTEGRACOT) 114-05 1	PVNIC LATRE	NECT FORDTRIN	INST. USNZA A VIRUS (STRAIM ACTION/TURKAII:NIA/18/72)	174.405	<u> </u>	<u>i</u>	:				
WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERACITE) 1114-05 WIGGERROTER WIGGERA A VERUS (STAJAN AUGGERA) AUGGERA A	PARTIN TARA	MICH BOSECUTEIN	THE LIFTER A VIRUS (STRAIN ACTEXACION)	378-405	T		-		-		
WCLEGROTH WCLE	CHIEF THE PARTY OF	NECT EDGE OF EN	MATHEMA A VIRILS (STRAIN ARTHORNADIA)	171.405	+						
WACLEGROTEN WELLEGA A VRIG (STRAIN ANCTORIANS) 111-405 WACLEGROTEN WALLEGROTEN WALLEGROT	PARTY INTER	MAIN COMPANY	INSTITUTE A VIDIO STRAD AMERICANT	178.405	1	-	$\frac{1}{1}$	+	-	1	
WOLLEGROTEN WELLEGAA Y WILL GITAMIN WOLLEGROTEN STIT-45	LANCE MUSS	NOCLEUT DE LE CONTROLLE DE LA	MATERIAL A COSTA STATE AND A ANALYSIS HELD		†				\mid	-	
NUCLEGROTER INSTITUENT A VARIS (STAIN AVAILGEMENTS) 174-45	PVMUC IAMIS	MUCLEOPROTEIN	INTLUENCA A VIAUS (STRAIN AVICTORIAN VIA		1		1	-	1	:	:
NUCLEGROTER INTELEGIA A VRIUS (STALIN AVWILEDANCIN D) 171-405 171-40	PVNC IAWHN	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AWITALEMAINUUSEKSA)	376-405			1				
NUCLEGROOTER NUCL	PVNUC IAWH	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ANVILALE/PACIFIC OCEAN/1976)	378-405		1	+	1			
MACLEGROUTH NELIBERA A VIRUS (STAIN ANGREGAS) 114-05 114-0	PVNCC IAWIL	NUCLEOPROTEIN	INPLUENZA A VIKUS (STRAIN AVVILSON-SMITHOUS)	378-403	1				$\frac{1}{1}$		
MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARS) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARS) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MRTLEBCA A VARIA \$18TAM AGWINEGARANYORG) 114-40 MACLEGROUTERN MACLEGRO	PYACC IAWIS	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AWISCONSINO) 2.178)	378-403	1		1	1			
MOLLEGAROTERN WOLLEGALA A VRUS \$TALAN ASWINGCAMINS 171-405	PVNUC IAZ29	NUCLEOPROTEIN	INFLUENCA A VIRUS (STRAIN ASWINEZWOT)	Q I	1	1	+		+		
MUCLEPROTEEN INTLUENCA A VRINS STALIN ASWINEDANIONGWAII) 111-405	PVMUC IAZ41	NUCLEOPROTEIN	INPLICACE A VIRUS (STRAIN ASWINE STATE)	200		1	<u> </u>	1		:	•
NUCLEOPROTERN PSTLEEZA A VIRIS (STALIA ASWIRGORDANONOSAS) 1714-05 17	PVNUC IAZCA	NUCLEOPROTEIN	INFLUENCA A VIRUS (STRAIN ASSWINDLAMITRICACTIOS)	(A-40)	1	1			1	-	
MICLEGRACIER INTLEAGA A VIRUS (STANIA ASSWIRGOURDANAY TO 1714-05) MICLEGRACIER MICLEGRAC	PVNUC IAZDA	NUCL EOPROTEIN	INFLUENZA A VIRUS (STRAIM ASWINE/DAMDONG/9/11)	378-403		-	+	-	1		
MICLEGROTERN WILLERGA A VILLS \$18 (ALM ASSWIRGOND RONGINS) 1714-05 1	PVNUC IAZGE	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWINEAUEXMANYZATI)	378-405	1		+			4	
MACEGRACIEN WILLIAGA A VILLIS STRAIN ASSWINGTON CONCULRANT 1714-05 1	PWC IAZHI	NUCL EUPROTEIN	INPLUENCE A VIKUS (STRAIN ASWINDINGER KONGO 10)		1		+	1			
MACE COPROTEIN STATUS A VILLE STACK A VILLES STACK NOWN STATUS 111-405	PVNC IAZHO	NUCLEOFROTEIN	INCLUENCE A VICUS (STRAIN ASMINISTRATIONS ROUGHS)		†		+			\downarrow	
MUCLEOPROTEIN INTLUENZA A VILLS STRAIN ASSINGEROWAND STATE OF STRAIN	PVNUC IAZHA	NUCLEOFICIED	INFLUENCA A VINUS (STRAIN ASWINGTONIA HASSI	200	1		1	+			
MACLEGROUDEN	PWNUC IAZII	NOCLEOPROTEDA	INTLUENCA A VIALIS (SI RAIN ASWINGTOWALY)	200	†		+	1		1	
NICLEGRADIEN	PVNC WZIZ	MOCLEOPTION FOR	INTELLEGICAL A VINITAL COTO A DA A REPORTATION A LACT				$\frac{1}{1}$		-	\downarrow	\downarrow
NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITALYDIN) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITALYDINS) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITALYDINS) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN DIFLUENZA A VIRUS (STRAIN ASWINEGITAL) 1714-05 NUCLEOFROTEIN MACLEOFROTEIN 1714-05 NUCLEOFROTEIN MACLEOFROTEIN 1714-05 NUCLEOFROTEIN MACLEOFROTEIN 1714-05 NACALINO 1717-05 NACALINIA 1717-05	PVAIL TAZE	MAIO EDECTEDA	INSTITUTENZA A VIRUS (STRAIN A/SWINE/ITAL Y/4)7/76)	11.405		-	+		-	-	L
MUCLEOPROTEIN DIFLUENZA A VRUIS (STRAIN ASWINE/ITALYRIAN) 1714-05 MUCLEOPROTEIN RELUENZA A VRUIS (STRAIN ASWINE/ALVRANA) 1714-05 NUCLEOPROTEIN RELUENZA A VRUIS (STRAIN ASWINE/ALVRANA) 1714-05 NUCLEOPROTEIN DELUENZA A VRUIS (STRAIN ASWINE/ARTERILANDS/12R) 1714-05 NUCLEOPROTEIN DELUENZA A VRUIS (STRAIN ASWINE/ARTERILANDS/12R) 1714-05 NUCLEOPROTEIN DELUENZA A VRUIS (STRAIN ASWINE/ARTERILANDS/12R) 1714-05 NUCLEOPROTEIN DELUENZA A VRUIS (STRAIN ASWINE/TENTESSED/AT) 1714-05 NUCLEOPROTEIN DETLUENZA A VRUIS (STRAIN ASWINE/TENTESSED/AT) 1714-05 NUCLEOPROTEIN DETLUENZA A VRUIS (STRAIN ASWINE/CNSIN/RS) 1714-05 NUCLEOPROTEIN DETLUENZA A VRUIS (STRAIN ASWINE/CNSIN/RS) 1714-05 NUCLEOPROTEIN DATLUENZA A VRUIS (STRAIN COALIFORNIATI) 1714-05 NUCLEOPROTEIN MALBURO VRUIS (STRAIN COPENIACEN) 1714-05 NUCLEOPROTEIN MALBURO VRUIS (STRAIN COPENIACEN) 1717-05 NUCLEOPROTEIN MALBURO VRUIS (STRAIN COPENIACEN) 1717-05 NUCLEOPROTEIN VALUOLA VRUIS (STRAIN COPENIACEN) 1717-05 NUCLEOPROTEIN<	PWRIC IAZZ	NIXT FORKOTEIN	INFLUENZA A VIRUS (STRAIN ASWINGATAL Y 12/19)	378-405		-	-		-		
MUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEATIALYRINRS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH PRELIDEZA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH MACLEORA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH MACLEORA A VRUIS (STRAIN ASWINEANCHS) 1714-05 NUCLEOPROTEDH VALUICA VRUIS (STRAIN ASWINEANCHS) 1715-05 NUCLEOPROTEDH VALUICA VRUIS (STRAIN ASWINEANCHS) 1717-17 NATA A MOSAIC POTENTA ROLLING 1717-17	PWRUC IAZIS	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWINEATAL Y/141/11)	376-405		-	-	-	-		L
NUCLEOPROTEIN NPTLEEZA A VRUS (STRAIN ASWINEJANTS) 114-03	PVAIC 1AZM	NUCLEOPROTEDI	INFLUENZA A VIRUS (STRAIN A/SWINE/ITAL Y/13/9/19)	378-405		-	-				
NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGACHELANDS/1/15) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGACHELANDS/1/15) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGACHELANDS/1/15) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGACHENTS) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGACHIN) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGANI/15) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGANI/15) 7714-05 NUCLEORIGIEM DGTLUENCA A VIRUS (STAJIN AGSWIEGANI/15) 7714-05 NUCLEORIGIEM DGTLUENCA C VIRUS (STAJIN AGSWIEGANI/15) 7714-05 NUCLEORIGIEM DGTLUENCA C VIRUS (STAJIN AGSWIEGANI/15) 7714-05 NUCLEORIGIEM DGTLUENCA C VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA C VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA C VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA C VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS (STAJIN AGSWIEGANI/17) 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGIEM DGTLUENCA VIRUS 7714-05 NUCLEORIGEM DGTLUENCA VI	PVNUC IAZIA	NUCLEOPROTEIN	INSTLUENZA A VIRUS (STRAIN A/SWINEJ/AMESBURG/42)	378-405							
NUCLEORIOTED NOTLECKA A VRUS (STAJIN ASSWIREMETHERIANDS/1245) 171-405	PYNUC IAZMA	NUCL EOPROTEIN	DIFLUENZA A VIRUS (STRAIN A/SWINEMAY/194)	378-405							Ц
MUCLEPROTEEN MPCLEPRICA A VRUS (STALM ASSWEDOTAL) 171-401 MUCLEPROTEEN MPCLEPRICA A VRUS (STALM ASSWEDOTAL) 171-401 MUCLEPROTEEN MPCLEPRICA A VRUS (STALM ASSWEDOTAL) 171-401 MUCLEPROTEEN MPCLEPRICA A VRUS (STALM ASSWEDISMUSS) 171-401 MUCLEPROTEEN MPCLEPRICA A VRUS (STALM ASSWEDISMUSS) 171-401 MUCLEPROTEEN MPCLEPRICA CAUGE (STALM MASSWEDISMUSS) 171-401 MUCLEPROTEEN MASSWEDISMUSS 174-401 MUCLEPROTEEN MASSWEDISMUSS 174-401 MUCLEPROTEEN MASSWEDISMUSS 174-401 MUCLEPROTEEN MASSWEDISMUS 174-401 MUCLEPROTEEN MASSWEDISMUS 174-401 MUCLEPROTEEN MASSWEDISMUS 174-401 MASSWEDISM	PYNUC IAZNE	NUCLEOPROTEDI	INTLUENZA A VIRUS (STRAIN A/SWINE/NETHERLANDS/12/18)	378-405							
NUCLEGRACIEM NUCLEGRACA VINUS \$18 NOA NOA NOTABLE 114-05 1	PVNUC IAZOH	NUCLEOFROTEIN .	INTLUENCE A VIRUS (STRAIN ASWINE/OHIO73/75)	207	1		-		1		
NUCLEOPROTEEN OPT.LUENCA A VOUS \$1 FALIN ASWERENISSEELOW 17 174-05 NUCLEOPROTEEN OPT.LUENCA A VOUS \$1 FALIN ASWERENISSEELOW 17 174-05 NUCLEOPROTEEN OPT.LUENCA A VOUS \$1 FALIN ASWERENISSEELOW 17 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN ASWERENISCONSINVIS 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN ASWERENISCONSINVIS 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN ASSET 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORP 174-05 NUCLEOPROTEEN OPT.LUENCA CVAUS \$1 FALIN FORE STAND FORE	PVNUC IAZON	NUCLEOFROTEIN	INTLUENCA A VINUS (STRAIN ASWINDON LAUGUST)				1		1		
NUCLEGRACIEM NUCLEGRACIA VALUS (STACIA ASMINEWISCUSSIVIS) 114-05 NUCLEGRACIEM DIFLUENCA CURUS (STACIA ASMINEWISCUSSIVIS) 114-05 NUCLEGRACIEM DIFLUENCA CURUS (STACIA ASMINEWISCUSSIVIS) 104-136 NUCLEGRACIEM MALBURO VALUS (STACIA MOSCE) 104-07 NUCLEGRACIEM MALBURO VALUS (STACIA MOSCE) 104-136 NUCLEGRACIEM MALBURO VALUS (STACIA MOSCE) 104-136 NUCLEGRACIEM MALBURO VALUS (STACIA MOSCE) 104-137 104-138 NUCLEGRACIEM VALUCIA VALUS (STACIA MOSCE) 104-137 104-138 NUCLEGRACIEM VALUCIA VALUS (STACIA MOSCE) 104-138 NUCLEGRACIEM NUCLEAR MOSCE VALUS 104-138 NUCLEGRACIEM NUCLEAR MOSCE VALUS 104-138 NUCLEGRACIEM NUCLEAR MOSCE VALUS 104-138 NUCLEGRACIEM NUCLEAR MOSCE VALUS 104-138 NUCLEGRACIEM NUCLEAR MOSCE VALUS 104-138 NUCLEGRACIEM NUCLEAR VOLVIERENCE 104-138 NUCLEGRACIEM NUCLEAR VOLVIERENCE 104-138 NUCLEGRACIEM NUCLEAR VOLVIERENCE 104-138 NUCLEGRACIEM NUCLEAR VOLVIERENCE 104-138 NUCLEGRACIEM NUCLEAR POLVIERENCE 104-138 NUCLEAR VALUE 104-138 NUCLEAR VALUE 104-138 NUCLEAR VALUE 104-138 NUCLEAR VALUE 104-138 NUCLEAR VALUE 104-138 NUCLEAR VALUE 104-138 NUCLEAR VALUE 104-1	PVNUC IAZTE	NUCLEOPROTEIN	INPLUENCE A VIKUS (STRAIN ASSWIND TENNESSEED ATT)	6	1		+	1	1		
NUCLEGRADIEN NUCL	PVNCC IAZWI	NUCL EOPROTEDA	INTELLEGIZA A VINCE OFFE AND ANAMERICANISMINES		\dagger		1		1	1	
WICLEGROTEIN WARBURG VEUS (STAAN MUSCRE) 166-407	PYRICE INCAS	MUCHOTAL EN	INTLUCATION AND (STEAT) ASSISTED TO THE TRANSPORT OF THE	99.136	7	167	+	+	1	1	
MACLEOPLOTEIN MACLEOPLOTEIN MACLEOPLOTEIN 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-407 164-118 164-11	PVAIL MARVA	NICLEOF COLUMN	MAKBURO VIRUS (STRAIN MUSOKE)	366-407	Т	-	l			\downarrow	
PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PROTEIN OIL PAPAYA MOSAIC POIEXVIRUS 158 KD PROTEIN OIL POTATO VIRUS OIL PROTEIN OIL PRO	PVALC MABVE	MICLEOPHOTEIN	MALBURG VIRUS (STRAIN POPP)	107-35	r	-		-			
PROTEIN OF VALIDA VALUE 1911 19	PV001 VACCC	PROTEINO	VACCINIA VIXUS (STRAIN COPENHAGEN)	1.37		909-	_				
153 KD PROTEIN FOXTAL MOSALC VIRUS	PVOOI VARV	PROTEIN OI	VANIOLA VIRUS	1.37		809-11					
16 KD PROTEIN NARCISSUS MOSAIC VIRUS 996-1021 116 KD PROTEIN PAPA'N MOSAIC POTEXVIRUS 116 KD PROTEIN POTATO VIRUS M (STAZIN RUSSIAN) 116 KD PROTEIN POTATO VIRUS M (STAZIN RUSSIAN) 116 KD PROTEIN POTATO VIRUS K (STRAIN X) 118 KD PROTEIN STRAWBERRY MILD YELLOW EDGE ASSOCIATED VIRUS 117-104	PVOR! FXXV	152 KD PROTEIN	FOXTAIL MOSAIC VIRUS	1023-1050							
178 KD PROTEIN PANAYA MOSAIC POTEXVIRUS 1914 KD PROTEIN 19	PVORI NAV	186 KD PROTEIN	INARCISSUS MOSAIC VIRUS	6201-266	1527-1561		H				
223 KD PLOTEIN POTATO VILUS M (STAAN RUSSIAN) 197-427 163 KD PROTEIN POTATO VILUS X 197-135 163 KD PROTEIN POTATO VILUS X (STRAIN X) 164 KD PROTEIN STRAWBELLY MILD YELLOW EDGE ASSOCIATED VIRUS 196 FROTEIN AUTOGRAPHA CALIFORNICA PURUS 113-142 113-142 114 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 113-141 114 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 114 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 115-141 115 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 115 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 115 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 115 KD PROTEIN AUTOGRAPHA CALIFORNICA PURUS 115 KD PROTEIN 115 KD PROT	PVORI PMV	176 KD PROTEIN	PAPAYA MOSAIC POTEXVIRUS	948.978	1481-1533			H	Ц		Ц
163 KD PROTEIN POTATO VRUS X 1941 KD PROTEIN	PVORI PVIME	223 KD PROTEIN	POTATO YIRUS M (STRAIN RUSSIAN)	597-627							
165 KD PROTEIN POTATO VALUS X (STRAN X.) 150 KD PROTEIN STRANBELLY MILD YELLOW EDGE ASSOCIATED VIRUS 171-347 P10 PROTEIN AUTOGRAPHA CALIFORNICA MUCLEAR POLYHIEDROSIS VIRUS 7-41	PVORI PVX	165 KD PROTEIN	POTATO VIXUS X	_	1017-104						
190 KD FROTEIN STANDELAT MILD TELLOW EDGE-ASSACIATED VIADS 112-12 P10 PROTEIN AUTOGRAPHA CALIFORNICA MUCLEAR POLYTIEIDROSIS VIRUS 7-41	PVOR! PVOCE	165 KD PROTEIN	POTATO VIXUS X (STIANN X))	Т	10.104	1	1				
PIOPROIEIN (AUTOMOTIA CALIFORNICA POLLEGA POLLEGA POLLEGA	PVORI SMYEA	150 KD PROTEIN	STIAMBEALY MILD YELLOW EDGE-ASSOCIATED VIRUS	Т		-	<u> </u>	1		-	
	PVP10 NPVAC	PIOPROTEIN	AUTOMATIA CALIFORNICA NOCLEAN FOCTIFICADOS VIRGAS			+	1		1	\downarrow	
5117	ACADI OTAN	FIG FROTEIN	CAROLIN TECHNOLOGICAL MINISTERNATION OF DESCRIPTIONS	T	77.		1	1	$\frac{1}{1}$		1
											١

PCT/US95/16733

FILE NAME FYFIG WTV FYFIG		VIRUS									
			767-62								
		ICE GALL DAMAS amos	_	227.254							
		WOUND TUMOR VIRUS	53-60								
			101.10								1
Ш			101:10								7
Ш		WOUND TOMOR VIRUS (STRAIN NI)	81.15								
11		ARTICHOKE MOTTLED CRUNKLE VIRUS									-
T		TOMATO BUSHY STUNTWINUS (STRAIN CHERRY)									
	SECUTED VEST	HERPESVIRUS SADKIN (STRAIN !!)	5								
	Ī	ECALINE MERPECYTRUS TYPE I (STRAIN ADAP)	16-6)								
		SEPRENDING CALVID (CTEAN II)	48-75								
_		TEATES VINCE OF SILVENIES VINCE ACCOUNTY OF A 1 STRAIN VACCINE)		410-433	632-662	907.934					
	-	AFRICAN HOMSE SICKNESS VINCE CONTINUES STATEMENT	913:146								
Ī		BLUETOWGUE VIRUS (SEROITYE 13/13/CATE UZA)	198.425						_		
		BLUETOWGUE VIRUS (SEROTYPE 1/ ISOCATE AUSTRALIA)	14, 11,								
T		BLUETOWGUE VIRUS (SEROTYPE 1/18/01.A1E.SCHIII AI RIK A)	•	107 707			_		_		
		EPIZOOTIC HEMORILIAGIC DISHASH VIRUS (SHROTYTH: 1)	ī								L
1		BOVING BOTAVIRUS (STRAIN IF)	٦								L
		BOOKING BOTAVIBLE STRAIN UK)									
VP2 ROTBU		SOUTH STATE OF THE PERSON WAS		533-567							ļ
Ļ		CANADA NOT A CANADA CAN	53-99	138-156	\$18-545	705.74b	-	1	:		
VP2 ROTPC	RNA-BINDING PROTEIN VP1		36.26				_			_	_
		SINIAM II KUI AVIKUS (SIIMAM) SINIAM II SIN	39.75	•							
		AFILICAN SWINE FEVER VIRUS (STRAIN E-12)	16.05								
L											
1										L	L
I.		-				\downarrow	-				L
_\	TOTAL SECTION BY PROTEIN VP)		101-02		1		1			L	
ı	POLYMENAN COMPLEX PROPERTY	•	182-012				1				L
1			64.102								ļ
VP35 NOVEM		VACCINIA VIRUS (STRAD) WR)	178-205						1	\downarrow	-
VP35 VACCV	DOMORODOM ENVIRONS	THE CONTRACT OF THE CONTRACT MUCLEAR POLYTIED ROSIS VIRUS	134-161	204.20			-				1
PV739 NOVAC		ORCYLA PERIMOTEUGATA MULTICAPSID POLYHEDROSIS VIRUS	263-290			1		1		1	-
JI NEVOF	N. C.	AFRICAN HORSE SICKNESS VIRUS (SENOTYPE 4 / STRAIN VACCINE)	133-159								ļ
VPJ AJBV4	VP) COOLE PROTEIN	BIT INTOMOLIE VIRUS (SEROTYPE 10/150CATE USA)	214-252				$\frac{1}{4}$		\downarrow	1	-
WPS BTV10	VP) CORE PROTEIN	BITTE TOWNER VIRUS (SEROTYPE 17/1SOLATE USA)	214-252								1
VPJ BTV17	VP) COAL PROTEIN	THE PARTIE OF IS VEROTOPE I / ISOLATE AUSTRALIA)	214-252								1
VP3 BTVIA	VP) CORE PROTEIN	BLUE LOWON THE LANGE AND STREET (SEROTYPE 1)	209-243	798-833			4		1	1	1
WI BOVI	VP) CORE PROTEDY	ENERGY OF THE LOCATION AND THE STREET AND THE 27 STRATH AUSTRAL	T (168-133			_	-		1		1
WEI ENDVA	VP) CORE PROTEIN	EVICOUR TEMOMONIC STATES	39-13	L							1
VAN GALV	P) PROTEIN	GRAPHINE FANCEA TIMES	39-66	129.184	L	L					1
NOT BOTTLE	INVER CORE PROTEIN VP.)	PORCINE KOTAVILOS (GROOF CASTING)	1992	350.37	451-497	619-692					4
West Britts	INNEX CORE PROTEIN VP3	SEAGAN II ROTAVIRUS (SI KALIF SATI)	440.470								4
000	CAPSID PROTEDY P40	EPSTEIN-BARK VIRUS (STRAIN BY)-4)	201.313	344.372		L		L	L		
	CANCEL PROTEIN PRO	HELVESVIKUS KADKIRU (STRALIV II)				-			L	L	
200	CARGO PROTEDI PRO	INTECTIOUS LARYMOTRACHELLIS VIRUS (STRAIN THORNE THEE)	200	55,50		-	-		L	L	L
	CANCELLE PROTEIN PRO	VANCELLA-ZOSTER VIRUS (STRAIN DUNIAS)		1700	1	1	-			L	L
200	COMPANY MENTERN VP4	SECTIVITY ROTAVIRUS (STRAIN SAII)			-	-			L	L	L
WAL KOISI	COLUMN TO THE PROPERTY OF	SDEAN II ROTAVIRUS (STIVADA SAII)	2		-	-	+				L
Wet Hors	COLEA CASSO FINANCIA PAR PRECIDENT	VACCINIA VIRUS (STIVAIN COPENHAGEN)	Ç		1	1	1	ļ	-	ļ	-
WALK VACCO	MACON CORE PACIFICA DA PERCITASON	VACCEMIA VIRUS (STRAIN WR)	Ç.			-	1	\downarrow	1		ļ
PVPAA VACCV	MAIOR COLE TROITER PAR PARCITION	VARIOLA VIRUS	48-75				1	1	1		ļ
PVP4A VARV	MAJOR CORE PROTEIN TAX PRECEDED	FOUND MY VORUS	00-110			1	1		1	1	1
PVP4B FOWPV	MAJOR CORE PROTEIN PAS PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	7:37			-	-	-	1		1
VP-4B VACCC	MAJOR CORE PROJEIN THE PRECENCION	UACCORTA VIBUS (STRAIN WR)	7.37		4			1		1	\downarrow
PVP4B VACCV	MAJOR CONE PROTEIN PAS PRECORSOR	VARIO A VIRUS	7-37				1	1	\downarrow	1	1
PVP4B VARV	MAJOR CORE PROTEIN MB PRELUKSUR	STANDARD IS VANIR (SEROTYPE 10 / ISOLATE USA)	34-61	\$76-603			4				+
PVP4 BTV10	VP4 CORE PROTEIN	BUTE TOWARD VALUE (SEROTYPE 1) / ISOLATE USA)	34-61	376-60)		_		-	1	1	4
WM BTVII	VP4 CORE PROTEIN	BLUE LONGE VIRUS (SEROTYPE 2 / ISOLATE USA)	34-61	\$76-603			$\frac{1}{1}$		1	1	+
PVP4 BTV13	VP4 CORE PROTEIN	SCHOOL STANDARD VINUS (STRAIN NCDV-LINCOLN)	552-622		-	1	1	1	-	-	1
PVP4 BTV2A	OUTER CAPSID PROTEIN VPA	POLYMER BOTA VIRIA (SEROTYPE 6/STRAIN B641)	195-629					4			-

TCCLAT.	107317814	All Vienzes (no baciertophages)								-	ſ
THE BOTH	CAN LEIGHT BEATEN US.	PURUS BOTA CORUS SETTA IN CARA	ABEAL	ABEA	77	AREA	AREAS	AREAS	ABEA 7 A	AREA !	AREA .
200	COLEA CASSIL FIGURE VE	BUVINE KULAVIKUS (31 KAIN C440)	573	SM-622							Γ
TALL BOILDS	WIEK CASID FIGURIN VP	BOVINE KOTAVIKUS (STRAIN UK)	595-629							-	
rvre ROIBU	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	112-146	492-562	\$52-629						Ī
WY KOTEH	OUTER CAPSID PROTEIN VP4	ROTAVIAUS (GROUP B / STRAIN IDIR)	5-32		L					T	Ī
PVP4 ROTGE	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 1076)	1.35	572-628				İ	T	\dagger	Ţ
PVP4 ROTHI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	1.35	279-306	\$3.621					+	T
PVN ROTHS	OUTER CAPSED PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN 69M)	5.55	112.139	584.629			T	T		
PVP4 ROTHS	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN 6941)	1-35	279.306	\$65.621			Ī	T	1	-
PVY ROTIED	OUTER CAPSID PROTEIN VP4	2/STRAIN DSI)	3	279. With	F. 6. 6.2.1	_	:				_
שונסא איי	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KI)		11.11	:		:	_	_		-
PVIM ROTION	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KU)	25.5	Т	279-106	\$27.621		T	\dagger	\dagger	
PVP4 ROTHE.	OUTER CAPSED PROTEIN VP4	HUMAN ROTAVILUS (STRAIN L26)	23	Τ.	26.63			T	†	+	Ī
POLLOW MANA	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVILUS (SEACTYPE I / STRAIN MJ7)	Š	633.610			1	1	\dagger	1	T
NOLLOW PANA	OUTER CAPSID PROTEIN VPA	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN MCN1)	1	19716				1	1	1	
PVP4 ROTHD	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIAUS (SEROTYPE) / STRAIN PI	T				İ		<u> </u>	-	:
PVP4 ROTHER	OUTER CAPSID PROTEIN VP4	HIDAAN BOTAVIRUS (SEROTYPE 1/ STRAIN BEN	T	Т				1	1	1	
PVP4 ROTHT	OUTER CAPSID PROTEIN VP4	HINGAN ROTAVIRUS (SEROTYPE 4/ STRAN ST THOMAS 1)		J	292-552				1		
PVP4 ROTHV	OUTER CAMED PROTEIN VP	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA70)		70.7	***		1			-	
PVP4 ROTHW	OUTER CAPSID PROTEIN VP4	HOMAN BOTAVIRUS (SEROTYPE 1 / STRAIN WA)	Ī	97.6	200			1			
PVP ROTPS	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTIPE S / STRAIN OSIN	į						1	1	
PVP4 ROTPC	OUTER CAPSID PROTEIN VP4	PORCONE ROTAVIRUS (GROUP C./ STRAIN COWDEN)	,	Т	50.			1		1	
PVP4 ROTPO	OUTER CAPSID PROTEIN VPA	PORCTHE ROTAVIRUS (STRADA GOTTFRIED)	T	Т	300			1	1	1	
PVP KOTPY	OUTER CAPSID PROTEIN VPA	PORCINE ROTAVIRUS (STRAIN YA)	T	.]_	367783		1	1	1	1	
PVP4 ROTHUM	OUTER CAPSID PROTEIN VPA	ALPESUS ROTAVIAUS	T	Т			1			1	
PVP4 ROTSF	OUTER CAPSID PROTEIN VP4	SBALAN 11 ROTAVIRUS (STRAIN SAIL-FEAD	Τ	OLY OLY			1	1			1
PVP ROTES	OUTER CAPSID PROTEIN VP4	SDAZAN 11 ROTAVIRUS (STRAIN SAII: SEM)	T	Т	(14.43)		1			+	
PVP WTV	NONSTRUCTURAL PROTEIN PNSA	WOUND TLANDR VIRUS	28-62	Т			T	1	1	+	T
PVPS AJESVA	OUTER CAPSID PROTEIN VPS	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)		117:16			†		1	1	
PVPS BTV10	OUTEA CAPSID PROTEIN VPS	BLUETOWGUE VIXUS (SEACTYPE 10/1SOLATE USA)	Ť	80.126				1	\dagger	+	Ī
PVPS BTVII	OUTER CAPSID PROTEIN VPS	BLUETOWOUE VIRUS (SEROTYPE 11 / ISOLATE USA)	Ī	93:136			T	1	\dagger	\dagger	
rvrs Brvis	OUTER CAPSID PROTEIN VPS	BLUETOWGUE VIXUS (SEROTYPE 1) / ISOLATE USA)	53-10				T			+	T
LALE BIAIN	COTEL CAPID PROTEIN VP3	BLUKTONGUE VIXUS (SEROTYPE 1/1SOLATE AUSTRALIA)		89-126	\				f		T
AND BINES	COLEA CASSO PROTEIN VES	BLUE LINGUE VIXUS (SERUTYPE I / ISOLATE SOUTH AFRICA)			148-182				-	-	Τ
PARK EURVI	COLEA CASIO FROIEN VE	BLUE LUMUUB VIKUS (SEKU) TYPE 1/1SOLATE USA)	1	П						-	Γ
ALA SAVA	CONTEX COAT PROTEIN PS	WARM TIME VIBIT	7	12.10	199-426						
PVPKI BTV16	VPA SECTION	BUTCH CALL COLOR ASSOCIATION ASSOCIATION	200								
PVPK! LOLDV	PROB NOWSTRINCT 41 9 KD PRO	MAIZE BOICH DWARF VINIS	(6)-101				1				
PVP61 NPVAC	61 KD PROTEIN	AUTOCRAPHA CALIFORNICA NUCLEAR POLYMEDROGIC VIRGI	707-46	1			1				
WALL BIVIO	VP6 PROTEIN	BLUETONGUE VIXUS (SEROTYPE 10/1501 ATE USA)	61.10				1	1	1	1	
PVP64 NPVOP	MAJOR ENV GLYCOPRO PRECURSOR	OROYTA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	ŝ	T			†	1	+	1	I
PVP67_NPVAC	MAJOR ENV GLYCOPRO PRECURSOR	AUTOGRAPHA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	17.7				1	t	\dagger	+	T
PVPS BTVII	VP6 PROTEIN	ALUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	157-119	Ī			†	\dagger	\dagger	+	T
PVM BTV13	VP4 PROTEIN	BLUETONGUE VIXUS (SEROTYPE 1) / ISOLATE USA)	137.189				T	t	\dagger	\dagger	T
PVT6 BTV17	VP4 PROTEIN	BLUETOWGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	157.189					T		+	T
PVP6 BTV1S	VP6 PROTEIN	BLUETONGUE VIXUS (SEXOTYPE 1 / ISOLATE SOUTH AFILCA)	161-191				\dagger	\dagger	+	\dagger	Ţ
PVP6 BTVZA	VP6 PLOTEIN	BLUETONGUE VIRUS (SEROTYPE 2/ISOLATE USA)	133-172				l		\mid	$\frac{1}{1}$	Ī
rvie tov	STRUCTURAL PROTEIN PS	IUCE DWALF VILUS		184-181					l	+	T
TVE 14 TATAL	PARTIES AND	AUTOMACHIA LALBURAICA NUCLEAR POLYREDROSIS VIRUS	П					-	l	-	Γ
AND MANAGE	SOUTH STATE OF THE	1	g	979-977					ŀ	-	Τ
PARTY NEWAC	Ver Cook Bentier			370-397				-	-		Ī
יייייייייייייייייייייייייייייייייייייי	MONETAL PROJECT PROTECT PART	WALLOW THAT THE THE THE THE THE THE THE THE THE TH	Ī					-		\mid	
PVPED NOVAC	CAPSID PROTEIN PRO	MICA MICTERS POLVEDBOSIS MATE	┑								
PVPR7 NPVOP	CAPSID PROTEIN 997	,	1	70.73							
VPR BTV10	HONSTRUCTURAL PROTEIN PR			1	1	1	1				
PVPE FOWPV	STRUCTURAL PROTEIN VP8 PRECURSOR		100	1	1	1	1	+	+	+	
					1	1	1	1	1	1	7

PCCENE	10711701	AB VITERS (IV COLUMN A COLUMN	AREA LO	1	2000					L
FILE MAME	PROTEIN	VIRUS	29.56	12-143			+			
1	CALTER CAPSID PROTEIN PI	WOOND TUMOR VIKUS	197.224							1
	NOW THE AT DECITE IN PASS	DOE DWALF VIRUS					-			
VO. CV	MAN STATE OF THE S	WORTH TIMOR VIRUS		1			-	L		•
VI WIY	STRUCTURAL PROTECTION	AND THE LABOR CONTINUES OF THE PARTY AND	122-49			1		-		<u>!</u>
PVP9 WTVN	STRUCTURAL PROTEIN P	STATES AND THE PRINCIPLE OF THE PORT WEED TO SEE VIRUS	196-223				1	-		1
PVPHE NPVAC	39 KD POLYNEDRAL ENVELOPE PROTEIN	AUGUSTICATE AND TICABEID BOI WIEDROSIS VIRUS	127-126	238-265			+			ŀ
ONAN APPAR	12 KD POLYHEDRAL ENVELOPE PROTEIN	ORGINA INEUDOI SUCATION SIES SON	167.194							-
TOPE APPLAIN	SATIONAL ASS	MOUSE ADEMOVIRUS TWEE								
1 V	NAME OF THE PARTY	HUMAN DANUNODEFICIENCY VIRUS TYPE I (ARVZSE I INDLA IE)				1	_	: -	:	
PVPU HVIAZ	VPUTRUITA	HINGAN NAMED DO SERVIENCY VIRUS TYPE I (IIIIIO AND IIXII) ISOLATIES)	7				-			L
PVPU HVIBI	VPU PROTEIN	THE PROPERTY VIEW VIEW TYPE I (BIG 150LATE)	21-48					1		
EVMI HVIBS	IVAU PROTEIN	HUMAN HAMOROGE SACRET TO THE TOP A PARTY AND THE A TEN	33.49							
	CATTERNER	HUNGA INDANAODEFICIENCY VINUS 17PB (BICAIN ISOLATE)								
NA BY	The state of the s	HIGHEN BOAUNODEFICIENCY VIAUS TYPE I (BAU ISOLATE)		Ī						L
TO HAVE	VPU PROJECT	WALLAND MAN MANDER CHENCY VIRUS TYPE I (CDC-451 ISOLATE)	20.70			1		+		
PAPE HVICE	VPU PROTEIN	AUMINI INTRODUCTION OF THE TYPE 1 (F) 1 (C) ATE)	(6.3)					1		
EVEL LIVIES	VPU PROTEDI	HUMAN DARCHODE KIERCT VINOS LITE I (ILLI SOCIETA	1			-				
		HUMAN BOADNOOFFICIENCY VIRUS TYPE I (II XILL I SOLATE)				-	_	L		
PVPU HVING		WALAN BANDADERICIENCY VINUS TYPE I (IH) ISOLATE)	67.7					-		L
PVPU HVID		THE STATE OF THE PARTY COUNTY TYPE I (TRESF ISOLATE)	57.7					1		
PVPU HV:78	VPU PROTEIN	HUMAN BANDADE ICENTO VIBILE TVPG 1 (U.2.) 15(1) ATE	15:32							
ADIOU		HUMAN WORLDWING THE TANK THE TOTAL T	152				_			
STILL OF		HIDAN BOACHODEFICIENCY VIRUS TYPE I (NUK ISULATE)							L	L
WAL HAIRD		MIDICAN BEACHNODEFICIENCY VIRUS TYPE I (PV22 ISOLATE)	7					-		L
PVPU HVIPV		HALL BACKBOOKENTENCY VIRUS TYPE ! (SF162 ISOLATE)	11.49					+		
ISIAH DAA		MORAN BRANCH CONTRACTOR OF CON	11-18		_			1		1
PATRICIA SPECIA	VINITED	CHING ANZES INMUNOCETICIENCE FINAS	20.77							
	No the Other Day	LACTATE DESTrongenase-elevating virus						-		
Vex LDV	VEAFFULLE	TANK TROPE MOSAIC VIRUS	1031-1078				1	-		
ENA BONV	ALPKA-A PROTEIN	CONTRACTOR OF CO	Ī					-		1
PUCOL ROTHS	VIN PROTEIN	BOVING KULAVAKUS LAKOUR CA STANIA	114.144							
A COMPANY	VAL PROTEIN	ROTAVOLIS (GROUP B / STRAIN AUR)	35 66					_		
W. W.	See an Overly	ROTAVILUS (GROUP B / STRAIN IDIR)			1		-		L	L
PVSOB ROLL	VICTOR IN	HUMAN ROTAVIRUS							_	L
SOC ROTHE	V2 TOTAL	PORPONE ROTAVIRUS (GROUP C/STRAIN COWDEN)	į			1				L
SOG ROTPC	VN PROTEIN	BOWNE BOTAVIETS (STRAIN KN-4)	2-29					1		1
PVS07 ROTBJ	CLYCOPROTEIN VP7	DOVER BOY AND THE AND LIKE	91-146	199-236			-	-		1
PVS07 ROTTBU	NOWSTRUCTURAL PROJECT PLANS	THE PART COUNTY OF A STRAIN OSU	91-146	202-236						1
PVX67 ROTPS	NONSTRUCTURAL PROTECN NOVE	MULTINE MOINT AND A COMPANIES OF THE PARTY O	91-146	199-336						1
Series Prints	NONSTRUCTURAL PROTEIN NCVP3	SDUCK II KOTAVIKUS (STAMIT SATI)	164.701			-				
	AND THE PROPERTY OF THE PROPER	BOVING ROTAVINUS (STILVIN UK)				-		L		_
VSOI KOTEU	MONE LANCE CONTRACTOR AND LANCE AND	GRATAN II NOTAVIRUS (STRAIN SAII)	107-901	107-17		1		-		L
VSOE ROTS!	NONSTRUCTURAL PROTEST PLANT	BOWNE BOTAVILLE (SENOTYPE 6 / STRAIN BOA!)	2-29					1		ļ
PVSO9 ROTTEA	CLYCOPROTEIN VY	20 THE SALVE OF SALVE AND ACT	1-19					-	-	1
PAYOR ROTES	CLYCOPIOTEDI VP7	BOVING RULA VIEWS (STINKER AC)	2.29		L					4
Are Borest	CAL VICIONED TEDA VP7 -	BOVING ROTAVILUS (STRAIN U.S.)	310.917		-	_	-	_		
20100	C. C. STANDARD CO. BOECH IN CO.	ROTAVILUS (GROUP B / STRAIN ADRY)	1000		1		-			L
VSO) KOTOA	C.T. Complete Williams	LINITAN BOTTAVIRUS (SEROTYPE 4 / STRAIN RV-4)	62-2				1			-
PV509 ROTHA	CLYCOPIOTED VF	CONTRACTOR OF CO	1.29							
ANTON BOTHA	CLYCOPROTEIN VP7	HUMAN KOIA TAKO ITE STORES	3.70		-					_
200	CI VONDEDITION VP7	HUMAN ROTAVILUS (SEROITYE G/ SIRAIN B)	1			-		-		
VSD KUIND	Control of the contro	HOMAN ROTAVIRUS (SEROTYPE 2/STRAIN DS!)	6.53			1				L
PVS09 ROTHED	G. TOURISEN VE	LIFEVAN BOTAVINUS (SEROTYPE 2 / STRAIN HOLI26)	3-29		_			1	-	ļ
VSO9 ROTHON	GLYCOPROTEIN VP/	SHELLAND BOT A CORING (CEROTYPE 1 / STRAIN MJ?)	1.12							1
PVC00 ROTION	GLYCOPROTEIN VP?	MUMAN ROLL THE SECOND S	2.70		L	_		-		
OTTO SOLVE	Calycopacited VP7	HEMAN KOTAVIKUS (SEKULTYE I) SIRAM PIO AND SIRAM	2.0	L			Ŀ	L		_
1	CH VOODBOTTED! VP?	HUMAN ROTAVIRUS (SENOTYPE 1/SINAINT)			+			-		L
200	On Concession (197)	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN S2)	69		1					L
VSO MULES	Carlotte and the second	HIDAAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	7.7							1
VS09 ROTHW	CE. TOWNOISM VE	PARTICIPATION (SEROTYPE 3 / STRAIN AT/16)	1.19			1		1		1
VS09 ROTP?	GLYCOPROTEIN VP	SAFAN BOTAVILLE (SPECTIVE 3 / STRAIN CRW-8)	2-29			1				1
VS09 ROTES	GLYCOPROTEIN VP7	CONCESSION IN CASE OF	5.29	-						4
VSO ROTS!	GLYCOPROTEDN VP?	_	125-152		-					
VALUE BOTHS	MONOR OUTER CAPSED PROTEIN		113.140				_			
10000	INCOMPTRINCTURAL OF YCOPROTEIN MCVI	•	١	114.146	+		-		_	L
1310 1013	LANCOR CHITER CAPSED PROTEIN	BOVING ROTAVIAUS (STRAIN UK)			+		-	-	L	L
Wall Kolbu	Manual Charles County	BOVING ROTAVILLS (STIALIN YARU)	2		+		-		-	ļ
WELL BOTTEV		151.00. 1.00 · L.10.								
		THE PROPERTY OF THE PARTY AND THE PROPERTY OF THE PARTY O	8=	_			-			1

PCCENE	1107x178x4	Att Virgan (as harderlanks per)	-							ŀ	-
FILENAME	PROTEIN	YIRUS	AREAI	AREA 2	AREA 3	ARFA 4	AREA S	AREA 6 AREA 7	Т	ARFAR	A LETA
PVSII ROTHS	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-S)	13.40	111-145					Т	T	
rvsii Roth	MINOR DUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS!)	13-40	111.145					$\frac{1}{1}$	t	T
PVSII ROTHW	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	111-145						\mid	Ì	T
PVS11 ROTAL	MINOR OUTER CAPSID PROTEIN	RABBIT ROTAVIRUS (STRAIN ALABAMA)	118-145							1	
PVS11 ROTS1	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 ROTAVIRUS (STRAIN SAII)	11.146							t	,1-
PVSH MUMO!	SMALL HYDROPHOBIC PROTEIN	ANDARS VIRUS	97						-	t	T
PVSH MUNDA	SMALL HYDROPHOBIC PROTEIN	INCINOS VIRUS (STRÁIN MATSUYAMA)	12-41		L			-			1.
PVSH MOOB	SMALL HYDROPHOBIC PROTEIN	MIDNES VIRUS (STRAIN BELFAST)	341						-	t	Ī
PVSH MOOR	SALALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN EXDERS)	9-46						-		T
PVSH MODO!	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN JEAYL-LYNN)	9-46						l		Ī
PVSII MUMPK	SMALL HYDROPHODIC PROTEIN	(MOMPS VIRUS (STRAIN KILLIAM)	97				İ		<u>.</u>		
PVSH MUMON.	SWALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	970					T	1	1	T
PVSH MOMPH	SMALL HYDROPHOBIC PROTEDY	MUNOS VIRUS (STRAIN MOYAHARA VACCINE)	13.51						+	1	
PVSH MUMOR	SMALL HYDROPHOBIC PROTEIN	MANOS VIRIIS (STRAIN IN)								1	1
PVSH LANDAY	KMALL LYTHE DELICATION DE CITETAL	LANCE VIEW ACTOR AND UNCORNER AND	Į.								
CACIA IIAA	SIGNA I PROTEIN BERCHEOD	PERMITTING THE ACTION OF ACTION AND	12:41								
PVCII BEOVI	SCHOOL STATEMENT OF COMME	PECVINOS (1176 27 217AIN DEARING)	10-63	2	23:161	200					
200	STORY I PROTEST PRECUASOR	ALUVINO (1 TELL FOR MAIN UNIONES)	4.10 4.10	130-193							
rvail AeOvi	SACRIA I PROTEIN PRECURSOR	REDVIKUS (TYPE I / STRAIN LANG)	4.52	75-104	113-160				-	l	Ī
rvsta Reovo	SKWA Z PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARING)	150-314						-		
rvsu Acovi	SICALA J PROTEIN	REOVINUS (TYPE 2 / STRAIN DS/YONES)	289-316						-	f	
TAND PROVE	SIGNA IS PROJECT	REDVIRUS (117E 37 STRAIN DEAUNG)	8-17						-		
rvata Aetuvi.	SKIMA I-S PRUIEIN	REDVIRUS (TYPE I / STRAIN LANG)	50-77							-	
1417 1417	PROTEIN TOA	CAPRIPOXVIRUS (STRAIN INS-1)	124-158						-	<u> </u> 	!
PVTS SFVKA	PROTEIN TS	SHOPE FIBROMA VIRUS (STRAIN KASZA)	150-217							t	
PVTER EBV	PROBABLE DHA PACKAGING PROTEIN	EPSTEIN-BAKR VIRUS (STRAIN B95-1)	234-290					T		\dagger	
PVTER HOMVA	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN ADIM)	417-451						<u> </u>	<u>:</u>	-
PVTER 115V6U	PROBABLE DNA PACKAGING PROTEIN	FFE 6 / STRAIN UGANDA. 1102)	136-201	!	:		:				
PVTER HSVII	PROBABLE DNA PACKAGING PROTEIN	ICTALURID HERPESVIRUS I	710-737							\mid	Ī
PVIER VZVD	PROBABLE DNA PACKAGING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DURIAS)	394-421							f	Γ
PVIP) TIVIV	VIXAL PROTEIN TPX	THERMOPROTEUS TENAX VIRUS I (STRAIN VT.)	169.196							+	Ī
PVIPA TIVI	VIKAL PROTEIN IPX	THEAMOPROTEUS TENAX VIRUS I (STRAIN KRAI)	169.1%		,					-	Ī
Y 1414	V PROTEIN	HUMAN PAKAIMTLUENZA 4A VIRUS (STRAIN TOSHIDA)	4.38							t	Ī
77 101 33 V	LOCALISTICAL IN PROPERTY	SULF COURTS VINUS-LIKE PARTICLE SNVI	23.65								
100	HINDONISTICAL ILLE CHESCHEN	SULFOLDED VIAUS-LIKE FAKIF F SOVI	Ş								
AND AND	UNDOTHER CALL II 3 P.D. PROTEIN	TOBACCO VELLOW DIVARE MALIE SAVI	30-78								Γ
SALLY ALLYS	MYOUTH IN THE PART CHECKE	ALTOCO AND CALIFORNICA MICHERALIA CUERTOCIO	37-63								Ī
PVINE SIVI	HVPOTHETICAL 113 KG PROTEON	ROUGHOUSE CALIFORNICA MULLECAN FOLTINEDADAIS VIRUS	2112								
PYI4K SSVI	HYPOTHETICAL 13.7 KD PLOTEIN	SUIFOLOBUS VIRUS-LIKE PARTICLE SSVI	9 9								
PYICK NPVAC	HYPOTH IN 39 KD PROTEIN STECTION	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRIIS	10.103	Ī				1		1	1
PY16K_SSV1	HYPOTHETICAL 15.6 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	13:11	T	Ī			1		+	1
PYIN SSVI	HYPOTHETICAL 13.0 KD PROTEIN	SULFOLOBUS VIXUS-LIKE PARTICLE SSVI	Τ	119-153			T	T		+	
PYIEK MSVN	HYPOTHETICAL 17.7 KD PROTEIN	MALZE STREAK VIRUS (NICEUAN ISOLATE)	16-61			T	T	T	+	\dagger	
PYISK MSVS	HYPOTHETICAL 17.2 KD PROTEIN	MAIZE STREAK YTRUS (SOUTH-AFINCAN ISOLATE)	19.5			Ī			+	+	
PYZOK SSVI	HYPOTHETICAL 28.4 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PÄRTICLE SSVI	76-103				T		+	\dagger	Ī
PY28K SSVI	HYPOTHETICAL 24.5 KD PROTEIN	SULFOLOBUS VIRUS-LIXE PARTICLE SSVI	93-164				T	ĺ		\dagger	Ī
172 SOON	HYPOTHETICAL PROTEIN 2	SOYBEAN CALOROTIC MOTTLE VIRUS	18-148						-	t	T
PYSIK SSVI	HYPOTHETICAL 11.3 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	24-97				Ī		-	1	
PY3ZK SSVI	HYPOTHETICAL 31.7 KD PROTEIN	SULFOCOBUS VIXUS-LIKE PARTICLE SSVI	233-267					Ī	-		Ī
PYSIK NPVAC	HYPOTHETICAL 33,7 KD PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS	133-184					T	<u> </u> .	+	T
V 5000V	HYPOTHETICAL PROTEIN 3	SOYBEAN CALOROTIC MOTTLE VIRUS	123-149							+	T
ANONA LA	HYDINE IKAL PROJEM /	SOTBEAN CALCHOILE WILLS							-	ŀ	Ι
PYBSK SSVI	HTFOIREIRAL 83.7 AM PROIEIR	SULPCIDED VIXOS-LUC PARTICLE SSVI		\$46-573	658-700					F	
PYS SOCIAL	INTO THE IKAL TRUITED IN STATE OF THE PROTECTION	SOURCE ON UTILITY AT THE WASHINGTON	╗				Ė				
PTBOI FOWEN	INTO INCIDENT AND AND OFFICE OF	FOW LOAN VALUE (ISSUENTE TOTAL HIMORICHI)		122-179	104:210						
PTB03 FOWPA	INVESTIGATION BANGACION SECTION	FOWEROX VIBILE GROLL ATE UP ANALYSING BANCHING	- 1							-	
FIBIN COURTS	HITOIRE BOMESTON IV INCIDENT	ונטאוייטט (ייטרייוב יוד אין שטיינה))	162-197	214-24	1				H		Π

PCGENE	167417814	All Viceber (no securing mages)	AREAI	AREA 1	ARTA	ABEAs	4	4	4		
FILE WAME	PROTECT	WIRUS	11.38								
MANUS CHEVE	HANDTHETICAL BANGE OFF 12 PROTEDI	FOWLYOX YAUS (ISOLATE PL-4) INTO CALL	121.167								
MUNUS LIEVA	HYPOTHETICAL BANGG-ON IS PROTEIN	FOWL FOX VIXUS (ISOLATE HP-434 MONICAL)	17.116								
ANT TO SERVE	REL'S PROTEIN	HUMAN SPUNALETROVIRUS	141.183								1
	LIVERTH SA I KD IN DAGE TREGION	HERPESVIRUS SAIMURI (STRAIN 414-77)									7
The same	MANAGED AS SECTION	HENPESVINUS SADAINI (SUBGROUP C/STRAIN 488)									
PYOH! HOVE	ALCOHOLD IN PARTY SECTION	HERPESVILUS SAINGRI (SUBGROUP C / STRAIN 488)									_
PYDIN HSVXC	HTMIRY'S WINDER JACKS	SOW! POX VIRUS (STRAIR FA-!)	î								
PYT26 FOWP!	HTTOTHER I CAL 23.9 NO PAOLEUS	COMPLEX VIBIR (STRAIN FP.1)	170.204								
PYF10 FOWP1	HYPOTHETICAL 36.9 KD PROTEIN	TOTAL MAIN COTAL WELL	37-64	95-126	144-171						
PYHEE VACCV	HYPOTH 21.3 KD NEWENIG-C PRO	VACUITY VIEW AND AND AND AND AND AND AND AND AND AND	31.50	179-206							
PVICE VACCY	HYPOTH HOST MANGE 27.4 KD PRO	VACURIA VIXUS (SIRVING WA)	121.00		L						
VKET FRV	HYPOTHETICAL BKATI PROTEIN	EPSTEIN-BARK VIXUS (STRAIN BY)-4)	18.53								
V#3 78.4Ve	HYPOTHETICAL BKRF4 PROTEIN	EPSTEIN-BARK VIRUS (STRAIN B93-4)	1				_				
TIME DO	NOTICE OF THE PERSON	HUMAN ADENOVIRUS TYPE 41	2							L	L
PTC13 AUEA1	HITCHIA MAN MAN MAN MAN MAN MAN MAN MAN MAN MA	EPSTEIN-BARR VIXUS (STRAIN B95-8)	37:34								
PYLIN EBV	HYPOINE II CAL BLACK FROM	CONTACT IN A VELLOW MOTTLE VIRUS	94.143								
PYORI COYNCY	HYPOTHETICAL 23 KD PROTEEN	CONDUCTION MOTTLE VIRUS	33.76								ļ
PYORE COTARY	HAPOTHETICAL IS NO PROTEIN	WANTE OF AVER APPRAIN VIRIE (STRAIN M)	64-94						\downarrow		1
PYOU WCHYM	HYPOTHETICAL 13 KD PROTEIN	WILLE COVEN MODEL OF STREET	63-95	L							1
PYOR 1 WOWD	HYPOTHETICAL 13 KD PROTEIN	WHITE CLOVER MUSALL VINOS (SINGER O)	92-119								
PACE APERI	INVESTIGATION 11.5 KD PROTEIN	AVIAN ADENOVILUS GAL! (STRAIN PHELL'S)	1					L			
1000	LIVECTHETICAL & 1 KD PROTEIN	THERMOPROTEUS TENAX VIRUS I (STRAIN KRAI)			1		-	L			
	INTERPORT SERVICES	THE NAME OF THE TENAX VIRUS I (STRAIN KIAN)								L	L
PYONE TIVE	ATTOINE MAN TO THE PROTECT	THERMOPROTEUS TENAX VIRUS I (STRAIN KRAI)	1				1				L
PYORO TIVI	MININE IN THE PROPERTY.	THER MOPROTEUS TENAX VINUS I (STRAIN KRAI)	3				-		-		L
PYORW TIVE	HYPOTHETICAL 12.1 KD PROTEIN	INC. TINCED RACTILIFORM VIRUS	44-71						1	1	1
PYP12 ATBV	HYPOTHETICAL PIZ PROTEIN	BICH Y INCHO BACH LIFORM VIRUS (ISOLATE PHILIPPINES)	44-73						-		1
PYPIZ RTBVP	HYPOTHETICAL PIZ PROLEAN	SICE TINCED BACKLI BORM VIXUS	59-101	8				1	\downarrow	1	ļ
PYTZ4 RTBV	HYPOTHETICAL PA PROJECT	TANCE THE PROPERTY FORM VIRUS (ISOLATE PHILIPPINES)	51-101	106-157					-	1	1
PYP24 RTBVP	HYPOTHETICAL PA PROTEIN	SICE HINDS BACH LIDORM VIRUS	156-107	197-231			1		1	1	1
PYP46 RTBV	HYPOTHETICAL P46 PROTEIN	THE HALP BACH I FORM VILLS (ISOLATE PHILIPPINES)	101-18	197-231			\downarrow	1	1	1	1
PYP46 KTBVP	HYPOTHETICAL PAS PROTEIN	THE LONG AN THOUNDS MILT FAR POLYNEDROSIS VIRUS	14-71								1
PYP63 NPVAC	HYPOTH PLO PA.S STREGION	AUTOCACA WEET HOTEL MAIN TICAPSID POLYHEDROSIS VIRUS	325-352	_							1
PYP6) NPVOP	HYPOTH 40.0 KD IN P6.5 STECHON	-	116-153								1
PYPOH NOVAC	HYPOTH 23.6 KD IN POLYHEDRIN SPELLIC		5-32								1
PYPOL DRIVE	HYPOTHETICAL 17.0 KD PROTEIN	_	15.3	89.68	156-183				4	1	1
PYQ) AMEDY	HYPOTHETICAL PROTEIN IN TRESTUCE	_	208-235								1
PYRFI HSV60	HYPOTHETICAL PROTEIN IV	THE SECTION OF VIETS CIVE A STRAIN GS	1233-257	168-299	Ц				1	1	4
PYTUT HSV60	HYPOTHETICAL PROTEIN ILT	HEATES SIMPLEA VANCE (* 172 A PA OS)	141-168						_		4
PYLL HSV60	HYPOTHETICAL PROTEDY RF3	HEIGES SUMPLEY UNITE CYPE & / STRAIN GS	1444								1
PYRF4 HSV60	HYPOTHETICAL PROTEIN RF4	HEAVES SMALLEA VINCE (11 TO STATE OF	<u>5</u>		_						4
PYRP2 DAVE	REPETITIVE PROTEIN ORF?	CHILD INDESCENT VINOS	7.34								4
PYVAO VACOC	HYPOTHETICAL \$3 KD PROTEIN	VACCINIA VILUS (S I MAIN CUPEATRACEA)	41.112				L	_			_
PYVAH VACOC	HYPOTHETICAL 14.5 KD PROTEDY	VACCINIA VIIIS (STRAIN CUPENHAGEN)	25.71	L	-	-					
777	HYPOTHETICAL \$ 5 KD PROTEDY	VACCINIA VINUS (STRAIN CUPENHAVER)	1	1	-	-		-	L	L	
TANKA BITALL	INDODUCTION AS KD PROTEIN	VACCINGA VIRUS (STRAIN WR.)		-	1	-	-				L
PYVDB VACE	THE STREET AT 9 2 KD PROTEIN	VACCINIA VIRUIS (STRAIN WR)	2	1	-	1	1	-	-		L
PYVDH VACEV	HINDER OF AN INCIDENT	VACCINIA VIRUS (STRAIN COPENHAGEN)	3	1		-	-	1	-	1	L
֭֭֓֓֓֓֝֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֜֓֓֓֓֓֡֓֓֡֓֓֡֓֡֓֡֓֡֓֡֓֡֓֡֓֡֡֡֡֓֜֡֡֡֓֡֓֡֡֡֡֡֡						_					

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

¥\$\$484					7		۰						
		Table 1			633-410								
	PROTEIN	AKK MUMDIE LEUKEAUA VIRUS	VIIIO		136:11	İ		Ī	Ī				
		AV MURDE LEGINERAL	N STATE		103.00		1						
		IK V MUSIDAR LE UNEMA	VINOS		_	115.402	Ī						:
	MYC TRANSPORMING PROTEIN	AVIAN MYELOCY I UMA I USIS VINUS CHIL	Cara viscos Centra		1	3,6 403		Ī					_
П		VIAM MYLLOCY I CAN	USIS VIRGO PAR		ī	1979	Ī	Ī			Ī		
i		AVIAN MYELOCYTONIA 10313 VIAUS MCA	USIS VIAUS ML.		ī					İ			•
	PROBABLE LI PROTEIN	AWAN PAPELDACAMEUN FIVE	7,4			1					İ		1
5		COVDE PERPESVIAUS T	130				Ī			Ì			
Τ	SWALL CHA	BOVING HERPESYIAUS TYPE I (STRAIN 14)	IPE I (STRAIN 14)				Ì					Ī	İ
Ī.		DOVING HEAVESMAUS !	PE I (STRAIN BAN)		-	1						Ī	
		DANK BAGBOOFFICE	MCY VIRUS (150LA)	(901)	_		631-693	1					
		THE PERSON NAMED IN COLUMN	A WASHER MEN A	I III	1	111.632	140-134						
		OVER PROPERTY OF THE	WIND ASSESSED.	144 61 61	104.33								
		DOVER LEUKENDA VIA	A STATE OF THE STA	The Control	100								
		POVER LEUKEMBA VIKU	AMERICAN ISOL	ile vom)		T							
Ī		DOVINE LEUKENDA VIAU	M (AUSTRALIAN ISO	LAIE)									
Ī		BOVING [EUREMIA VIALIS (BELGIUM ISOLATE LETIT)	IS (BELCIUM ISOLAT	(61011)				-			İ		
Ī		BOVING LEUKENDA VIRU	IS (BELGIUM ISOLA)	re t.ess)								1	1
1		ACVINE LEINE MILA VIRI	IS CLAPANESE ISOLA	TE BLV-1)	104-111				1		:	-	•
Ī	TO THE PROPERTY OF THE PARTY OF	SOVOR PARAINSTURING	PARAINSI UENZA I VIRUS		(F3)			İ					i
		AND COMPANY PARTIES	A 1 VIRUS		16.91	155-262	313:314						
	THA POLYMETA SE ALPINA SUBURILI	TO THE PARTY OF TH	111111111111111111111111111111111111111		=======================================	ī	189.489						
VGU PID	FUSION CLYCOPROTED PRECUISOR	BOATINE FAILANT COUNTY STATES	211017		301.131								
PYNAT PIJE	MATRIX PROTEIN	BOVING PARAMALUEN	A J VIRUS	100000									
ļ	RNA POLYNGBASE ALPIN SUBUNIT	BOVINE RESPIRATORY S	WCVIAL VIRUS (S	I KAIN ASITON	1		1	977					
Ī	STREAM CO VCOPROTEDN PRECURSOR	BOVDE RESPONDED	THE TITLE WINUS (S	FRAIN ASIBOD	ş	202							
Ī	ALTERNATION OF PROPERTY IN	BOVDE RESPIRATIONY	THEY TIAL VIRUS (S	I RAIN ASIBOL)	2								
Ť	MAIN'S W. L. O'ROLLING	VACATA IN COMA TON	THE TITE VIEWS 13	TRAIN AS 1904)	219-246								
1	KAIKIX PRUIELM	VACUATION AND AND AND AND AND AND AND AND AND AN	WASTINE VISITED	ITHADA COPENDIAGEN	1 22 1	154.303	116.743		411-533				
Ī	FUSION CLYCOPROTEDY PRECURSOR:	CONTRACTOR OF THE VIEW OF THE	ALC: NICK	THAM COPENITAGEN	121								
		A STATE OF THE STA	The state of the s	TRADIDALI	3	134.203	316-241	177	111.333			. !	
	PUSION CLYCOPROTEON PRECURSOR ,	BOVING RESTRAINED	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		10.00								
PENV MEVCS	ENV POLYPROTEIN	CAS BR. I MORDAE LEUK	EPHIN VINUS		-	311.310	10.00	2.6.514	53.63				
Γ	ENV POLYTROTEIN	CHIP CANZER INDIVIDUAL	ביונות יותם										
Ī		CHID-D-ANZEE IND-CHOOPETICIEMCY VIPUS	EFICIENCY VINUS		_	1							
	IEN	CHISOTANZEE DOMINOR	EINCIENCY VIAUS (S	SIVICEZII									
		COTTONTAL LABBIT (S	HOPE , PAPILL OPLAY	TAUS (STRAIN RANSAS)	-								
T		COTTONIAL BABBILLIS	HOPEIPAPILLOMAY	TAUS (STRAM KAMSAS)	=		_						
NE COL		DENGLE VIRUS TYPE !	STRAIN SINCAPORE	Stiling	1151-103	20.02	_					1	
٦	CONCRETE TO LITERAL DE LA CONTRE DELA CONTRE DE LA CONTRE	NEWSTER VINITE TYPE I	STRAM LAST		1304-1371	1656-1165	2901-3935	1962-1916	3117-314	_			
_		SECOND STREET TYPE 3	STRAIN IGAIL POKS		24-131	1650-1165	-	200.2935	3113-3016	3113.3143	_		
		S SEASON	CIBADA MANERAL		346-131	1656.1113		_	1146-1111				
	GENOME POLYTROTERY	THE PROPERTY OF THE PARTY OF TH	1100111		1515.1531	1154-1119	1905-1912	100		3343.3370			
			TO TOWN TO THE	CONTRACTOR OF THE STREET STREET STREET		100.00			_				
					133.164	1342-1369	183.1884	3006.2531	1910-3014	1345-1372			
l		DENCOL VICES 1172			3111.3110		-	_	_	<u>-</u>			
1	GENOME FOLYPROTEIN	DENGUE VALUE I THE	Total Concession	11 NEC 1501 ATE 511									
1014	DHA POL TAGRASE	DUCK PEPATITIS B VIRUS (BROWN SIGNATURE 32)	DEACH STANCE	MI DOCK TOUCHE TO									
POPOL 10 LDC	DHA FOL THERASE	DUCK IEPATITIS B VIR	S (STRAIN CIUMA)										
WORDS INCH		DUCK (GPATTIS B VIN	US PARTIE SHANGAU	AI DUCK ISULATE STIT				1					
Value of the	PROTEIN	EPSTEIN BARA VIAUS (17 KB 83 C					-					
200		EPSTEIN-BARR VOIUS (TAN BUS C			2							
	N BBLS1	EPSTEIN BARR VIRUS	ITAM BOS. I)		77	_							
À		SPITED BARK VIRIS	I KAN DIS II		115-3121	69).814							
THE STATE OF THE S	-	EPSTEIN BARK VIAUS (STRAM BOLE)	STAMBOLES	00	9								-
		ENSTERN BARN VOILS	SIRAM BILLI		107-144	961-196							
MAN ED		EPSTEIN BANK VINUS	STATE BY IN		10.17								
W.W. 124	LYCOPROTED	ESTEN BASE VAUS	STAM BIS.		=								1
	ğ	EFSTEDIONAL VIRUS	STRAIN BUS-6)			3							-
VGL EBV	2	EPSTEM-BALL VIRUS	STAIN BIS I)		349.536	19.61							
PVCLH EBV		PITALS GOVE CONTRACTOR	CTRAIN BOLLS		104 149								

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PENV MON	ENV POLYPROTEIN	NUMM CELL FOCUS FORMING NUMBE LELIKEMIA VINUS	100								
PENV ME VAIO	ENV POLYBOOKEN	HUNK CELL FOCUS FORMING KIURINE LEUKENIA VIAUS (1501.ATE CL.)	10.00								
PENSI MONVS	PROTEIN	MATTER FOLKER LEUKENIA VIRUS	2							Ī	1
PICIE MCMVS		MARINE CYTOLICAL DURING STREET, SALING	Ξ						Ì	Ī	-
PVCILB MCMVS	_	MAJAINE CYTOREGAL OVIRUS (STRAIN SMITTIN								Ī	
PVE 3 PCPVI		PITITURE CYTONIC GAL OVINUS (STRAIN SMITIN)	1								
PVES POPV	PROTEIN	LYGMY CHIND ANZEE PAPIL LONIAVIAUS TYPE I	267.794	137.361							
PENY MENTO		AADIATION OF THE TANK OF THE 1	2						Ī		
PPOL MAYON	POL POLYPROTEIN	BADIATION STREET FURENITA VIRUS	497.538						İ	Ī	
PENV MEVRK		A DIA TOUR OF THE PARTY OF THE	3	103-111					Ī	Ť	1
POL PEVAK		AADIATION MURINE FIRE LAIA VIDIS CERALIS AND AND AND AND AND AND AND AND AND AND	3								1
DAME SCHACE		SIMIAN CYTONIE GAL OVIRUS 15TRAIN COLBURNO		2		i					Ī
TOTO IDAYS	GENOME POLYPROTECH	SPUANIE PATITIS A VIRUS (STRAIN AGAL IT)				j					;
PENY CIVAL	ENV POR VAROTEIN	STATION A VIRUS (STRAIN CY.143)									-
PPOL SIVAL	POL POL VPROTER	SUCIAN DOUBLE FOLE NO VINUS (AGNISS ISOLATE)	369 310	181.181	90 619	10.00	407.134	-	-		
POL SIVA	POL POL YPROJERY	CINIAN MAINTON ICE IN THUS (AGNISS ISOLATE)	-		119 419			Ī	Ī	Ī	
PENV SIVAG	ENV POLYPROIER	SINIAN MACHINIST NIEWS VINUS (AGNISALISOLATI)							İ		
POL SIVAG	POL POLYTROTEIN	CHEME T VIRUS (AGAI) (SOLATI)	00 00 00 00	166 573	197 614	136 bis	017.10	İ		Ī	
POL SIVAL	POL POLYPROTEIN	TOTAL VINUS (ACAT ISOLA II)	19 46		3				Ì	Ī	-
PDV SIVE	DAY POLYPROTEIN	PARADOR IN THE VIEW OF VIEW OF THE PARADOR IN THE P							Ī	İ	-
PGAG SIVSA	GAG POL YPROTEIN		_	-	099 219	90			Ī	İ	
20.20	POL POL YPROTZIN	PCIENCY VIBILS OF SEASONS INC. A SE	1							Ī	i
PENV SIVA	DAY POLYPROTEIN	KIENCY VIAIIS IISOLATE AGAICEI ONE CALLE								İ	i
PCAC STVAL	GAO POL YPROTEIN	KIEMCY VIRUS JISOLATE AGNIZOLOSE CALLI			8	914.70					-
ZA ZA	MEGATIVE FACTOR	HEIEMEY VIRUS ISSOLATE AGNITCH ONE CRITI									-
200	CL CL THOILIN	MURACUE IN CIFICY VINUS LISULATE AGAIN CLONE CALLI	- 11.010			1					į .
PENV SIVE	ENV POL VEGOTTEN	ICHEME Y VIRING (150LATE AGM / CLONE GRI. 1)	-	-		-			į		_
POL SIVE	POL POL YPROTECN	ICIEMO VIPIUS (1SOLATE GOL)	_	1112	30 610	10.00			-	!	-
1	ENV POLYPROTEON	US HSOL ATE GRID		- 949-919			Ī	-	!	i	1
L	GAG POLYPROTTIN	CIENCY VIRIS (NOW ISOLATE)	200			İ		Ī	-	Ì	
	POL POLYPROTEIN	CENCY CHEST AND SOLATE	2					-	Ī	-	!
IJ	ENV POLYMOREIN	APAINODE HE IENCY VINIS IN 19 1504 A 11	3						<u> </u>	-	i
DV SVAI	ENV POLYPROTEIN	FCIENCY VIAIIS (ARAINS 19 150) A 183		1						<u> </u>	i
1	ENV POLYMOTEIN		12								
PENY SIVE			110	311.316		Ī		Ī	İ	i	
			- 1	310.303	646.122			Ī	İ	1	j
POL SIVSP										İ	-
1	DAG FOL TROILIN	SPOAN BORINODE HERMY VIRUS (STATISOLATE)	1=	1		Ī					
			ī	15.19	18	100		Ī	İ	i	
PREV SIVAT	REV PROTEIN		12.63	Ī	T	Ī	Ī	İ	İ	1	-
PEN LONN			3		Ī	Ī	Ī	Ť	İ	$\frac{1}{1}$	_
PHOL MONTH	POL POL YPROTEIN	SECAN MASON SECTION	0.7			Ī		İ	i	1	ī
PGAG LOTAY	GAG POL YPROTEIN	- Children	_ :	10000		Ī	Ī	İ	-	<u> </u>	_
PEXON VZ 45	ALKALINE EXONUCLEASE	RIS (STRAIN DUNIAS)	92 ::	Ī				Ī	<u>-</u>	<u>:</u> -	i
BAZA ITDIA		SIRAIN DENIASI							<u> </u>	<u> </u>	
	ACE CHA	R VIRUS (SIRAIN DURLAS)	1	2				Ī			<u> </u>
T	٦	(STRAIN DUMAS)		19.1450	Ī	1	Ī			_	<u> </u>
נוניון אלאם	2				T	Ī	İ	1		<u></u> 	_
7	-	N VIRIIS (STRAIN DUNIAS)	-100	Ī	Ī	1	Ť	i	1	<u>- </u>	
					1		1		1	\dashv	

PCC EME	10711704	AS ANDRES 100 DECEMBER 1	ARTAILA	REA 1	3	1	RIAS IA	NEA 1	SEA1	17.4	2020
THAM WE	PROTEIN			ļ		Ī					
	WORLDWICE NO PROTEIN	A 20SILA VIRUS (SI	1		1		İ	Ì	Ī	Ī	
		CALCALL A SOCIAL PARTY OF THE PARTY IN THE P	_	200	-	601-01					
22	GENE 31 PROTEIN	277 777 777 777 777 777 777 777 777 777	30.164	Ī				_			
SAY SAY	HOST SIGNOR VINION PROTEIN	A COSTER VIROS ISTRACTOR OF THE PROPERTY OF TH	1	. 346	İ					-	;
5	CENT IS MENDIALME PROTEDY	VARICELLA ZOSTER VIRUS (STRAIN DUNIAN)					Ī	Ī	Ī		<u>.</u>
3	PACIA NA MEP GENE 6 PROTEIN	LLA 2051FR VIRUS (STRAIN DUPIAS)		-	İ				Ī	Ī	
	1	VALICALLA 2051EF VINUS (SIRAIN PUNIAS)	22.52	İ	Ì				Ī		
אמני אנאם	CAT CORDIEIN OF	TA POST IN VIEWS AND	174.108	32.52			j				_
0.7× *4.4	CAPSIO PROTEIN PAU	1	180-061				_				i
PYTER VZVD	PROBABLE DNA PACKAGING PROTEIN	ILA COST CALLED TO THE COST OF									
PVELE VZVS	CLYCOPROTEIN CAV	ZOSTER VIRITS (STRAIP SCOTT)		Ī	İ	Ī					
AND MAY	DAY PALYS BASE	KIRPATITIS VIRUS I		İ	ĺ						
	100 100 100 100 100 100 100 100 100 100			j			1				İ
POPCE. WHYS	DAY FOLT PLANTS	TATAL STATE CITY S		= 0							-
POPOL WHY	DNA POLYMERASE			100							
POPOL WAYS	DHA POLYMERASE			11.0	Ī		Ī				
POPOL WINE	DHA POLYNERASE	WOODCINCK HE PATITIS VIRUS I	1								

TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

Т	1071.17824	Prohamatic Sequences	AREA L	AREA?	AREA 2		7		1000		1
П		PICKETTSIA BICKETTSII		П	35.312	276-572	100	1100-1404			
	NO KO SUNFACE-EXPOSED PROTEIN	DICKETER TYPHI	67.94						77.00	1621 1631	1771.1750
Г	17 KD ANTIGEN PRECURSOR	POCKETTIN BICKETTIN	241-268 4		607-634	24.71	23.62	16.40	2671-3071		
PISOK BUCH	IN KD ANTIGEN PRECURSOR (CELL SURFACE)	MOVE I SILV MOVE IN THE PROPERTY OF THE PROPER	2065-2096 2	3							
П		PERIO FURDCOCCUS MOBILIS	18-51	29.00	20-14						
P22KD DESMO 2	22.6 KD PROTEIN	VIRBIO ANGUILLARUM	153-196								
HOKD VIBAN	40 KD PROTEIN PRECURSOR	FSCHERKCHIA COM 1	511-534								
	60 KD DWER-MENGRANE PROTEIN	PROTEUS MILABILIS									
PHODM PROPAGE	SO KD INNER MEMBERANE PROJECTI	ZYMOMONAS MOBILIS	95-132	\$ 2.24							
SKD ZYDOLO	65 KD PROTEIN	MACTILIS SUBTILIS		21.46							
WIND BACKU	PROB 6-PHOSPHOGLUCO	ECASE ICHA COLI	205-232								
Г	6-PHOSPHOGLUCONATE DEHYDROGENASE	SCHOOL OF TABILITIES	205-212								
PERCO SALTY	6-PHOSPHOGLUCONATE	SALMONELLA TITIES OF SELECTION AND SELECTION AND SECURITY	150-477								
Ц	6.ANDVOCLYCOSIDE N.ACETYLTRANSFERASE	STAPHTLOCOCCUS ACREOS	Т	115.212							
	ASPARTATE AMINOTRANSFERASE	BACILLUS SP	т				L				
Г	ASPARTATE AMINOTRANSFERASE	ESCHENCHIA COLI	136.201						_		
П	ABC PROTEIN	ESCHENCHIA COLI	٢	130.204	(12.602				-		
A PAT LACTA	BOATIVE PHAGE RESIS	LACTOCOCCUS LACTIS	t								
TACK ACREU	RANSCHETTIONAL REP	AGROBACTERUM TUMERACIEMS	2017								
PACEA ECOL	SOCITIVATE LYASE	ESCRETACHIA COCI	15.00			L	_				
MACKET	ACONITATE HYDRATASE	BACELUS SUBTILIS	T	613.640							
TOUS NOUVE	ACONITATE HYDRATAS	ESCHENICHIA COLI	L								
PACTA ALCEU	ACETOIN CATABOLISM REG PRO	ALCALIGENES EUTROFIUS	1			L					1
TOOL COV	ACYL CANNER PROTEIN	ESCHEDICHIA COLI	213.247								-
TIOUS VOVE	ACTUAL AVON RESISTANI	ESCRETCHIA COLI	130.331			L					
LION ECOL	ACHIELAVIN RESISTANCE PROTEIN B	ESCHENICHIA COLI	\$12.550	126-753		L					
	ACRUFLAVON RESISTANCE PROTEIN F	ESCHENCIA COLI	157.184								1
PACT STRCO	PUTATIVE KETOACYL REDUCTASE	STREFTOM TLES COELICOLOR	Т	\$76.603							
	ACTIN-ASSEMBLY INDUCING PROTEIN PRECURSOR		1129.3163		L		Ц				1
A DOM WORK	ACV SYNTHETASE	NOCAULA LACTAMBONAS	136-170		L						4
PADAA BACSU	METPHOSTRESTER.DI	BACULUS SUB (ILLIS	198-425	187757	\$22.556	1005-1032	2		•		1
PADDA BACSU	ATP-DEPENDENT MOCLEASE SUBUNIT A	PACE 1 US SUBTILLS	257-264	100-011	41.917		1	1	1	1	1
PADDB BACSU	ATP-DEPENDENT MUC	CI OSTRIDIUM ACETOBUTYLICUM	284.311					1	+		1
PADHI CLOAB	NADPH-DEPENDENT BUT AND, DENTUROUS AND A		198.125						1		1
PADHA CLOAD	NADH-DEPENDENT BUTANOL DEHYDRUGENASE A		298-325					-	1	1	1
PADING CLOAN	NADH-DEPENDENT BUTANOL DEHYDRUGENASE B		633-610	179.806					1		\downarrow
PADIE CLOAD	ALCOHOL DEHYDROGENASE	RECHEDICHIA COLI	271-298			_	-	1		1	1
PADHE ECOLI	PADHE ECOLI ALCOHOL DENYDROGENASE	FSCHENCIAL COLI	45.72				_	_			1
PADIY ECOLI	PUTATIVE REGULATORY PROTEIN ACT	MYCOPLASMA GENTRALIUM		697.724	23.62	101-066	100	2	!	-	
PADPI MYCGE	140 KD ADHESIN PRECURSOR	LYCOPLASMA PNEURIONIAE	1357.1514				+		1	-	1
PADPI MYCH	ADMESTA PI PIECURSON	ROCETTSIA PROWAZEKII	176-307		-	1	-	\downarrow	1		-
PADT NOR	ADPATP CAUGA PROTEIN	AEXOMONAS HYDROPHILA	278.305			1	1	-	-	-	-
PAESA AEUN	AEROLYSIN PRECURSOR	STREPT OCCICUS MUTANS	41041)	20.63		-	\downarrow	1		-	L
PAGAL STUMO	ALPRA-CALACIOSENSE	PSEUDOMONAS ATLANTICA	36.51	1	-	1		1	-	-	L
PAGAR PSEAT	BELANDONE TREEST ATOR PROTEIN	STAPHYLOCOCCUS AUREUS	129-139	2		1	-	+	-	-	
PAGE STAND	CCESSORY GENE NEX	YEASDNA ENTEROCOLITICA	19-40		1	-	1	-	1	-	-
AND AND	ATTACH INVASION	ESCHENICHRA COLI	0	8	201.330	+	1	1	-	-	ļ
PAK H	L	ESCHEDICHIA COLI		60			+	-	-	-	
PAKH EQU	ASPACE OF ALTER AND BETA SUBUNITS	S BACILLUS SUBTILIS	2		1	+	+	+	-	-	-
PACS BACSU	SAMINE KINASE A	т	?		1	1	1	+	+	-	-
PAKAB CORGL	AVAKTAIB MAASA		26.316		1	+	+	\downarrow	+	+	-
TO TW	ALCONATE MICKYN TRANSL REG PROTEIN ALCB	PSEUDOMONAS AERUGINOSA	3		+	+	+	\downarrow		-	L
MG PACE	ALCINATE BIOSTINE		9		1	1	+	+	-	-	ŀ
A L	THE ANY CREMENTAL REGULATORY PROTEIN ALGE				-	1	+	-	-		
7	ALK ANE, I MONOOXY	Ħ	11.11	111.365	1	-					
200 P	BITTH FEDOXON-NAD(+)	PSEUDOMONAS OLEOVORAMS			+	-					-
ALA! Farm					_	_	_	_	_		-

PCCENE	10717244	Probarotic Semestra					-	-	-	-	Γ
EILE WAME	PROTEIN		ARIAI	ARIA	AB1.A3	NR.A.	AHPASAN	AREAG	AREA 7 AR	AREABAN	ABEAS
PALA BACST	ALANINE RACEMASE	HERMOPHILUS					-		ī	7	
PALSR BACSU	ALS OPERON REGULATORY PROTEIN	ATILIS	119.146					<u> </u>		-	Ī
PALYS BACSP	AUTOLYSIN PRECUA	BACILLUS SP	157.187				-		-	H	Ī
PALYS BACSU	AUTOLYSIN PRECURSOR		147-191						<u> </u>	-	i
PALYS STANU	AUTOLYSIN									-	Ī
ANG SILVE	AMIA PROTEIN PRECURSOR		z	297-118	446.473						
	AMIDASE	PSEUDOMONAS CHILORORAFIRIS	85.2								
TANKE SINCE	ANIMALE INCOME PROTEIN ANIE		107.214				:	-	į		
AND GRAM	METAL ACTIONS ME	ESCAPATIA LANGERGES		177.226		1		-	!		İ
1017	A SOUTH A SOUTH							+	-		
1	A MINORERYTORSE N		-	8.7				7		<u> </u>	
	WINGTED I DASE IN		2000			j					
	A-FRO ANIMOREY I ID.		100								
WAT THEY	AMINOPERTIDASE T		201.300								
LYMA DECIM										<u> </u>	İ
L CANALITY OF THE PARTY OF THE	ALTHA AMTLASE 2	LUNI	151-176	507-534				·			
PAMY: SALTY	CYTOPLASMIC ALPHA-AMPLASE		10-104					-	-	H	
PANY) DICTA	LPHA-AMPLASE)	MOFIIII.UAI	280-307				-			<u>:</u>	Ī
PAMMS BACCI	BETA-AMYLASE PRECURSOR		11-11					-			
PAMME BACKO	ETA-AMMLASE			166-293	1143-1184		-	_	-	-	
	BEIN-MATLASE, THERMOPHILIC PRECURSOR	ERMIOSULFUROGENES			459.486					-	
AATO CLOSP	AUCOAMMASE PRE			480.510				-		-	
PAMMIN BACST	PAMYM BACSTIMAL TOGENIC ALPHA-AMYLASE PRECURSOR	BACILLUS STEAROTHERMOPHILUS									Γ
PAMYR BACS	MAW-STANCH-DIGESTING AMYLASE			435.465	613-642					-	Γ
PAINT AEUNY	ALPHA-AMYLASE PRECURSOR		415-453					Ŀ		-	
PAMY ALTHA	ALPHA-AMMLASE PRECURSOR		166-193					-		-	Ī
TAMP BACAN	ALPHA-AMYLASE PR	FACIENS						-	-	-	
LAMY BACE	ALPIA-AMTLASE PRECURSOR	BACILLUS CIRCULANS	•	437-474							
TANK BYCKE	LINA ANTA LOSE PR		П	<u>\$</u>							Ì
	ALTHA-AMILANE PRECURNOR	4.5	╗		П						
	MATERIAL ALONG A REC		1	26.57	279-606	795-822					
THO WAY	LI PUA ALVI ACE BE		7								
7 1812 /2714	AL MANAGE PRECIONAL	CTOS INDIVIDUAL INFORMACIONE SAN CONTROL OF	1	9:50							
POST VALVE	MITTOCEN RIVATION		82.								
PANED AZON	MITEOGRAM OF THOM THOM AT PUA CHAIN	AZOTOBACTES VINELARDII	67777		1						
MOZY X9VV	NITROGENASE BLON-		771-64			1	1	1			
PANCE VIBAN	ANCR PROTEIN		1	100.07		1	+	+	1	1	
PANCE FREDH	PHYCOBILISOME 120 KD LINKER POLYPEPTIDE	NON	T			1		+	+	1	T
PAPCE STYLING	PHYCOBILISOMIE LIDIKER POLYPEPTIDE		Τ	\$15-615		1	\dagger	+	1	+	Ī
PAPCE STYPE	PHYCOBILISONG 130 KD LINKER POLYPEPTIDE		52.79				-	+		\dagger	T
PATHE SALTY	ALKYL HYDROPEROXODE REDUCTASE C12 PROTEIN	7	61-29				\vdash	-	l	+	Ī
AN AOUT	MOTEASE I MECURS	LYTICUS	478-505			-	-	-		\vdash	Ī
יאירכ בכסוד	PROBABLE CYTOCHROME OXIDASE SUBUNIT	ESCHENICHIA COLI	=							-	Γ
TATE DEAL	ALALINE PROTESSE SECRETION PROTEIN APPL		7	╗					L	-	
PANE PONE	Т	FUTURE ICHA CON I	1	201-23	247-277					Н	П
PANU TIGET	80	ANOI ICITE	101.71		Т					1	
PARCA MYCAR			1	7	28.9()	967-1014	1210-1254 138	1381-1408	1	+	
PARCID ECOLI	LEAGBIC RESPONTION CONTROL PROTEIN ARCB		٩	1.	100.436	†	+	1	+	1	
PARCO PSEAE	ROBABLE ARGININEKORNITHINE ANTIPORTER	RUGINOSA	T	Т		\dagger	+	+	+	\dagger	Ţ
PARGA_ECOLI	AMINO-ACID ACETYLTRANSFERASE		Т			\dagger	+	t	+	+	T
PANGT ECOLI	YS-ARG-ORN-BINDING PROTEIN (LAO) PRECURSO		11.78			\dagger	1	+	1	\dagger	Ī
PAROA STAAU	HOSPHOSHIKLMATE I-CARBOXYVINYLTRANSFER	AUREUS	16-120		Ī	İ		+	+	+	T
PAROC ECOLI	HONSMATE SYNTHASE		61.95				-		ŀ	+	T
PAROC SALTI	CHORISMATE SYNTHASE	SALMONELLA TYPHI	68-95					+	-	\vdash	Γ
PAKUD BALSU	POLITICACIONALE DEHITORALASE		49.76				Н			-	Γ
											Ì

	PROTEIN		•				7				L
					Т	г					
		ESCHERICHIA COU	Ţ	637.63	366-126						
	000	STREPTOCOCCUS PYOGENES	1	T							
	N THE CONSTR	ESCHENICHIA COLI	737.77			1					
PANY ECOLI	19484	ESCIENCHIA COLI	201-238								
	NO AIRASE	CONFESCIONA COLI	-			1					L
ISB ECOLI		TANK OCOCCUS AUREUS		200				T			
	ARSENICAL PUMP MEMBRANE PROTEIN	STANISH OCOCCIIE YA'I OSUS	27.71	295.322							
REE STANY	ALSENICAL PUND MEMBRANE PROTEIN	SIATILITY OCCUPIES A INCIDE	16-91								
PARCE STAND	ARGENICAL RESIST OPERON REPRESSOR PROTEIN	STAMILLOCOCCUS AGREED	05.5								
	ANTA PROTEIN	ESCIENCHIA COCI	2	211-240							
7	PRANCEMET SYSTEM PROTEIN ARTI	ESCHERICHIA COLL	T								
WILL ELON	THE STATE OF STATE OF THE PROPERTY AND THE	ESCHENCHIA COLI	┱	100	190.836	149.896					
7	TRANSPORT STREET THE PROPERTY OF THE PROPERTY	ENTEROCOCCUS FAECALIS	7	200							
	AGGREGATION SUBSTANCE PRECURSOR	SCOTT DICHIA COLI	137-158								_
_	ASPARTATE-ANONONIA LIGASE		7.5						_		
	ACPARACINE SYNTHETASE II		116-111					İ			1
	BESTER A LOUBY PROJECT ASPAC	ויאט אווראואנאציו									
-	ALCONOMINATION OF SECT	BACILLUS SUBTILIS	:							L	
	ASTALIA AMPLIANIA LI ASE	ESCHERICHIA COLI	204-236							L	L
_	ASPARTATE ANGIONIA-LTASE	PERMATIA MARICECTENS	34-33								L
Τ.	ASPARTATE ANOMONIA-LYASE	SCHOOL PROCESSION	252.208					:		_	_
_	LASPARAGINASE	BACILLUS LICHERING	116.31			_					4
	1 ACBARAGINASE PRECURSOR	ERWINIA CHRYSANIIII: NI									
ASPO ESAME	TANK AND AND ASSESSED.	ACINETOBACTER GLUTANINASIPICAMS							L		
ASPO ACIOL	GLUI AMINASE-ASI AN	ESCHENICHIA COLI	134-381						_	L	_
PASSY ECOLI	ARGININOSUCLINATE STREET	INCTHANOSARCINA BAJIKERI	207.314								_
ASSY METBA	ARGINIMOSUCCIMATE	CTANAN OCOCCUS AUREUS	41-68	101-245							-
PATRP STANU	OTENTIAL ATP-BINDS	SI CONTRACTOR ENCLAINE	91.10	343.334						1	1
Valley Valley	POTASSITUACOPPER.TRANSPORTING ATPASE A	ENTERUCCUS PACACIO	200,110	450.477	\	L					4
	DOCA SSUIMACOPPER.T	ENTEROCOCCUS PARCALIS	9								4
ATKS EVIEW	A TOTAL STATE OF THE PARTY AND	SALMONELLA TYPHINDRUNI	2000		1						
PATHOS SALTY	Y MC(1) I KANSTON! AND STATE OF THE STATE OF	SYNECHOCOCCUS SP	237.662			1				L	
PATPS STICK	AIF STRINGS A COMM	VIBRIO ALGINOLYTICUS									L
PATH VIBAL	ATP SYNTHASE A CHAIN	ANABAENA SP	9.36	١	1		1		<u> </u>	ļ	<u> </u>
ATTA ANASP	ATP SYNTIMSE ALTER CITATIO	BACKLUS MEGATERIUM	4.36	€ €					-	-	-
PATPA BACHE	ATP SYNTHASE ALTEN CINE	ESCHENCHIA COLI	486-513							-	L
PATPA ECOLI	ATP SYNTHASE ALPHA CRAIN	ENTEROCOCCUS FAECALIS	4-36	5					\downarrow	ļ	L
PATPA ENTFA	ATP STATHASE ALPHA CHAIN	ACCOUNT ASMA GALLISEPTICUM	362-409							1	1
PATPA MYCGA	ATT STATHASE ALPHA CHAIN	A DOMESTICAL MODESTUM	6-36							1	1
ATPA PROMO	ATP SYNTHASE ALPHA CHAIN	ACCOUNT 1 AA BITTELLA	165-200	987-650					 -	1	+
VATE ANDRU	ATP SYNTHASE ALPHA CHAIN	Management of the second of th	111.343	\$ S	L					4	4
ATTA CON AC	STEEL UP AC ATTRACE ALPHA CHAIN	SULPOLOBUS ALLIXA ALLIXAS	77.								4
	ATT CONTINASE ALPHA CHAIN	SYNECHOCOCCOS SP		143.180			L				-
NI V	THE COUNTY OF ALL PHA CHAIN	STATECHOCOCCUS SP		1	-	-	L				
LATEA STRUTO	ALCONOMICE ALPHA CHAIN	SYNECHOCYSTIS SP								L	L
PATPA STATS	ATP STRICKS AT SULA CUANA	THE LANGETHEIR BACTERUM! PS-3	9-36		-	1			-	L	 -
PATPA THEP?	ATP STRIPAGE ALTER CLAN	VIBRIO ALGINOL YTICUS	661-513			\downarrow		+	1	-	-
PATPA VIBAL	ATP SYNTHASE ALTHA CRAIN	ANABAENA SP	280-307	36.33			\downarrow	1	1	1	-
PATTPB ANASP	ATP SYNTHASE BETA CHAIN	BACTIUS FIRMUS	163.190	331.315					1	+	\downarrow
PATES BACK	ATP SYNTHASE BETA CHAIN	LAYONE A CALA GALL ISEPTICUM	115-402					-	1	1	\downarrow
PATPB MYCCIA	ATP SYNTHASE BETA	a Local Committee in the Billian in the Committee in the	339-316	L					1	1	1
PATPE BHORU		ACCOUNT ACTION AND AND AND AND AND AND AND AND AND AN	164-191	L	_	L				-	1
PATTER SIRAC	ATPASE BETA CHAIN	SULPOROS ACIDOCACIO	181-408		L	-	L	L			4
	ATP SYNTHASE BETA	SYNEOHOCOCCUS SP	301.116	107	-						-
PAIRS SING	ATE CONTILASE BETA	SYNECHOCOCCUS SP			\downarrow	+	ļ	-	-	L	-
PATE SYNDS	ATP SYNTHASE BETA	SYNECHOCYSTIS SP	5	1	$\frac{1}{1}$	+	1	-	\downarrow	L	-
PATPB SYNT	A IF STATINGE DEL	ANABAENA SP	60.5	200	\downarrow	+	+	+	-	-	L
PATED ANASP		BACELUS FIRMUS	8	3	1	1	1			-	l
PATPD BACFI	ATP STRINASE DEL	BACTLUS MEGATERUM.	133-159		1			1	-		-
PATPD BACKE		ENTEROCOCCUS FAECALIS	3		+	+	1	1	+	-	-
PATPO ENTIA	ATP SYNTHASE DEL	PROPIONICENTUM MODES TUM	9 19	2		+	1	+	+	ļ	\vdash
PATED PROMO	III STRIPASE DE	RHODOPSEUDOMONAS BLASTICA	135-152		+	+	+	1	-	-	\vdash
PATTED MIDBL	ATP SYNTHASE UE	MIRRIA I I PROPOSITION	119.146	_			_				

PCGENE	107117814	Proharyolic Scaures								r	
FILENAME	PROTEIN		ARAL	AREAL	AREAL	ANEA	AREAS	AREA 6	AREA? A	AREA &	AREAS
PATPD SYNP!	ATP SYNTHASE DEL	SYNECHOCOCCUS SP	- Se-								
PATED SYNYS	ATP SYNTHASE DEL	SYNECHOCYSTIS SP	<u> </u>								
PATPD VIBAL	ATP SYNTHASE DEL	TICUS	5								
PATPE BACFI	ATP SYNTHASE EPS		<u>≅</u>								
PATPE MYCGA	ATP SYNTHASE EPS	-	99-176								
PATPE PROMO	ATP SYNTIMSE EPS	PROFIGNICATION NODESTURE	200								
PATE SING	ATE CONTINCE D'OUTE		8				1			1	
PATPE BACK	ATP SYNTHASE B CHAIN	Aire	Ţ	T		1			†	1	
PATPE BACKE	ATP SYNTHASE B CHAIN		1	07.1.70		1				Ì	
PATPE MYCGA	ATP SYNTHASE B CHAIN	TICINA	Ţ	2		Ī				†	T
PATPF SYNDI	ATP SYNTHASE B CHAIN		Τ							1	
PATPE SYND	ATP SYNTHASE B CHAIN		T	1				T		1	
PATPE THEPS	ATP SYNTHASE B CHAIN PRECURSOR	ERIUNI PS. 1	T						Ì	\dagger	T
PATPO ANASP	ATP SYNTHASE GALDAA CHAIN		26.310					Ī		Ť	
PATPO ECOLI	ATP SYNTHASE GAMMA CHAIN	ESCHENCHIA COLI	253.283		Ī		Ī				
PATPG MYCCA	ATP SYNTILASE GAMMA CHAIN	MYCOPLASMA GALLISEPTICUM	Т	92.140		Ī				T	
PATPG RHORU	ATP SYNTILASE GALMA CHAIN	AUDDOSPINILLUM RUBRUNI	L							\dagger	
PATPG SYNDI	ATP SYNTILASE GANDA CHAIN	4	[Ì					T	
PATPO SYNYS	ATP SYNTILASE GAMMA CHAIN		921-90	210.307							
PATPI MYCOA	ATP SYNTHASE PROTEIN I	A GALLISEPTICUM	133-167								
PATPX ANASP	ATP SYNTHASE B'C										Γ
PATPX BACFI	ATP STATHASE BET		162.189	156.363							
PATPX MHORU	ATP SYNTHASE B' CHAIN	טפאטע									
PATPX SYNF!	ATP SYNTHASE B. CHAIN		П	138-155							
PATPX SYMM	ATP SYNTHASE B' CHAIN	SYMECHOCOCCUS SP	8								
PATPX SYNY)	ATP SYNTHASE B'CHAIN	SYNECHOCYSTIS SP	20.13								
FAIFE BACKE	AIP SYMINASE PROTEIN !	BACILLUS MEGATERUMI	29-								
PAVER PERC	AVELLE ENTE & PROTEIN	1140		1							
PBA71 EURSP	7-AI-PHA-HYDROXYSTEROID DEHYDROGENASE		1	087-117	1					1	Ī
PBA72 EUBSP			5.5	T						†	
PBACH HALIPM	HALORHODOPSEN	HALOBIUM	145.170					T	\dagger	\dagger	T
PBACH HALSG		dS.	180-214						-		Ī
PBAES ECOLI	SENSOR PROTEIN BAES			П		П					
PBAG STRAG	IGA FC NECETON PRECURSON	AGALACTIAE	┪	19:30	267.306	343-318	487.524	\$62-589	1014-1041		
PBAHO VITSP	BACTERIAL MEMOGLOBIN	VITAEOSCILLA SP	19.146								
COAL CUBS			D() .								
PBASS ECOLI	SENSOR PROTEIN BA		Т	60.00	1				+	1	
PBAT HALMA		IALOBIUM	40142	T	T			Ī	1	1	
PBAX ECOLI	BAX PROTEIN		3								T
PBCCP_ECOLI	BIOTIN CARBOXYL (6.35							-	T
PBCHEN NHOCA	METHYL TRANSFER	NHODOBACTER CAPSULATUS	1000-1033								
PBCHP NIOCA		MHODOBACTER CAPSULATUS	٥								
PBCNS CLOPE	BACTENOCIN BONS			\$15.646							
PBCPA PROAF	BACTERIOCHLOROPHYLL A PROTEIN	PROSTIGECOCHLORIS AESTUARII	18:13								
PBCSD ACEXY	CELLULOSE SYNTH	ACETOBACTER XY, INIA	十	2101-6601	T	T	1	1	+	†	
PBENA ACICA	BENZOATE 1,3-DIOX	ACINE TOBACTER CALCOACETICUS	117.8		T		\dagger		\dagger	\dagger	T
PBETT ECOLI	HIGH AFFINITY CHOLDIE TRANSPORT PROTEIN		243-270	T	T		T	T	†	\dagger	Ī
PBEXA HAED	BEXA PROTEIN		П			Ì			-		
PBEXC HAED	BEXC PROTEIN		П	276-253					-		
PRESO HAEIN	BEXD PROTEIN	HAEMOPHILUS INFLUENZAE	105-239		İ						
PROA2 FOR	EVOLVED BETA-GALACTOS DASE ALPHA-SUBLINIT	FINANCIAL WINDOWADSKYI	200.000			1	1				
PBOAL BACST	BETA-GALACTOS/DASE	BACALUS STEAROTHERNIOPHILUS	599-611	T	T	1	T		+	\dagger	T
						1				1	7

	Frankline Sequence	Г	6 7497	L V SQ V	ARFAL	2 X X		2000		3
710/11/01	ORGANISM	Į.	Т	Т		Т	1	Г		
CANAL CALACTORDACE	CLOSTIUDIUM ACETOBUTYLICUM	26-137								
PBOAL CLUAB BELA-OALACIONES	CLOSTRIDIUM THERMOSULFUROCENES	161-161			1				i	!
PBGAL CLOTU BETA-CALACTUSIDASE	VI FROME DA PAPELIMONIAL	143-212						1		
DETA-GALACTOSIDASE	I ACTORACII FIIS DEL BRIJECKII	305-332							Ī	
PBGAL LACDE BETA-GALACTOSIDASE	STATES OF THE MODELLINE	116-215								
BETA-GALACTOSIDASE	SIRETIMOCCOS INCINCIO	100	139.206							
RETA-GALACTOSIDASE	SULFOLOBUS SOLP A LAKICUS	130.146								
RETA GALACTOSIDASE SMALL SUBUNIT	LEUCONOSTOC LACIES									
THE CALL FIRST AND ACTOSIDASE	SULFOLOBUS SOUFATARICUS		1	Ī	1	!		i		
SELL COSTA CE A	CLOSTRIDIUM THERMOCELLUM	22:380		1						
POCLA CLOTAL DETA-CLUCUSIONASE A	CLOSTRIDIUM THERMOCELLINI	259-286	23:409	24.20	62					
THERMOSTABLE BEIN-	TOUR COLD	461.194	\$36-563							
BETA-CLUCURONIDASE	EX NEW COLI	177								
SECTION ACTION TO THE PARTY ACT INCOSIDASE	AGROBACTEMUM SP	Т	***	210	718.765					
THE ACTION OF A	BUTYNUVIBRIO FIBRISOLVENS	_	701-165							
BELAGLUCOSUASE A		200					•	:		•
POTENTIAL DNA-INVER	MINIST WILLIAM IN THE PARTY OF	163.197								
	SIATILITY COLUMNICA	141.00					•			
	STAPHYLOCOCCUS AUREUS						-			
	BACILLUS SPIIAERICUS	8						Ī.		
FERNA BACOT ATTICONOMINATION OF THE PERSON O	BACILLUS SMIAENCUS	27.1-01								
	SECTION OF A COLL	130-157								
BIOTIN SYNTHETASE	DACH THE COURSELLY	144-171								
PRIOD BACCH DETHIOBIOTIN SYNTHASE	BACILLOS STANENCOS	11111	278.105				_			
1	BACILLUS CENEUS	95,55	16.70				L			
BEYA ! ACTAMASE ROS	HAEMOPHILUS INFLUENZAE									
BEI A CHANGE BE	BACILLUS CEREUS	16-67	277.107							
PRIAL BACCE BETA-LACIAMASE PACCONSON	DACH IN CO	19:67		, ,						
BETA-LACTAMASE PR	2007470	15.83	95-129	L		L		,		
PRI AT BACCE BETA-LACTAMASE PRECURSON, TYPE III	BACILLUS CEXEUS									
Т	PSEUDOMONAS AERUGINOSA	2								
PBLAC PSEAL BELACIAMENT SECTION TO THE	BACILLUS CEREUS	30-66 20-66	200-227							
PBLAD BACCE BETA-LACTAMANE PIECUASON, 111C.	BACTEROIDES PRAGILIS	33-49								
BETA-LACTAMASE PRECUISOR, 1 Tre !!	200100000000000000000000000000000000000	93.120	176-303	_						
PRI AC BACCE BETA-LACTAMASE PRECURSOR, TYPE I	BACILLUS CENEUS	1	86-111					_		
	BACELUS LICHENIFORMIS									L
BETA 1 APPANACE PRECIESOR	PROTEUS MIRABILIS	177:16								
SELV-CACION SELVING	PROTEUS VUICAUS	4-38	240-267							
BETA-LACIAMASE	CTOCOTOMY FE ALBUS G	4).70								
BETA-LACTAMASE PR	The state of the s	21.14	L							
PRI AD RIEPN BETA-LACTAMASE PRECURSOR	KLEBSIELLA FREUMONIA	16.31	90.126			L	L			
PENCOL MASE REPR	STAPHYLOCOCCUS AUKEUS					-		_		L
BETT : ACTANAGE PR	ESCHENICHIA COLI	8	707-667		1	1				L
SECTION AND A SE	ESCHENCHIA COLI	155-196								
BEINGALIAMOREI	MACHILUS LICHENIFORMIS	129-156	\$15-552							1
REGULATORY PROJE	ETABLIS ALMENS	13.114	132-161	234-261	281-312	503-519				
REGULATORY PROTE	SIAMILE CONTRACTOR OF THE PARTY	113.746								
BASIC MEMBRANE PR	I REPORTED THE PORT	27.75					L			
Т	BACILLUS SUBTILIS					-			L	L
٦.	PSEUDOMONAS PUTIDA			\downarrow	-	-		_		L
т	PSEUDOMONAS PUTIDA	2				1				
BENEFIC LA SIGNI	PSEUDOMONAS PUTIDA	179-213								\downarrow
_	THE VITTE OF CORDS AND IVALENS	157-237	242-290	311-355	391-425	340-373				
-	PERIODIONAS AFRUGINOSA	260-287	313-340							1
CARRIER PROTEIN	Persimonana Applicable	254-281	_	-		-				
PRIME PSEAE TRANSPORT PROTEIN BRAE	Paculomona Arabanasa	77.5		-			L			
BRAG PROTEIN	PSEUDUMONAS ACAGOIMOSA	710 444					-	L	L	
VITAMIN BIZ RECEPT			-		-	-				
VITAMIN BIS TRANSI		6	1	-	1	-			L	
O S S S S S S S S S S S S S S S S S S S	Г	174.203					-		l	1
	BONDETELLA BRONCIOSEPTICA									1
SON ELICISISM CONCRETE CONTRACTOR	BORDETELLA PERTUSSIS	116.143						1		1
E PERIPLASMIC PROTEIN BYOB TACCORDO	BONDETELLA PERTUSSIS	. 19-66	202-239						_	
PBVGC BORVE SENSOR PROTEIN BVGC	T	113-143	14:36	201.53	L					
IN VINULENCE BYGS PROTEIN PRECURSOR	T	113.140	616-729	Т	815-842	151-493	968-995	1159-1207		
DENT CHARD INDITITION NEUROTOXON TYPE A PRECURSO	CLOSTRUIUM BUTULIAUM		Т	Т	Т	T	ŀ	١	L	L

PCGENE	107117314	Prokaryatle Sequences	╗	П	_	Т			П		
THE CAPIE	POTENTIAL PROPERTY OF STATE OF PRESCHIEGO	CIOCHISM	7	J	Т	285	AREAS	48146	7454	AREAL	AREAS
Carried Carried	BOTOLINOM NEUK	CLOST RUILDING BOTTON CHIEF	Т		Т	Т	830-892				
200	BOTH BUT WEIN	CLOST MAINTENANCE CONTRACTOR CONT	T	076-076	21		747-147	90.00	1000		
	BOTTO SAIN MEIN	CLOSING BOILDING	T		20.75		114.048	6101-266	113-1149		
PBYT CLORO	ROTTH INC. METER	CLOSTREMENT BOTH BAR	40.00		66.60	200					
PCSSO MOCAE	CYTOCHRONG CSS	MICHOCYSTIC APPLICANCE	Т	,	616.74		7711-0001	0171-611		I	
PCADA BACTI	PROBABLE CADACT	BACILLUS FIRMUS	200	100.131	165.102	174.10K	(11.44)				
PCADA STAAU	ROBABLE CADMIL	STAPHYLOCOCCUS AUREUS	382.309	536-570		Т					
PCADC ECOLI	TRANSCUPTIONAL ACTIVATOR CADC	ESCHENCHIA COLI	× • • • • • • • • • • • • • • • • • • •	413-443							
PCATA YEAVE	I CAPSULE ANCHO	YERSINIA PESTIS	203-240	416-457	530-557	619.646					
PCAPA BACAN	CAPA PROTEIN	BACILLUS ANTHUACIS	108-138								
PCAPB BACAN	APB PROTEIN	BACELUS ANTHRACIS	36.70								
PCAPP ANAM	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANACYSTIS NIDULANS									
PCAPP ANASP	PHOSPHOENOLPYR	ANABAENA SP		157.184	687.728						
TAY CONT	PHOSPHOEMOCPYR	CORYNEBACTERUM GLUTHICUM	~ ~								
	PHOSPHOENOLPTRUVATE CAUBOXYLASE		200					-			
CARA BACSO	CARBAMOYL-FIOSPHATE SYNTIASE		24.319					•			
PCARE BACSU	CAUGAMOYL PHOSPHATE SYNTHASE		100.00								
200	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAI		₌								
TALE STAN	CHICACAMPHENICAL ACETAL TRANSPERASE	STAPHYLOCOCCUS AUREUS	-	=							
	CARCING IN MANCHESTER		1								
X X X X	CATECHOL 1,3-DIOXTGENASE	ACINETOBACTER CALCOACETICUS	Ş€								
באיא פארצו	TEXOXIDASE I CA I	BACALUS STEAKOTHERANOPHILUS	207								
TOTAL PROPERTY.	LAIALASE PUI	EXCHENICATA COLI	270 606								
AL VINE	CATAL ASS LINE	FULL LOCATION TO SELECT									
PCATE BOOK	CATAL AGE MAIL	ECONDITION ON I	Ť	103-000							
00 TO	CHORANDHENICOL ACETYLTRANSFERASE	CAMPYLOBACITER CO. 1									
	CHE ORANGEMICON	COSTRIBILATION							Ì		
	CHEORANDHENICOL	ESCHERICHIA COLI		1	1		Ì			Ì	
PCAT PROM	CHLORANDPIENICOL ACETYLTRANSFERASE	PROTEUS MIXABILIS		Ī		1			Ì		1
PCAT STAB	CHEORANDHENICOL ACETYL TRANSFERASE	STAPHYLOCOCCUS INTERNEDIUS	Т	1.							Ī
PCAT STRAD	CHLORAMPHENICO	STREPTOCOCCUS AGALACTIAE	Π	11:18			Ī		Ī		Ī
PCBINE COXBU	CAME PROTEIN	COXIELLA BURNETII	209.336								
KART THEN	CARBOXIPEPTIDASE Y PRECURSOR	THERMOACTINGAIYCES VULGARUS	48.35							T	Ī
NCA ECOL	THWA PUCLEOTIDY TRANSFERASE	ESCHENICHIA COLI	1079							T	
PCCACK SYND)	CO2 CONC MECH PROTEIN CCND	SYMECHOCOCCUS SP		П							
S S S S S S S S S S S S S S S S S S S	COS CONC MECH PR	SYMECHOCOCCUS SP		271:111	445.486						
200	TO OFFICE TOPES	THE UNOANAEROBACTER ETITANOLICUS	П								
YOU DO	CYCLOMAL IODEXT GLUCANOTRANS PRECURSOR	BACILLUS MACERANS	_	7							
	TCLOMALIODES!	BACILLUS PIACEKANS	7	936-466	615.642						
	CYCLOGAT TOREST CLUCANOTALNE PRECINSOR		Т	7	20.00						
	TYCH DAIN TODE Y			27.7	294-647						
PODG! BACK	TYCLOMAL TODEXT		ī	177.71							
MODEL BACKS	CYCLOMAL TODEXT		Т	т		1					
MOOT BACS	CYCLOMAL TODEXT		L	111.463	1777					1	
PCDGT BACSP	CYCLOMALTODEXT		Т	Т	615.642	Ī			Ť	1	
PCDOT BACSS	CYCLOMAL TODEXT		Т	Т	394-631	T					
PCDOT BACST	CYCLOMAL TODEXT	BACILLUS STEAROTHERMOPHILUS	216-626			T					
PCDOT KLEPY	-		212.239	T	T			T	Ť	Ť	
PCEAL ECOLI		ESCHERICHIA COLI	15.3	215.326	Ī	Ī	Ī	Ī	1	T	
PCEAL SHISO	COLICINE 1 PROTEIN		Т	Т	413.440	T			1	T	
MEAN ECOLI	COLICIN E2	ESCIENCIA COLI	334-368			Ī	Ī				
	COLICINED		334-368								
MEAN ECOL	COLICINES	ESCHENICHIA COLI	134-368								
752	LOTTON B		25.34	1	1						\prod

17.1333	107.170.4	Sequenting	A 1 4 1 4 4	A KELL L	AMIA JAMIA	_				:	i
T	7,51044		1	-	Т	$\overline{}$				i	١
THE LANGE	CALLED TO THE PARTY OF THE PART		+	+			<u> </u>				
PCEAD ECOL	COLICINO		┪		1		1	-			
	COLICINA		7	3		1	<u> </u>	1	i	i	į
CEAN ECOLI	COLICIAN	CNDII	220-250			1	1	t	-	Ī	
KEA CITTA		LIGERUS	330-307	╗	┪	1	+	+		T	
KEID STROL	SOPENICILLIN N EPIMEMASE		50-09			20:43	1		1	Ī	
POEM ECOL	COLICINIA PROTEIN		68.69	185.282	378-412 415	415.452	1		İ	ĺ	
1002			9.69				4	1	 	1	
20.00	INTERMENTAL PRANSFERASE	LINUM		T					-		
1	THE THE PERSON AND THE PARKETS OF THE PARKETS OF		7	7				 	l		
			٦	80		+	t		l		
						+	+	t	Ť		
	_		180-207	144.271		_	1		1		
Г	CHAIR PAGRILAL SUBUNIT E	•	10.53					1			١
	14 KD CHAPERONIN	ACYNTHOSIPHON PISURI STRIBIUTIC BACTERS		Ť	-	-	-				
	A P. CLAPEBORDA	┰		T			-	-			İ
	TOPO GOVERNO	_		1			-	•			
Ollo Oc.18	I THE PARTY OF THE				1	+		T			
DO3 OHO	IO KD CHAPEKURIA		68-95		1	1	\dagger	1			
PCHIS HAEDU	10 KD CHAPERUNIN		57.84				1	Ì	t		
PCHIN LEGAL	10 KD CHAPERONIN	KIUSIII	65-93		1		+	†	İ		
STORIO BLOCK	10 KD CHAPERONIN	134	16.99					1	1		
PCHIO TIGERS	IN KD CHAPERONIN	TIC DACTERIU	73177					1	1		
300	AN KIN CHAPERONIN	ווי מעניביים	T	119.170	425.466					~	
	A TO CUANCE CAME	T	1	T			-				
DIAM AGAIN	OR NO CONTRACTOR	1	┪		1						
CHES AMORS	60 KD CHACEAGAIN		┪	137.30	1	1	1				
INCHED BYCEN	60 KD CHAPEKURIN	ROBERT IA BURGOON'EN	٦	199.368	+		1	Ť	İ		
DENOS OFFICE	60 KD CHAPERONIN	Tan Mana VIII	117.144	339.366		1		j	1		1
POTES BRUAB	60 KD CHAPERONIN	SAUCES AND SECTION AFF	15.3		1		1	1	1		
NA DO ONLO	60 KD CHAPERONTN	COLONIA TO ACTIONA TIC	1		<u>-</u>			1			
TI DO ONLO	IN KD CHAPERONIN	Charles Indiana	100-127		ľ		_				
MUDO OTTO		CHACMATION VINCOUR	234.332	117.364	455.482						╛
870 C STILL		CLUST MUSICAL COOL I C. C.	117.168	413-444	-						
	AN IN CHAPERONDY	CLOSTRUDIUM PERU RUNCERS	100.001	144.162							
		COXDELLA BURNETII	***	417.444							
	MINO CONTRACTOR OF THE PARTY OF	HAEMOPHILUS DUCKEY!	30.466					Ī			
OHO INEDO	TO ICO CANCELLIA	LEGIONELLA MICDADEI	299.333					Ī			L
NOTE OF CASE		I FGHONELLA PNEUMOPHILA	296-332	452-479		1	1	1			L
POHO LEGIN		A CONTRACTOR IN A LIBRATE	125-152	236-263	337.364	-			1		1
TOWN OWNER	~	MTCUBAC I EMUM LETIME	135.152	117.164							
	•	MYCOBACTEROM TOBERCOCOSIS & CO.	110.166			-					
		PSEUDOMONAS AERUGINUSA		111	377.757						
300	_	ILHIZOBIUM LEGUMENOSARUM		346.316	30.00		T				L
	_	NCKETTSIA TSUTSUGAMUSHI	103-130	21.13	200	1	T	T			L
DCH60 TUCHS	_	SYNECHOCOCCUS SP	301-333	337.310		1	1				
PCHES SYND		CYMECHOCYSTIS SP	338-365	455.489							1
CTARS SALDS	_	STREAMPHILL RACTERITAL PS. 3	137.364								1
(43th 640)	1	STATES OF ALL BIR C	16-148	337.364							1
A CA	60 KD CHAPERONIN 2	SI KEY TOM I CES ALL BOS O	21.48	172.799							1
AN AND	_	VIBIO HARVETI	207	19.00							
	-	BACTLUS SUBITLIS	700 700								
	CARACTA XIS PROTED	ESCHEMICHIA COLI									L
	CHEST AND PROTEIN CHEA	SALMONELLA TYPHINGRUM	104-10				Ī				L
DEA SALIT	TOTA SO STATE	BACALUS SUBTAJS	134-131			1	Ì				
OFF TAC	CHEMOLOGICAL STATE OF THE PROPERTY	ESCHEMICHIA COLI	611.3			İ	1				
PCHEW ECOL	MUNICIPAL OF CALL	SALMONELLA TYPHINGRUM	<u>=</u>			Ì					ļ
PCIEW SALT		E CONTRICTION COLL	57-78 73-48								\downarrow
POLEY ECOL		EAT MONEET A TYPHINITINIAN	13-49								1
POPEY SALTY	CHEMOTAXES PROTEI	SAA ECCES OF FECA	100	× 50.50							1
POIG BACCI	_	STANDARD CO.	345.372	L							1
5	Т	ALI LEGINORAS SI			ļ						
		,		_	-						

The contract between the con	PCGENE	107.178.4	Probaryolk Sequences				:				•
Internate Description Seccing Color Section Sect	FILE RAME	PROTEIN	ONGANISM	J	Т	<u> </u>	AMA LAN		_	4	48.4
INTERNATE OF STREETH	PCHID BACCI	CHITINASE D'PRECURSOR	BACILLUS CIRCULANS	T	9.716	+		+			
INTINATES IN PECUNON STATISTICAL PROPERTY 19-10-10-10-10-10-10-10-10-10-10-10-10-10-	PCHIT SACEA	CHITINASE	SACCHAROPOL YSPORA EXTINAEA	411.26	+	\dagger	1	+			
STATE STAT	אונג דוניר	CHITINASE 63 PRECURS	SIRETIONICES FLICATOS	1000	+	\dagger					
The Property of	PCHOAD BACSU	CHOILSMATE MUTASE	DACILLOS SOBJECTS	101.100	+	t	1		-	† !	!
International Control of Contro	CHOO BICE	CHOLES IEACL UNIDASE PRECURSOR	VIBER CITY EAST	70.104		+					
United State Unit	CHIA VIKE	APPLEAN EN IEROIGAIN, A CHAIN PRECONSON	AGROBACTERING TARES ACIENS	Ī	1.208	\mid		-			L
THOO VISION HOUTENAY CITIODACTES REENDING 144-119	PUNK ACETI	BECEPTOR PROTEIN CAVE PRECIASOR	AGROBACTERUMITUAGEACIENS	£	-	-	-				
International Processor International Pr	PCIN CHE	CITROL YSIN PROTEIN 1	CITROBACTER FREUNDII	433-462	-	\mid					L
TATULE STREET, TATULE STREET, TATULE STREET,	PCIRA ECOL	COLICINI RECEPTOR PR	ESCHEALCHIA COLI	146.173							
Interference Inte	MICH BACK!		BACQLUS SUBTILIS	118.405	-				_		
ITALE SOUGHA TYPOOT SALMONELLA TYPHINDUNAL 194-11	NATION VALUE	CITRATE SYNTHASE	ACINETOBACTER ANITRATUNI	143.170							
11/16/16/16/16/16/16/16/16/16/16/16/16/1	MICK BACCO	CITATE SYNTHASE	BACILLUS COAGULANS	24.51		-					
INTERFECTORIAL STATE STANDWINELLY DIVIDUAL 194-21	AL IN CALL	12	SALMONELLA TYPHINIURIUM	154.181	-	-					
SALANGELLA PULDUAN SALANGE	769 14 74104	CITEATE COMMA EVAPORT	KLEBSIELLA PNEUNONIAI:	194-321		-					!
INTATE_SOOUGH SYAFON SALAONELLA FULLORUM 19.18		CITATE CONING SYMPORT	SALAKONELLA DUDILIN	194.221		-					
THE CHORGE IN THE CONTRIBUTE THE CHORGE IN THE CHORGE		CITE ATE COOKING CONTROL	SALMONELLA PLILL ORINA	194.221		\dagger		-			
THE PROPREMENTARY PROTEIN STOTE KICHIA COL	111111111111111111111111111111111111111	CHI GOOGATECHOL 13 DIOXYCENASE	PSEUDOMONAS PUTIDA	13.36		-			-		L
TANIN LENGTH DETERMINANT PROTEIN 19:217 139:217	1000		ESCHERICHIA COLI	133.167	<u> </u>	 	<u> </u>				
STATE STATE STATE STATE STATE STATE	C DI ECOLI	CHAIN LENGTH DETERMINANT PROTEIN	ESCHEDICHIA COLI	T	20.237	-	_				L
CLOSTEDIA/ARI PRECINSOR CLOSTEDIOM HISTOLYTICUM 105-18 407-15;1	PCLD SALTY	CHAIN LENGTH DETERMINANT PROTEIN	SALMONELLA TYPHINIUMUNI	Г	\$1-212						
17.7 STROGROUP CONTENT 191-901	PCLOS CLOM	ALPHA-CLOSTRUPAIN PRECURSOR	CLOSTRIDIUM HISTOLYTICUM		97.534						
The PRODUCE OF PROTECT In Fig. 1997 The PRODUCE OF PROTECT In Fig. 1997 The PRODUCE OF PROTECT In Fig. 1997 The PROTECT The PRODUCE OF PROTECT In Fig. 1997 The PROTECT OF PROTECT In Fi	TOO Y TO	ATP-BINDING SUBUNIT CLPA	ESCHENCHIA COLI	655.695							
17.24 PARCIC OF ROTE PACTEROPIES NOOOSUS 118-131 442-149 151-159 17.24 ROMOLOG PROTEIN ESCHENCIAL COLI 118-131 118-131 118-131 17.24 ROMOLOG PROTEIN AZOTOGACITER VIDELANDII 118-131 118-131 118-131 17.24 ROMOLOG PROTEIN ESCHENCIAL COLI 100-131 118-131 118-131 17.24 ROMOLOG PROTEIN ESCHENCIAL COLI 100-131 118-1	PCLPA RHOBIL	CLPA HOMOLOG PROTI	RHODOPSEUDOMONAS BLASTICA	439.406							
115.749 115.740 115.749 115.	PCLPB BACNO	CLPB HOMOLOG PROTE	BACTEROIDES MODOSUS	П		1.595					
13-151 1	PCLPS ECOL	CLP8 PROTEIN	ESCHENICHIA COLI		63.590						
135-127 135-	PCLPX AZOVI	CLPX HOMOLOG PROTE	AZOTOBACTÉR VINELANDII		12-350	H					
15.176 1	PCLPX ECOL	ATP-BRIDGHG SUBUNIT CLPX	ESCHERICHIA COLI	135-282							
CONTINUE DEALOGALISE ESCHERICIAL COL. 100-139 100-139	NONI ECOLI	T.T.CYCLICANIC T.PHOSPHODIESTERASE PRECURS		30.77							
CONCRETENCE MOTENT BACELLUS SUBTILIS 104-131 18-210 CONCRETENCE REGILATORY PROTEIN BACELLUS SUBTILIS 15-130 CONCRETE RESISTANCE ROTEN B PLECUKSON STEUDOMONAS SYUNGLE 15-130 SOPA FROTEN 15-10 15-10 AGRELLUS SUBTILIS 15-10 AGRELLUS SUBTILIS 12-22 AGRELLUS SUBTILIS 12-22 AGRELLUS SUBTILIS 12-22 PODE COAT PROTEIN E BACELLUS SUBTILIS 13-40 CYTOCHOME CONDASE POLYPETIDE I BACELLUS SUBTILIS 13-40 CYTOCHOME CONDASE POLYPETIDE I BACELLUS SUBTILIS 19-50 CYTOCHOME CONDASE POLYPETIDE I BACELLUS SUBTILIS 19-43 CYTOCHOME CONDASE POLYPETIDE I BACELLUS SUBTILIS 19-43 CYTOCHOME CONDASE POLYPETIDE I BACELLUS SUBTILIS 19-43 CYTOCHOME CONDASE POLYPETIDE I BACELLUS SUBTILIS 19-63 CALVANDE ROTER BACELLUS SUBTILIS 19-76 CALVANDE ROTER BACELLUS SUBTILIS 19-78 CYTOCHOME PASI DEC STRENOMYLYTICANOTES S 19-13 CYTOCHOME PASI DEC <td>PCODA ECOLI</td> <td>CYTOSINE DEAMINASE</td> <td></td> <td>1</td> <td></td> <td>+</td> <td></td> <td></td> <td>_</td> <td></td> <td></td>	PCODA ECOLI	CYTOSINE DEAMINASE		1		+			_		
OPPER RECURS OF A PROTEIN BY ROTE IN BACKLUS SUBTELS 194-197 OPPER REAST RACE ROTEIN B PAECINSON 15 LAND ROTEIN B PAECINSON 15 LAND ROTEIN B LAND ROTEIN COLL 17 LAND ROTEIN B LAND ROTEIN COLL 17 LAND ROTEIN B LAND RO	PCOM! BACSU	A COMPETENCE PROTEIN I		7	10.70	+			-		
STATE STAT	PCOMO BACSU	CONDETENCE NEGULA	BACALUS SUBTILIS	27-57	1	+		+	1		
VALOREGICANCE AND INSTITUTE VALOREGICAN VALOREGICAN COLLING	POOPS STAND	OP-6 PROTEIN	SIAMILUCUCUS AUREUS	100	+	+	-	+	-		
The color of the	PCOP PSESA	COPPER MESIS I APPLE P	ESCHEDICHIA COLL	14.161	+	1	<u> </u>	-			
FOOLE COAT PROTEINE	POOR ECUL	MACINESIUM COBALI	SALMONELLA TYPHINDRUM	134-161							ļ
CTOCHGOME CONDASE POLYPETIDE BIAADYNGZOBIDM IAPONICUM 180-407	TO THE PACE OF	CPORF COAT PROTEIN	BACILLUS SUBTILIS	42.92	-						
PAMCICOLOGE CONTIANS POLYPETIDE PAMCICCUS DEMITIWICANS 111-110	PCOXI BRAJA	CYTOCHROME COXIDA	BRADYTHIZOBIUM JAPONICUM	380-407							
VANDORAGE COURTAIN PARTIES SPINAR S	PCOXI_PARDE	CYTOCHROME COXIDA	PATACOCCUS DEMITMFICANS	383.410							
SACELLUS FUNDS SACELLUS FUNDS SACELLUS SUBTILIS SACELLUS SUBTILIS SACELLUS FUNDS SACELLUS SUBTILIS SACELUS SUBTILIS SACELUS SUBTILIS SACELUS SUBTILIS SACELUS SUBTILIS	PCOXI MOSH	сутосноване с охара	RHODOBACTER SPILAEROIDES	38.423							
NEISSELLY FACTOR BACELLUS SUBTILIS 19-76	PCOXX BACFI	OXIDASE ASSEMBLY FA	BACALUS FIRMUS	16-63	+	1					
NESSELA GONDALOGEE 12-79 163-309 163-3	PCOXX BACSU	OXIDASE ASSEMBLY FACTOR	BACILLUS SUBTILIS	7		1	-	4			
MANOSE - INTOCRIMA	PCPPB NEICO	CRYPTIC PLASAMD PROTEIN B	NEISSERIA GONORINIOEAE	7	62:50 62:50	1	-	+	_		
PRODUCE PLANT PROPERTY PROPETTY PROPERTY PROPETTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROP	PCPSB ECOLI	MANNOSE: I-PHOSPHA	ESCREMENTA COUL	917.00		1			1		
Trocheme Process Trocheme	PCSB SALTY	MANNOSE-I-PHOSPHA	SALMONELLA I TRUMONOMI ESCHERICHA COLI	346.318	+	\dagger	+		1		
DEGYTERTITIONOLDE B (DEB) HYDROXYLASE SACCHANOPOLYSFORA ERYTHUAEA 111-180	ביים	CATOO TO A TRUIT OF A 10 100	CAR EPICALON CONTRACTOR			1	1				
Triccincincincincincincincincincincincinci	COXC SINS	PLOCHECIME TAN IS	SACCHABORON VANORA FRATHRAFA	36	\dagger	1	+		1		\downarrow
ANALES A	LAND SALEA	DEDATEATING OF PAIN IN	SACRETIC CITE TO 15	1100		1		-	-		
NOTE CASE NOTE NO	PCYON BACSO	POBABLE CYTOCHO	ANABAENA SP	98-133		†					
17 KD CRYSTAL FROTEIN BACEL LUS THURANGIENSIS 153-187 9 KD INSECTICIDAL TOXIN BACEL LUS SHIAFBICUS 276-304 19 KD INSECTICIDAL TOXIN BACEL LUS SHIAFBICUS 276-304 10 KD INSECTICIDAL TOXIN BACEL LUS SHIAFBICUS 276-304 10 KD INSECTICIDAL TOXIN BACEL LUS THURANGIENSIS 20-234 20-234 230-24 20-234 230-24 20-234 230-24 20-234 230-2	יייייייייייייייייייייייייייייייייייייי	SVD COVETAL DROTE	BACK LUS TARRINGIENSIS	181-181	+	t	+	+	-		ļ
19 KD INSECTICIDAL TOXIN BACIL LIS SPIAFBICUS 176-108 19 KD INSECTICIDAL TOXIN BACIL LIS SPIAFBICUS 216-108 10 KD INSECTICIDAL TOXIN BACIL LIS SPIAFBICUS 216-108 10 KD INSECTICIDAL TOXIN BACIL LIS THURMGIENSIS 20-234 20-234 230-234 25 KD INSECTICIDAL PROFEEN 20-234 25 KD INSECTICIDAL PROFEEN 20-234 25 KD INSECTICIDAL PROFEEN 20-234 25 KD INSECTICIDAL PROFEEN 21-34 25 KD INSECTICID	PACE SACE	STATE PROTEIN	BACO LIS TRURINGIENSIS	133-117	1	T		+			1
19 KD INSECTICIDAL TOKIN RACII LUS SPILAERICUS 176-306 19 KD INSECTICIDAL TOKIN RACII LUS SPILAERICUS 176-306 19 KD CRYSTAL PROTEIN DACII LUS THUADACIENSIS 101-334 133-379 15 KD CRYSTAL PROTEIN RACII LUS THUADACIENSIS 17-46 135-359	PLACE BACIN	LOKE DISCONDING	BACII LUS SPHAERICUS	276.308	-	t	+	-	1		
10 KD INSTCHICINAL TONIN 84CH LUS SPHAERICUS 176-108 10 KD CRYSTAL PROTEIN 0ACHLUS THUADACHENSIS 101-134 133-379 15 KD CRYSTAL PROTEIN RACHLUS THUADACHENSIS 17-46 113-159	PUBLIS BACKE	N. N.	BACHIUS SPILAFRICUS	176.308					L	ļ.	
TO END CRYSTAL PROTEIN DACILLUS THORUNGIENSIS 101-234 231-279 15 END CRYSTAL PROTEIN RACILLUS THORUNGIENSIS. 17-14 [125-159	PCR43 BACSH	41 9 KD INSTICTIONAL TOWN	BACITE US SPHAENICUS	П	П						
75 KD CRYSTAL PROTEIN PACIL LUS THUMUGIENSIS. 121-16 135-159	PCR70 BACTD	70 KD CRYSTAL PROTEIN	DACILLUS TINURINGIENSIS	П	П	9-463					
	PCR 70 BACTO		RACILLUS THURUNGIENSIS.		П	7-464		H	Ц		

-COMP	10111114	Freharyothe Nequences	•		AREAD	AREAS	ARIAS	SHAS	AMA	AKKA	3
THE NAME	PROTEIN	PRCAMISM	87.28	12.00	т						
LUV S	TO KD CRYSTAL PROTEIN	BACILLUS TITUTURCIENSIS	т	Т	\$52.615						
A VICTOR	WED CRYSTAL PROTEIN	BACILLUS THUMINGIENSIS	T	Т							
	22 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	T	Т	117.191						
AT VE	WED CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	L	T							
PCR77 RACTI	77 KD CRYSTAL PROTEIN	BACILLUS TITURURGIENSIS	01110								
TEC BOOK	SENSOR PROTEIN CREC	ESCHENCHIA COLI									
1003	DOJER MEMBRANE PROTEIN CRED	ESCHENICHIA COM		137,154							
רטה בססרו	CATABOLITE GENE ACTIVATOR	ESCHENCHIA COLI A									
Ł		SHIGELLA PLEANER	5	23.154							
PCR. SALTY	CATABOLITE GENE ACTIVATOR	SALMONELLA TYMINURIUM									
		KLEBSIELLA AEROGENES							L		
PCD TI SEVONE	PHYTOENE DEHYDROGENASE	ERWINIA HERBICOLA	717.00								
TOTAL STATE	MAYTOFNE DEMYDROGENASE	RHODOBACTER CAPSULATUS	34.410	47.	100					L	L
12011	CRITIMENTED	RHGDOBACTER CAPSULATUS	201-16			į	1	!		:	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	113 KD CRYSTAL PROTEIN	NACILLUS TINIRINGIENSIS	1212		2001	İ	!				
NAME OF THE PARTY	IN KO CRYSTAL PROTEIN	BACILLUS THUMINGIENSIS	100		2001-1001						L
CATS DACIE	THE CONCEAN PROTEIN	BACILLUS THURMGIENSIS	736-770	2	130						L
מעוב	CONDITION OF A PROPERTY	BACILLUS TIIUMMGIENSIS	252	2	201.01		1		L		
PERTS BACT	TO KE CENTER PROTEIN	BACILLUS THURINGIENSIS	111:11	76.60	201-102						L
PARTS BACIN	SACTOR VETAL PROTEIN	BACILLUS THURINGIENSIS	136-170	2			:	<u>:</u>	:	-	_
CATS BACIS	TO CONTACT PROTEIN	BACILLUS THURINGIENNIS	100	7		İ	i				L
CAYL BACIA	STATE OF STA	BACILLUS THURINGIENSIS	765.77	2				1			
PCKT BACIE	TO CALCALL PROJECT	BACILLUS THURINGIENSIS	117-231	334-314	101-10	, () . mg/			ļ		
PCRYT BACT!	IJUKU CRISIAL FROIEIN	BACK LUS THUNDNGIENSIS	ויגינון	29. 19.			1				1
CAYT BACTK	DAKE CATSIAL PROTEIN	BACILLUS THUMNGIENSIS	136.770	88	1				1		1
CRYU BACTA	IN CRESIAL PROJECT	BACILLUS THURINGIENSIS	217-231	2.5	174-401						1
אל אליי	INCRESIAL PROJECT	BACILLUS THURNGIENSIS	138.772	166.193	1034-101					\downarrow	1
CRYU BACTK	K 131 KO CATSTAL TROTEIN	BACILLUS THUNUNGIENSIS	117.711	165.892	1053-1030				1		1
PCRYV BACTA	IN TO CATE IN THE	BACILLUS THURINGIENSIS	1013		3			1		1	1
CATV BACII	TO THE CALL THE PROPERTY	BACILLUS THURNGIENSIS	136-370	180.0				1		1	-
CAYV META	TIMEN CONTAIN PROTEIN	BACILLUS THUMNGIENSIS	4				1				
TALK BACE	TOTAL PROTEIN	BACILLUS THUNINGIENSIS	MOB-650	8			1 00.1			ļ	L
CATA BALL	THE KIN CHASTAL PROT	BACILLUS THURMGIENSIS			3			1			ļ
TALL BALL	COLUMN CYNTHESIS 63	ESCHERUCHAA COLI	A0-7-						ļ	-	Ļ
	CS1 PILL SYNCHESIS 41	ESCHENICHIA COLI			7	1	1	-	 -		Ļ
	CEL PRI SYNTHESIS 13 KD PROTEIN	ESCHENCHIA COLI				1	1				-
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CELL SIMPACE GLYCOPROTEIN PRECURSOR	HALOBACTERIUM HALOBIUM			1		-				-
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	CELL SIMPACE GLYCOPHOTEEN PRECURSOR	HALOBACTEMUM VOLCANII	2			1	-		ļ		-
TO LOTTE	1	METHANOTHERNUS FERVIOUS					1	ļ	-		L
319	CELL SURFACE GLYCO	NETHANOTIE LATUS SOCIABILIS			1	-	-			L	L
1000		ESCHENCHIA COLI		1							_
A CLOSE	COA-TRANSFERASE SU	CLOSTRIDIUM ACETOBUTY LICEN	14.30		-	1	-			L	
NOD LILLY	COA. TRANSFERASE SU	CLOSTUDION ACE TOBUTALICON		1	-	-		L			
PCTRB NEDGE		NEISSEAN NEWWORLDIS		134.151	69	152.715	-				
PCTX PSEAR	CYTOTOXIN PRECUR	PSEUDOMORAS ACADOMOSA	3	16).219							
PCVAA ECOL	COLLICTIV V SECILE TION	ESCRENCIA COLI	1			L			L		Ц
KVAS ECOL		ESCRENCIA COL	197.234		1010-104	-					
PCWPM BACBR	MEDDIE CETT WALL	BACKLUS BACK 13	9:7	Т	247.988						
PCWPO BACER	A OUTER CELL WALL PROTEIN PRECURSOR	BACILLUS BACATIS	2.3	633.639	т		-				
PCYAN BORD	E ADENTLATE CYCLASE PRECURSOR	SCHOOL LAND TO STATE OF THE STA	343.387	393.630							4
KYAA YEU	A ADEMIATE CYCLASE	SOBRETEI A PERTICAL	241.368		_						
KYAB BORP	E CYAB PROTEIN	PONDETELL A PERTUSSIS	178.212								4
PCYAD BONDE	E CYAD PROTED	BONDETELLA PERTUSSIS	113.340								+
KYAE BORDE	E CYAE PROTEIN	NHODOBACTER CAPSULATUS	18-65			-		4	+	4	+
AND MOCA	CTIOCHACHE B	ESCHEDUCHIA COLI	3.30	182.409				4			4

ANJUJA	100000	Park agreed of Commerce	-	ľ		I	Ì			ľ	
PILENAME			AREAI	AREAL	AREAS	ARFAC	ARTAS	AREA CAREA	7	AWVAR	4864.
CYMO ACISP			Т	Т	Т	Т	7	Ţ	7-	Т	
PCYNT SYNP?	CARBONIC AMIYDR		136.200	Ī		İ	İ	Ī	İ	İ	
PCYNX ECOLI	CYNX PROTEIN	ESCHENCHIA COLI	5).80			Ī	Ī			Ť	-
PCYOB ECOLI	CYTOCHRONGE OUR	ESCHENCHIA COLI	===						İ		
PCYPH SYNP?		SYNECHOCOCCUS SP	107-141								
MCYSA ECOLI		ESCHENCHIA COLI	10.13								
CYSE ECOCI	CYS REGULON TRANSCRIPTIONAL ACTIVATOR	ESCHENCIA COBI	.30								
A PARTIE	_	SALMONELLA TYPHINIUNI	2			j					
200	SEKINE ACETYL IN	ESCHEMCHIA COLI	164-191				1				
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	-	HINDRON	2.2								
7 ECOL	SIROPEM STYTHASE		405-432					~			
200	SUCREM STATIONSE	HAIURIUM	405-412		1	1	1				
1	SULTAIL AUGUILA		- A	1	1				j		
100	SOLANIE TEMMEASE W TRUILIN	SAME LIGHT LOLI	27:102	1		Ì	1			7	
THE RELATIONS	CATION ESTITIVE OF THE COURT OF THE		Т			1				1	
	ATKIN FEET LIX CV		207:107	T	104-301	1		1		1	
POACE BACSU	PENICEL IN-BODONG PROTEIN S- PRECURSOR	BACILLIS SIMILIS	101.03	Ì	\dagger	\dagger	Ī		1	1	
PDADA ECOLI	S-ANDWO ACID DEK	ESCHERICHIA COLI	127.154	Ī		İ			1	1	Ī
POACA ALTHA	ANOH DIKED DAL	LOPLANKTIS	11:11	T	\dagger	T	T			1	
POLICE ECOLI	DANCE PROTEIN		Т	149.110	+	T	T	T		†	
PDAPA ECOL	DONYDRODDICOLIN		Τ	137.184	\dagger	T		Ī	T	T	
PDATI BACSU	NA-PROTEDICYS	\$	Γ			T		Ī		T	
PDBHA ECOLI	HA-BINDONG PROT	ESCHENICHIA COLI	13:39	Ī						T	
PDBH CLOPA	NA-BRIDDING PROT	TEUNANUNI	13:53				T				
PDCAM ECOL	ECAUDOXYLASE P		146-173			l					
PDCDA CORGL D	KAMENOPPOELATE	CUM	134-161								
POCOA PSEAE	DIANDAOPONELATE DECANDOXYLASE	RUGINOSA	17.84								
DOE: ECOL	GLUTAMATIE DECAI		4-31								
POCHS ENTAE	HESTIDINE DECANDOXYLASE	ÆS			,						
	THOMAS RELEACE THE THE DECAMENTAL ASE	MEBSIELLA PLANTICOLA		1		1	1				
TOTAL COLOR	DEFETTION THE ANGEOGY PROTEIN DOLLD			1		1	1				
PDCLY HAPAI	LYSINE DECARBOXYLASE		111	\dagger	1	T	1		1	1	T
POCOA KLEPN	OXALOACETATE DECARBOXYI ASE ALPHA CHAIN	METANOMAE	Τ	147.166	+	T	†			1	I
PDCOA SALTY	OXALOACETATE DECAMBOXYLASE ALPHA CHAIN		Т	342.369	\dagger	1	\dagger	T	†	†	T
PDCOB SALTY	OXALOACETATE DECARBOXYLASE BETA CHAIN		Т			\dagger	T	T	T	\dagger	
PDCTD NAME	TRANSPORT SENSOR PROTEIN DCTB	OSARUM	111411							1	
LOCUS KHOWE	TRANSPORT SENSOR PROTEIN DCTB	211	┑								
מאפ נינסת	ATP-DEPENDENT KNA HELICASE DEAD		╗	£							
TOTAL VIEW	ATP-DEPENDENT IN A PELICASE DEAD	KLEBSIELLA PREUMONIAE	T	29.546	1	1					
TOTAL POPUL				97.	-		1		1		
SOUN CHECK			Τ.	T	127.724	1	1	1	1	1	
PDEOC ECOLI	DEOXYXIBOSE-PHOSPHATE ALDOLASE	170	19.5	T	\dagger	1	1			1	
PDHAL PSECUL	ALDEHYDE DEHYDROGENASE	EOVORANS	=		I	1			Ì	1	
PDHAS BACSU			1 × ×	T	\mid	T	T	T	T	\dagger	Ī
PDHAS CORGL		M GLUTAIICUM	11.70	12-339		T	T		T	T	Ī
rollus Ecolu	ASPARTATE SEMIALDEHYDE DEHYDROGENASE		119-156								T
PDHAS VIBCH			309-336						T		Ī
PDHA BACSH			149-176								
PDHA BACST	ALANDAE DEHYDRO	MOPHILUS	94-121			Ī					
104E1 CLOO	NAD-SPECIFIC GLUTAMATE DESTYDROGENASE	Т	\neg								
POET PEAS	DISPECTIC GLUTAMATE DEHYDRUGENASE	FLY TOS TREP TOCOCCUS ASACCHAROLYTICUS	=	35.310					Ė		
DIO POLICE	HADP-SPECIFIC GLU			***	1	1	1				
PDHGA ACICA	GLUCOSE DEHYDROGENASE.A	ACINETOBACTER CALCOACETICUS	Ŧ	11.00		1	1		1	1	
					1	1	1	1	1	1	7

12.00	103013004	Preharyelit Sequencei	V V V V V	ABFAL	AREA 3	AHEA 4	AMEA S	ARTA 6	1		
200	PECTAIN		Т	Т	т	Г					
ALCO COLOR	CHARLE LINE HYDROGENASE B	ENUM									
NG BACKE	CLUCOSE PENYINGGEN		10-40		T	Ì					
		OLACEORUBER	61-105								
PDICK! STRVN	KETOACYL KEDUL I ASE		192-219								
	LEUCINE DEJIYDROGEN	•	117.344								
PDIEDO AGATA	D-LYSOPINE DEHYDROGENASE	SN:	133-117	90-234							
POPUL METEX	METHANOL DEHYDROGENASE SUBUNIT I PARC		Г	190.224							
DAY METOR	METHANOL DENYDROGENASE SUBUNIT I PREC		T								
PANALI BARDE	METHANOL DEHYDROGENASE SUBUNIT I PAEC	Sperimentary		I							
	NAME AND POST OF THE PARTY OF T										L
PDIONA BACS	MADH DENI CANOCIANOR							Ţ			L
PA ECOL	NADH DEHYDROGENA		73-107	406-433							
PHON BACSU	HOMOSEAINE DEMIDA	C. HTANCIAL	105.132								
1000	WOMANGE DESTUDENCE DESTUDENCE										
The state of the s	VIEW PARTY IN THE PARTY	CUS									
DHON BACK	TENTAL ANIME DEN		482-512								
POHSA ECOLI	SUCC DEHYDROGENASI		16-113	130-161							
PHILE ANALY		ANABAEMA LILINDRICA	9				L				
	SALING CENACE CHAIL SUBUNIT	SYNECHOCOCCUS SP	201.00								L
POHISS STAFF	OLUGE RI DANCE	METHYLOTROPHUS METHYLOPHILUS	433-400								L
POHTM METHE	TUNE INTERNATE DESIGNATION OF THE PARTY OF T		514-611								1
ING ECOL	ROBABLE ATP-DEPEN	D. C. D. C.	24.83	114.141							1
STATE OF THE PARTY	DIVISION INSTINCTION PROTEIN		06.					_	_		
	PRINCIPOLITICA MIDE DESTYDROGENASE			760					L		
	THE PROPERTY OF PR	AZOTOBACTER VINELANDII	î	0/7-0/7							L
TDH AZOVI	CIPOANIUE DENIENCE CO.	PACH I US STEAROTHERMOPHILUS	12-124								
PDLDH BACST	T LEGAMIDE DEHTDROVERASE COPO (E)	BACRITIC CIRTILIS	13:109								
PIN IN INCSU	L'IPOAMIDE DEHYDROGENASE CONO (E.)		101.13		L			į			
1 100	DINYTHE OF THE DESTROY OF THE PROPERTY OF THE	ESCHENCHIA COLI		1							
5	THE PROPERTY OF THE PARTY OF TH	PSEUDOMONAS FLUORESCENS			1						L
POLDH PSET	DIRTURGLOOMING	PCELITIONANAS PUTIDA	63.90								
POWON PSERU	PHENOL HYDROXYLASE PUPROLEIN	2.544 lie 6100 ftl 16	497.524	\$48.501							
PENA! BACSU	DNAK PROTEIN	BACILLO3 SUB-ILLIS	456.483							İ	
NAME AND	DNAK PROTEIN	BACILLUS SUB IRLIS	910								
	A PACKA A A A A A A A A A A A A A A A A A A	BACILLUS SUBTILIS		***		144.444				L	L
2	Mary Control	BORNELLA BURGDOM EN	97.71						_		L
NAY BURB	CALL TO SECURE	BUCHDELLA APHIDICOLA	8		201.16						L
DYAN BULN	UNION TRUITING	ESCHENCHIA COLI	266-400					-			L
MAN EGOL	DWAAFRUIEIN	MICEOCOCCIISTIMEUS	385-415			1					
PONAA MICLU	DNAA PROTEIN	ALCOCATA PAREITO IN	3.	3.113	274.310	350-369					1
WAA ACYCC	PONAA MYCCA DNAA PROTEIN	MICOLOGICA CAN ACCOUNT	141.100			L		_			
1	DNAA PROTEIN	PROTEUS MIKABILIS								_	
W. W.		PSEUDOMONAS PUTIDA	398-439					-			L
DAMA ISEN	DAM FRUIE	SPIROPLASMA CITRU	45.72	76-110	43.160						
DKA SPICE	DNAA PROTEIN	CLIN ANOTHER THACHOMATIS	112-333		_						1
POWAL CRLTI	I DNAB-LIKE PROTEIN	Contraction Co.	\$2.109		_	L	_				
TOUR EVINE	INNA PROTEIN	ESCHEMONIA COLI	2								
	MANUAL PROPERTY	SALMONELLA TYPHINURUM	601.0					L			L
TOWN SALE	Supplied States	ESCHENCHIA COLI	40.1%								L
DNAL ELLOL		BACALUS MEGATERIUM	407-524					-		-	1
PONAK BACHE	E DRAK FROIEUR	BORRELLA BURGDONERU	312.594								1
DNAK BONB	U DNAK PROTEIN	SPINCELLA OVIS	148-275	512-546							1
PDNAK BRUOV	V DNAK PROTEDY	CASA CALATTER CRECTENTUS	361-588							4	4
PDHAK CAUCA		CACCOMPTENT OCTOBITION OF THE	400.576			L					
PHAK CLOAB	B DNAK PROTEDY	CLUSI KIDIUM ALEI DOOT I LICUS	406.537					_			
TANK CLOS		CLOSTICUM PER MAGENS	93 669		ļ						
TO A STATE OF	ANDNAK PROTECT	METHANOSAKCINA MAZEI			1	1			L		L
	THE PROTEIN	MYCOBACTEMUM TUBERLULUSIS				1	ļ				
TOWN WITH		STREPTOMYCES COELICOLOR	2/-6			-		+	-		-
STATE STATE	-	ESCHENICHIA COLI				\downarrow	1	1		-	-
DNIK ECOL	Party 1 Party	2 YMOMONAS MOBILIS .	2			1	-	1	\downarrow	1	-
OWORLZ THOU	ন		24.51				1			1	1
POPUL STUE	_		104-172				-				1
PDOCK SULSO	O PROBABLE MONAL RECOGNITION		\$1.15	417.444	1382-1416	9		4		1	1
PDPJA BACSU	7		77.104					1		4	4
PDPJA ECOLI	_	A TANGET A BOARD I CONTINUE A TANGET I	130.969	L	L	_	_	_	_	_	_
	1	CALL HARDING TANKS EN LINES			_						

JA JOUG	1445-196-4	Part - mails					-			
ELLE MANE	PROTEIN		П	ARIAL	AREAZ	AHEAL	ARYA S AR	AREA 6 AREA?	A? AMEA!	AREA!
PDPJA SALTY	DNA POLYMERASE I	INUMUM	П							
FUP BACSU	DNA POLYMERASE I		213:239	!						
PDP3B BOKBU	DNA POLYMERASL I	BORRELIA BURGDORFERI								
Succession of the succession o	DNA POLYNERASE I		٦	306-359						
TOTAL MOOD	DNA POLYMERASE III, BETA CHAIN		=				+			
STATE OF THE PARTY	DNA POLIMERANS III, BETA CHAIN	MICOLLASMA CAPACOLUM	2 5				+			
Poets at add			T	130 133	91.	1	+		+	
PDP3X BACSU			1	Т			1	1		
POPCE ECOL			196-363			1		$\frac{1}{1}$		
PDPCA ECOLI	DNA PRDIASE TRACA		4-10				+			1
PDPND STRPN	DPND PROTEIN		79.120	Ī		Ì	1	1		
POPOI BACCA	DNA POLYMERASE I	BACILLUS CALDOTENAX	201-335				_	<u> </u>		
PDPOI STRPN	DNA POLYMERASE I		Т	391-425	\$71.598	643.633		1		Ī
PDPOI THEAQ			1	Т	Т			-		
PDPOI THEFT	DNA POLYMERASE	SO:	Т					-		
PDPO2_ECOUL	DNA POLYMERASE II		569.998						<u> </u> 	
PDPOL PYREU	DNA POLYMERASE		746.773				-			
POPOL SULSO	DNA POLYMERASE	5		П		747.774		L	-	
PDFOL THELL	DNA POLYMERASE	ALIS		\$51.580	926-261	1004-1031	1153-1194			
PDP LACIA	DOPERTOYL PEPTIDASE IV		116-753						_	
PDP LACIC	DOEPTOYL PEPTOASE IV	TIS	116-753						_	
DOS ECOL	DNA PROTECTION DURING STARVATION PROTEIN									
DRNI STREO	DEOXYNUBONUCLEASE PRECURSOR	STREPTOCOCCUS EQUISIMILIS		291-318						
PORCA STIVE	DAUNORUBICIN RESISTANCE ATT-BINDING PROTEI									
51	DIMYDROPOLATE RE	STAPHYLOCOCCUS AUREUS	4	7						
PEAR FOR	ATTACHMO AND REFACING PROTEIN			Т	Т	٦	1			
Τ.,	EBO OPERON REPRESSOR PROTEIN		261-171		76.67	62/-160	077-20	\$20.17	1	
PEBR STANU	ETHEDRIM BROWEDE	AUREUS	16-19	T		\dagger	+	1		
PECHINI MIDCA	ENOYL-COA HYDRATASE HOMOLOG	LATUS	222-249		1		+	-		
PECPD ECOLI	CHAPERONE PROTEIN ECPD PRECURSOR		20.47			T		-		
PEDD ZYIONO	PHOSPHOGLUCONATE DEHYDRATASE		П					-		
PEDIT STAND	ET CALCULATE ACTOR &	STAMPLOCOCCUS AUREUS	7	19.146						
,	ELONGATION BACTOR 3				1					
	EL ONGATION PACTOR 2			1		1	1	1		
		110	Ť	46.180		1	+	1	1	
1			Ť	Т	236.347	1	-			
L_I			Т	Τ		1		1		
		ESCHENICHIA COLI	234-261				-	T		
	ELONGATION FACTOR O	•		330-357						
TEO SALIT		SALMOMELLA TYPHIMUMUNI	Т							
Т						1		-		
_	2	MICESTALIS				1	1			
PETT STILLA	201		200			1	1		1	
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_	U-18		1	Ī	1	+	+	+		
PETTS SING		2	T	134.161	1	1	+	1	1	
PETTU BACK		BACTEROIDES FRAGILIS	~ ~	220.156	1	\dagger	1			
PETTU BACSU			Τ	10.70	1	1				
PETTU BURCE	ELONGATION FACTOR TU		Γ		Ī	Ť	+	+		
-		ACHOMATIS	218-245			Ī	+		<u> </u>	
PETU DELS	ELONGATION FACTOR TU		230-257				-	-		
PETU FLESI	ELONGATION FACTOR TU		221-248							
PETU PALMA	ELONGATION FACTOR TU	IMLOARCULA MARUSMORTUI	=				H			
		غر ا								

JA COL	107.174.4	CONSTRUCTOR SECURIOR	ADFAI	ABFAS	ARCAS	AREA	ANT O		1	į	
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	EL DAMA TION SACTOR TU					T					
D 10 MCTO	CLUNCATION FACTOR 1			:	į	:	:				
NYCHO PACHO	LUMUATION	71	230-24	_		_		•			
TU MYCLE	FLONDATION FACTOR	SINORE	220-247								
PLYTU MYCTU	LUNGATION FACTOR 1	SA SILVERS A BITTER OF A SILVERS OF A SILVER	26.51								
PEFTU SHEPU	ELONGATION FACTOR T		332.259								
PEFTU STROR	ELONGATION FACTOR TU		141-168								
PELAS PSEAE	PSEUDOLYSIN PRECURSOR	PSEUDOMORAS ANTONIOS	31.101								
_	TA ABILE ENTEROTOXIN A CHAIN PRECURSOR	ESCHENCINA COLI		·	!						
1	TELANH E ENTEROTOXIN A CHAIN PRICURSON	ESCHERICHIA COLI				_					
	ACADEMAN STREET	RINGS NS	2				1	-		-	
	T-LABILE ENTEROION	ECCHERICITACOLI	24.11								
PENTED ECOLI		PASSING A TYPICAL MILES	14-61								
WA SALTY	•	SALMOMELLA I Trainionomi	97.5	35.33	290-125	117.421	11.189				
APAR CTARS	113 KD MEMBERNE ASSOCIATED MOTEIN	STAPHYLOCOCCUS EPIDERCHIDIS									
7		STAPHYLOCOCCUS EPIDERNIINIS	?!		-	1		-	1	:	:
PEPIC STALL	ENDERGIN BIOSTNINGS FROM	CTAPHYL OCOCCUS EPHYL RAHITIN	7.55	197.124	i	i			: : :	_	:
PEPIP STAEP	SEAINE PROTEASE EVIP PRECURSOR	PATAMINA COCCUS SPIDE WASHING	20.00					•			
Y STAEP	HYPOTHETICAL 16 7 KD PROTEIN IN EPIA S'RIGION	SIAMITUACOS ELIMENTES	8								
410.00	HYPOTHETICAL PROTEIN IN EMA S'REGION	STAPHYLOCOCCUS LFIDERCHINIS									
	COTE BACKING SEA PROTEIN	ESCHEMCHIA COLI									
LAY ET OF	CAN PROPERTY OF THE PROPERTY O	SACCHAROPOLYSPORA ERYTIIRAEA	100.11								
PENBS SACER	SENSORY INCASOULTION TROPIES	ESCHEDICHIA COLI	2.64	143-170							
703 13	EXTRACOMYCIN ESTER	SACCULA DOPON VCMORA FRYTIGAEA	9.36	87.93	= 3.15						
Y) SACER		SALCTON COLUMN STATES	31.155								
PESTA STRSC		SINE I UNITED SCHOOLS	163.189								
Section 1	ARYI FSTERASE	PSEUDOMIDIAAS PLUDIKESU EMS		20,							
1	TOTAL DESCRIPTION TARE C. I PRECIDE SOR	STAPHYLOCOCCUS AUREUS	76-	3							L
3	CALL TO TO THE PARTY OF THE PAR	STAPHYLOCOCCUS AUREUS	76-117	133-500							
C STAND	ENIEROIOMAINEC	STAPHYL DCOCCUS AUREUS	<u>√</u> -11	185-306	,						1
C STANU	ENTEROTOREN TITLE C	STABUST OCCUSAUREUS	36-69	165-192							
PETXA STANU	ENTEROTOXON TYPE A	A DOTAIN PERFERENCENS	208.236								
PETXO CLOPE	PSILON-TOXIN, TYPE B PRECUASUR	STANDA OCOCOTIC ATMETIC	101-20	173.207							
TO STANU	INTEROTOXIN TYPE & PRECURSOR	SIATH LOCOCCUS AUREUS	153.200				L				
PETAD STANU	INTEROTOKIN TYPE D PRECURSOR	STAPHTLOCOCOUS AUREUS	36.49	1				L			
VAT STAND	SYTEROTOXIN TYPE & PRECURSOR	STATTICKUCUS AUREUS	91711								
ALTER STREET	THANGLAMINE AMMONIA-LYASE LIGHT CHAIN	SALMONELLA TYPHIMIUMIUMI	200							L	
	MITATIVE TRANSCRUPTION REG EVGA	ESCHENICHIA COLI	68-70			13.75	20 85				
	т	ESCIENCHIA COLI	63:18	0/7-657							L
TANK STATE	TO THE SECOND IN	ESCHENICHTA COLI	226-253								1
	EACOLON INCIDENT	ESCHENICHIA COLI	10-107								
	BIOTOL I PICK I INCHASONI EXCIT PROTEIN EXCA	KHIZOBIUM MELILOTI	110-207								1
PEXON MODE	SUCCEMBER TOWN BIN	STREPTOCOCCUS PNEUMONIAE	216-254								1
COA STRUM	EXODEDATABORDELEASE	BANZORITA MELILOTI	236-270	327-361							
PEXOF NUDAE	EXOF PROTEIN	SUNTOBIO MET IN OTI	151.279								
PEXOH NOOG	SUCCINOCL YCAN BIO	ALIZOPHA MET IN OFF	311.342	27.799	186-951		L				
DON NOO	SUCCEMOCE YCAN BIO	MENSION MELEN	3	177.204							
DOS PO	FATTY OXEDATION CO	ESCHENCHIA COCI	330.343			L			L		_
PEATE FOOL	FATTY ACED TRANSPO	ESCHENCIAL		157157	503.551					L	L
tym gury	OUTER MEMBRANG PI	ESCHENICHA COLI									
1200	VII LONDE FORBRIAL	ESCHERICHIA COLI	3								
1	CAND PROTEIN PRECT	ESCHENICHIA COLI	8		200			1			ļ
	MATURE PROTECTION	ESCHENICHIA COLI	<u> </u>								1
PANE ELUCI	THE PLANT OF THE PARTY OF THE P	ESCHENICHTA COLI	2						1		1
PLANT ELLOS		ESCHENICHTA COLI	13-141							1	1
VAN ECO	PANHTRUIEMPRES	PSEUDOMONAS FRAGI	7	295-323		_					1
PFAOS PSEFE	т.	WOLINELLA SUCCINOGENES	2.5							1	1
PEDE WOLSO		ESCHENICHIA COLI	613-640							1	1
PEDE ECOL	POWALE DEATON	PSEUDOMONAS SP	49.76	366-393							1
POST PSEST	PURMA IE DEN IDAG	ESCIENCIA COLI	381-315	22.53	68-730				1	1	1
PLONG ECOL	THE ANGEO TO SECUTE OF THE CURSOR	ESCHENICHIA COLI	33:36					\downarrow	1	1	1
THE CY BOOK	TA ANGEORY PROTEIN	ESCHENICHIA COLI	210-217					1	1	1	1
					•						

PUCENT	107:120-4	Probarrato Consesses					-	-		
THE HAME	PROJEIN		AMEAI	AREA 1	AREAJ	AREA 4	AREAS AREA	A AREA?	ANEAS	AREA .
PFEMB STAAU	POSSIBLE PROTEIN	KUREUS	22.56						ı	
PFENA SYND?	FERREDOXIN-NADP	SYNECHOCOCCUS SP	=							
אני במר	FERUIC ENTEROBACT	ESCILENCHIA COCI	7					-		_
PEED ECO.	FEMALE ENTEROBACTIN FRANSPORT PROTEIN FEPT	ESCHEDICHIA COLI	T	201-102		1			Ī	
PERU ANAGO	SERREDOYN RETER	ANABARNA CD			T			+		I
PFEUX ANASP	EXTEDOXON-LIKE P		2.5					1		T
PFHAS BORPE	BLAMENTOUS HEM		ŝ	1359-1386	2063-2114	2841-2868 30	3051-3085 3167-3194	18		Ī
PFHAC BORDE	AEMOLYSIN-LIKE P	russis	142-369			-			İ	Ī
PINEA ECOLI	FORMATE HYDROGE		16-63	150-114	401-428					
PEHUA ECOLI	FEAUCHROME-INON	1	458-415					<u> </u>		
PENUS ECOL	PROTEIN FHUB PRECURSOR		117-154							
PEHNE ECOLI	OUTER-MEMBRANE									
		2	٦	126.367						
PFIC ECOLI			2:2							
FIC SALTY	CELL FILAMENTATION PROTEIN FIC	SALMONELLA TYPHINIUNI	7							
TO ECO.	CHAPERONE PROTEIN		(1.3	740-301		1				
FIND ECO.			Ī.,	458.485	\$34.561	161.590			İ	
	TYPE I FINBRIAL REGULATORY PROTEIN FIME		Т		Т					Ī
PFIMY SALTY	FINERIAE Y PROTEIN	IINUKIUN	49.76			-				
PFIMZ ECOLI	FINGRUAE Z PROTEIN		47.69	167-193	196.130			-		Ī
MINZ EALTY	FINDRIAL Z PROTEIN	HINDRICKI	175-209					_		
FINO ECOL	FINO PROTEIN		145-173							
PICA MOU	FIRA PROTEIN	NICKETTSIA NICKETTSII	162-189							
1000	PLACE TROIGING							-		1
ALVE AND A	SENECIA PROTEIN FIXE			75. 150		1				
PELA! BORRE	EL ACELLAR PRI AMENTAL KO CORE PROTEIN		T	30.16						
PELA! HALM	FLAGELLIN AI PRECU	ICNI	L	23.00	-	T				
PELA I METVO	PLACELLIN BI PRECI	METHANOCOCCUS VOLTAE	11:37	33.55			-			
PFLAS METVO	FLAGELLIN BY PRECL		38.66				_			
PILLY MALHA	FLAGELLIN BI PRECI		36-63							
W.W. METVO		METHANOCOCCUS VOLTAE	7							
Y Y	PLAGELLIN BY PRECI		T	2						
TELS PARTY	FLACELLIN OF THE UNITED A	MACHINE ELECTRIC	T		1		1			
CAN CAN	FLAGELL IN A				757 607	†				
PILA CAUTE	LAGELLINA		١,	Т	100,000	1	+	1		
PILAA METVO	FLAGELLIN A PRECURSOR		Т	Т		T		+		T
PFLAA PSEAE	HAGELLIN	CINOSA	1	===	97.124					T
PILAA NOGE				228-265	160-091					
PFLAA SPIAU	FLAGELLAR FILAKENT PROTEIN PRECURSOR		٥							
THA TIEN	FLACELLAR FILAMENT PROTEIN PRECURSOR	TENAE	П	219-215						
WINA THEY	_		٦							
200	PLACELLIN B	CANCEL COLLEGE COLL	Т	┪						
_	EL ACETTO D		907-077	10-333	20.33			-		
200	EL AVOCAMA		1	ī	60.00	160-341				
TAY CALCE	BEGIN ATORY PROTEDUFLAY			457 (3)		1				
PFLA BACSU	LAGELLIN	BACILLUS SUBTILIS	Т	***		†		1		T
┖	FLAGELLAR BASAL-BODY ROD PROTEIN FLGG		1		Ī	\dagger		1		Ī
1 1	FLAGELLAR HOOK-ASSOCIATED PROTEIN I	INTURI	П	Т	456-540					Ī
	FLACELLAR HOOK-ASSOCIATED PROTEIN 1		П	239.366						
ארטי צערע	FLAGELLAR HOOK-ASSOCIATED PROTEIN 3	SALMONELLA TYPIUMURIUM	٦	29-266						
1	FLACELLAR OPERON RNA POL SIGNA FACTOR	HIGHORA	10.00	T		1	-			
								-		7

15.00 15.0	295-339 136-131 136-131 136-136 136-136 136-131 136-131	335-359 335-359 335-359 335-359 335-359 335-45 403-33	99 176-403	 	\coprod
SALMONELLA MUENCIEN SALMONELLA MUENCIEN SALMONELLA MUENCIEN SALMONELLA MUENCIEN SALMONELLA MUENCIEN SALMONELLA TORISTA SALMONELLA TORISTA SALMONELLA TORININA SALTENODES NODOSUS SALMONELLA TORININA SALTENODES NODOSUS SALTENOS SOLTENOS SOLTENOS	136-184 116-117 116-104 116-200 116-200 116-104 116-10	- 	\dashv		\prod
SALMONELLA PARATYPHIA SALMONELLA PARATYPHIA SALMONELLA PARATYPHIA SALMONELLA PARATYPHIA SALMONELLA PARATYPHIA SALMONELLA PARATYPHIA SALMONELLA PARATYPHIA SALMONELLA PARININUM SALMONELLA PARININUM SALMONELLA PARININUM SALMONELLA PARININUM SALMONELLA PARININUM SALMONELLA PARININUM SALMONELLA PARININUM SALMONELLA TYPHIMURIUM SALTERODES NODOSUS SALMONELA SONOSUS SALMONELA SONOSUS SALMONES NODOSUS SALMONELA SONOS	16-177 116-116 116-100 11-200 10-200		╛		1
SALJONELLA RUGISLAW 3-41 34 34 34 34 34 34 34	196-184 116-196 15-196 15-199 150-187 1 150-188 1 150-188		(1	
SALMONELLA TYPHIMATION SALMONELLA TYPHIMATION SENDATORIA TYPHIMATION SENDATORIA TYPHIMATION SENDATORIA TYPHIMATION SENDATORIA TYPHIMATION SENDATORIA TYPHIMATION SENDATORIA TYPHIMATION SALMONELLA TYPHIMATION SALTISTOUES NODOSUS SALTISTOUES NODOSUS SALMONELLA TYPHIMATION SALTISTOUES NODOSUS	116-194 116-200 116-200 116-187 116-18		+		1
SALJONELLA TYPHINGUINA 141 151	116-200 15-89 160-187 1 255-289 1 156-187 1 156-188	1111	+		\downarrow
STATITA MARCESCRIVE 15-66 10	35-89 166-187 235-299 361-318	111	Т		
TEM 3 ESCRENCIA COL 13:46 10	235-299 235-299 261-318	$\neg \neg$	175-571		1
150 150	355-299	403-438	-		-
LIE BACILLUS SUBTILIS 1915-161 1916-			+	-	-
ACTILUS SUBTILIS 21-161 19 19 19 19 19 19 19			+	1	-
CAUTOBACTER CRESCENTUS 24-21 235 24-21		1	1		
SALMONELLA TYPHIMUNIUM 144-129 144-124	1111		+		
SACELLUS SUBTILIS 134.2	iell	1	+		-
ESCENCIA COL	<u> </u>		1		
INCLLUS SUIFILIS 1946 11 ACCILLUS SUIFILIS 17114 11 ACCILLUS SUIFILIS 177114 11 SACILLUS SUBTILIS 19-11 11 ACCILLUS ILLUS SUBTILIS 19-11 11-11 ACCILLUS SUBTILIS 19-11 11-11 ACCILLUS SUBTILIS 19-11 11-11 ACCILLUS SUBTILIS 19-11 11-11 ACCIDADANCES VISCOSUS 11-11 11-11 ACCIDADANCES VISCOSUS 11-11 11-11 ACCIDADANCES VISCOSUS 11-11 11-11 ACCIDADES NODOSUS 11-11 11-11 ACCIDADES NODOSUS 11-11 11-11 BACTERODES NODOSUS 11-11 11-11 BACTERODES NODOSUS 11-11 11-11 BACTERODES NODOSUS 11-11 11-11 BACTERODES NODOSUS 10-11 11-11 11-11 BACTERODES NODOSUS 10-11 11-11	_	:			
ACCILLUS SUBTILIS 13.11	1		+		
SALMONELLA TYPHINUMIUM 19-118 17-104 18-105 17-104 18-105 17-104 18-105 17-104 18-105 17-104 18-105 18-			+		1
BACTELUS SUBTILIS 17-104 11-113 13-113		:		:	!
BACTILLUS SUBTILIS 100-113 101	┪		†	-	-
SECIEDACHIA COLI 101-113	108-178		+		
SALMONELLA TYPHIMURIUM 100-131		1			
AACTELUUS SUBTILIS		1			
ESCIENCIA COLI 131-121		1	+		-
CAULOBACTER CLESCENTUS 16-11		1	†		-
ESCHELIAT TOPHINITION 19-16	-				
FALLMONGLIA TYPHINURIUM 7-46 0 0 0 0 0 0 0 0 0	1	1			
FAECURSON SCHELLINGSA 198-87		+		-	
PRECUSSOR ESCHERICHA COLI 11-34					
SOR SCUELCHA COL 14-131 15-131					
ACTIENCIDES PRODOSUS 114-141	79 417.444	-			Н
ACTEROIDES NODOSUS 110-131					+
BACTERODES NODOSUS 101-114					1
ACTERODES HODOSUS 101-114					1
BACTEROIDES MODOSUS 110-137				1	+
SACTEROIDES NODOSUS 121-150					1
BACTEROIDES NODOSUS 102-141		1		1	+
BACTEROIDES NODOSUS 91-112					1
BACTEROIDES NODOSUS 111-145		1			1
BACTEROIDE # WODGS 13	1	1	1		-
PSEUDOMONÍA A RENIGINOSA 19691					+
OTEN FACT BACTEROIDES NOCOSUS 106-144		+			-
105-104 105-	2	+			+
PARTICULAR PRECURSOR PROPERTY PARTICULAR PARTIC	22	+	1		-
TOUR THOUSEN PRECURSOR NEISSELLA MENTAGITEDIS 10-97 TOURILL PROTEIN PRECURSOR NEISSELLA CONOUNHOEKE 66-97 TOURILL PROTEIN PRECURSOR NOONGELA NOVILONGE ACTENS TOURILL PROTEIN PRECURSOR PERUDOMONIS AERUGINOSA 10-61 TOURILL PROTEIN PRECURSOR 10-63 TO 1-63 T		+			-
FUGBLIL PROTEIN PRECURSOR NEISSELLA CONOULHOEKE 105-17 FUGBLIL PROTEIN PRECURSOR NORLIQUEE ACIENS 105-14 FUGBLILL PROTEIN PRECURSOR FELLOCHOMNS AERUGINOSA 10-63 FUGBLILL PROTEIN PRECURSOR 10-63 FUGBLILL PROTEIN PROTEI	1	+			-
FEBRUAL PROTEIN PRECURSOR MONAXELLA MONALOUE ACTENS 106-10 FEBRUAL PROTEIN PRECURSOR 156-51 FEBRUAL PROTEIN PRECURSOR 156-51 FEBRUAL PROTEIN PRECURSOR 156-51		-			
FOREILL PROTEIN PRECURSOR PSELDOMONAS AERUGINOSA					-
A LONG THE PARTY OF THE PARTY O	-	+		-	-
FRAME AT PROTEIN PRECURSOR		+			-
FESCHENCIAL SUBUNITA PRECURSOR ESCHENCHIA COLI	2	+			
CALIFORNIAL SUBUNITA PRECURSOR ESCHENCHIA COLI		-			
MAJOR FEMBRIAL SUBUNIT PRECURSOR	214 111.365	131.458	\$17.555 652.686	111-156	
AU FIBRONECTIN-BINDING PROTEIN PRECURSOR STANFOLOGICAL SAUREUS (13-15)	Т				
FOLYLOLYGLUTAMATE SYNTHASE ESCHOOLING CASE					+
I POLYLOLYGLUTAMATE SYNTHASE					$\frac{1}{1}$

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PCGENE	107117314	Protestell Sements									
EILEHAME	ROTEIN		AREAI	AREA 3	AREA 3	AREA 4	AREA S	AREAG	AREA 1	ABEAG	ABEAS
PFILDA ECOLI	UMARATE REDUCT		Г	Т	Г			١.	Т	Т	
PFILDA WOLSE	UMARATE REDUC	NES	Г	407-514					ĺ	<u>-</u>	i
PFRZE MYXXA	LIDING MOTILITY	MYXOCOCCUS XANTHUS	1342	478-505						T	
PFTHS CLOTH	FORMATE - TETRAHYDROFOLATE LIGASE		163.190							T	
TELE MET H	FORMALTIKANSFE	NI THERMOAUTOTROPHICU	176								
PETER PACSO	CELL DIVISION PROTEIN PLAN		╗								
	CELL DIVISION OF	ESCHENICHIA COLI	=	33:418							
	CELL DIVISION PROTEIN ETC		-								
PETSN ECOL	CELL DIVIGON PROTEIN BTCM	ECORE I CUITA COL	R.								
	CFL DIVISION PROTEIN STCK										
PETEV POR	CELL DIVISION PROTEIN RESC		278.305					1			
1003	I. HINDAR DEFENSIVE TOR		2,02,00								
1000	EINA BATE LICES		Ŷ								
TO VALUE	UMAKA IE HTDKA	HERMOPHILUS	280.312								
DELLE VERRE	FURNITATION OF STATE	BACILLUS SUBTILIS	ž.	:	:			:			
	SAC S BUT DE DE UNE		27.130						:		
AUAUA PER	CENT OF THOSE DELICATION OF THE SECOND SECON		102-129								
1000	CT VOT A BLOCK PRINCE OF THE SECTION	AMABAERA VANABILIS	87-114								
ALVANA CALLA	CHAIL STRUCK DEMINACIONANCE 3		162-189	_							Ī
מינים ברסת	OF VC 3 MICE RELIGIOUS CONTROL										
TOTAL BACKET	CLOC PENOS DENTURCUENASE	COM		117.271							
DON'S STORY	7		49.76							Ī	
TOTAL STREET	CLIC FIND DESTURBINASE		259-286								
A INFO	GLTC 3-PHOS LIEHYD									T	Ī
LOOKE BACS	AUCUSE - MUSTIN	THERMOPHILUS	103-143	241-268						T	
	CLUCUS & PHUSPHATE I-DEHYDROGENASE		301-324							T	
LOND ZYMONO	GLUCUSE PHOSPHATE I-DEHYDROGENASE		163-192								
TACK DEPT	CTANIDE CUNTROL PROTEIN	S	178-205						İ	t	T
TOWE SALIT	CALACTORUNASA	_									T
NAL.	GAL-I-FROS URIDAL YLTRANSFERASE		П	119-269	-				T	T	T
200	CAL ACTORE CHEST	LACTORACILLOS PELVETICOS	304-338								
POAT B UARRA	CALACTOSE OFERON		25.6								
POAL PREFI	DE DOAL ACTOUR LIDEHYDROGENAKE		602.20		1						
	OTP CYCLOHYDROI ASE II										
		LEIOGNATHI	201.01			1					
PGCSH ECOLI	CLYCINE CLEAVAGE		Ť		1				1		
PGCSP_ECOU	CLYCINE DEHYDROG	ESCHENCHIA COLI	216.246	1	1.		1	1		1	
PGCVA_ECOLI	_		76-09	T			1	1	1		
PGENK ECOLI	PROTEIN K		5.5	T	1			1	1		
PGERI BACSU	SPORE GERMENATION		19.83	182.216	350-384		1	Ì	1	1	
PGENU BACSU	SPORE GERMONATION		_	Г	T		1	Ī	T	\dagger	Ī
PCENE BACSU	GELMINATION PROTEIN GENE		3-40						T	t	T
			6-33						T	t	
V 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ANIBACIEMAL PROJEM 3	HAEMOLYTICUS	ŝ				ļ		Ť	\dagger	
	GEOCOSE INFUBILIED	BACILLUS SUBILLIS	196-423							\mid	T
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CLOCOSE INVIDENCE IN VISION PROTEIN A		533.568								Ī
PCIDA BACCI	GLINOSE INMIBITED		239.266								
PGDB PGFM1	CHIEF AND SOUTH		3	1					l	-	
CCC SYNY	GLUCOSE TRANSPOR			1							Ė
PG DA BACST	GLYCEROL DEHYDRO	The Bridge and The	777-177								
Т	GLYCOGEN SYNTHASE		20-70	1							
	GLUCOSE I-PHOSPHATE ADENTLYLTRANSFERASE			1	1						
_	SFERASE	IDAURIUM		1	1	1	1				
			209-243	†	T	1	Ī		\dagger	1	
_	GLNB-LIKE PROTEIN I	THERMOLITHOTROPHICUS	25.55	1		\dagger	1		1	1	
		7							1	1	7

PCGENE	\$67277514	Proharyotic Sequences		П	$\overline{}$	-	ıT	_	П	П	Π
TILE NAME	ROTEIN		4	<u> </u>	7 7 7 7	AREA	ARCA!	AREA A	AREA AREA	ARA.	<u>a</u>
PGLNA ANASP	SLUTAMINE SYNTHETASE		-	1	1		1	$\frac{1}{1}$		1	T
PGLNA BACSU	SLUTAMINE SYNTHE		Ţ	1		1		1		$\frac{1}{1}$	T
PGI NA CLOAB	GLUTANINE SYNTIETASE	CLOSTRIDIUM ACETOBUTYLICUM	413-440							-	1
PGI NA ECOL	GLUTAMINE SYNTHETASE	ESCHERICHIA COLI	144-171							-	7
PGI NA METVO	CELITAKINE SYNTHETASE	METHANOCOCCUS VOLTAE	301-130							-	
UNO NA PROVU	GLUTANDNE SYNTHETASE	PROTEUS VULGANS .	143-169							-	
PCI NA PYREU	PCHAR PYTEU CLUTAKINE SYNTICETASE		161-421								
PGUNA SALTY	GLUTAMINE SYNTHEY		144-171								
PCI NA STRCO	CLUTAMINE SYNTHE		112.98	· :	1			_	_		_
TO THE PARTY	NITEOCIEM BEGIN ATO	AZOSPIKILŁUM DRASILEMSE	:67-51			_		:			
1000	NITEOGRAPHICA ATORY PROTEIN P. II		15.49			Ī		-	-		
200	NITEOCEM RECIEMATORY PROTEIN P. II	SYNECHOCOCCUS SP	\$3.79		İ				_		
CCAS STATE	MINISTER ACCOUNTS TANKED ACC	ECCHE PICHIA COLL	١	151:178	l	T					Ī
ינראם בינה	CONTRACTOR OF THE ANGELONGE	CALLACATE A TYPHILLIPHIA	۲			Ť	İ			<u> </u> 	1
FGLND SALIT		TOUR MICHIGAN	T	11.60	107.17	Ī	-	-	-		_
PCLNE ECOL	ADENYLYLIKANSFERASE	בארוווא רסבי	T	7		İ		T		<u> </u>	Ī
PGLNH ECOU	CLUTAMINE-BINDING PROTEIN PRECURSOR	ESCIENCIALOLI		1	Ì		1	1		+	T
PCLNQ BACST		BACILLOS SI EAROTITERATORILLOS		1	1	1	1	1		$\frac{1}{1}$	T
POLPD BACSU	AEROBIC CLYC.) PHOS	BACILLOS SUBILLIS		1	1	†		+		+	Ī
PGLPD ECOLI	AEROBIC GLYC.)-PHOS		1000	1	1		1	†	1	+	Ī
PGLPF BACSU	GLYCEROL UPTAKE FACILITATOR PROTEIN		217:67	İ	Ì		1	†	1	$\frac{1}{1}$	Ī
POLPK BACSU	GLYCEROL KINASE	BACILLUS SUBTILIS			1		1	1	1	$\frac{1}{1}$	T
POLPK ECOLL	- 1	ESCHERICHIA COLI	8		1		1	1		+	T
PGLPR ECOLI	GLYCEROL J-PHOSPHATE RECULON REPRESSOR		2.2		1				1	+	1
PGLPX ECOLI	GLPX PROTEIN		297.324		1				$\frac{1}{1}$	1	
PGLPX SHIFT.	GLPX PROTEIN	SHIGELLA FLEXMERI	247:324		j	j			1	-	1
PGLIX ECOL	GLUTAREDOXIN	ESCHERICIIIA COLI	26.51	`				_		1	1
POLTB ECOL	GLUTAMATE SYNTHA	ESCHENCHIA COLI	483.500								1
ומדוף בכסנו	PROTON GLUTAWATE	ESCHENCHIA COLI	119.146		1					+	
POLVE ECOL	PHOSPHOTIVANSFERA.	ESCHENICIÓN COL!	130-153		1		Ì		1	+	1
PGLYA BRAJA	SEALNÉ HYDROXYNŒÎ	BRADYTHIZOBIUNI JAPONICUNI	9.60	1	Ì				1		1
PGLYA CAMPE	SELINE HYDROXYNETHYLTILANSFERASE	CANDYLOBACTER JEJUNI	176-403	Ì			1	- !	1	+	1
PCLYA HYPAGE	ELINE HYDROXYME!	HYPHONICROBIUM NETHYLOVORUM	٦	-	j					1	
PGMG7 BACSU	COMO OPERON PROTEIN ?				Ì	Ì		1		+	1
PGNTK BACSU	LUCONORDIASE			1	1	1	1	+	1	+	T
PGP ID CALTA	VIRULENCE PROTEIN			i		j			1		T
CP2D CR.TR	VIAULENCE PROTEIN			İ		İ	İ	i	-	+	
20 OG TE		CHLAM IDIA IRACRIORIA IIS	٦,	9,	1		1	Ì	1	+	T
100 OF 12	VALUE DACE PROTEIN		T		\dagger	Ť	T	1		+	Ī
70°70 CR.TR	VINCE DICE PROTEIN		161.76	1		T	1	t		+	Ī
MONTH OF THE	VALUENCE MOTEUN FORT-U				T	T	T			+	T
NOT YES	TRANSCELL TO THE PERSON OF THE		11.11	T	1	\dagger	\dagger	\dagger		+	Ī
CAN EACS	COLUMN TANKS	1011	2	Ť	†	T	Ť	l	1	+	Ī
	CANESTONE CANTEN	CLOSTROPINA ACETOBUTYLICUM	12:43	Ì		T	T			+	Ī
	Carlotting & Cortherase	BACOLUS BREVIS	١	790.876	140.812	1035-1062	T	t		╀	
	THE A VACCION S STATES	BACULUS BREVIS	41.75	Т	Τ		1213-1240 2	2162-2189 25	2559-2586 2819-2846		1606.1633
I DUST INDUSTRI	GUTAMATE CYSTE	ESCIENCIA COLI	339-266		Г					-	
POST BOOM		ESCIENCIA COLI	70.00	115.92						-	
PCCIA PCCAE		PSEUDOMONAS AERUGINOSA	10-114						-	-	
DOG PACSU	STARYATION-DEDUCE	BACELUS SUBTELS	Г	365-396		ļ				-	
POCO DIVICA	MOTEDY D PLECURSO	EAWDIA CAROTOVORA	258-285	316-343	819-616	T				-	
PCOD FRVOR	PROTEIN DIMECURSOR	5	П	Т	\$51.578	989-659	-			-	
MG KI ENA	PROTEIN D PRECURSOR	KLEBSELLA PNEUMONIAE	259.286						-	-	Γ
ACON DIVICA		EAWDIA CAROTOVORA	329-367						ŀ		Ī
PCSTE ELWOH	-		129-367								
POSTE EL DY	PROTEINE	/	П								
MOSPE PSEAE	PROTEIN E	PSEUDOMONAS AERUGINOSA	122-149	131.369						\dashv	

A SECTION AND DESCRIPTION OF THE PERSON OF T											
FILE NAME DECYT	200	Frahitrodic Sequences			_						
PGSPF XANCP PROTEINE	22	VKVATSN	AKIAL	AREA	ARCA 2	AREA	AKEAS	AREA 6	AREAS	ARIAR	100
PCSPH PSEAE PROTEI	NH PRECIDENT	PEEL MONON S CAMPES INS	30.33						Т	_	
PGSPL AERHY PROTEIL	PROTEIN PRECURSOR	ASEQUATIONAS AERUGINOSA	<u>.</u>								
PGSPI ERWCA PROTEIN	N PRECIPEOS	ACKUMIONAS IITUROFIIILA	17.61						Ī	Ī	-
PGSPJ KLEPN PROTEG	2000 C 20	ERWINIA CAROTOTORA	15-62							Ī	
POSPE ERWCA PROTEINE	A PART CASON	ALLESIELLA PREUNIONIAE	140-167								
POSPE FRANCH PROTECT	12	ERWINIA CAROTOVORA	28-55						Ť		
POST KI SPN PROTECT	12	EXWINIA CHRYSAUTHENII	18.33								
POCEN PORAR PROTECTION		KLEBSIELLA PNEUDIONIAE	8.7					T		1	
POCH COMPLETE	¥ E	PSEUDONIONAS AERUGINOSA	262.289				Ì				
TOTAL ENACH PROTEIN	1	ERWINIA CHAYSANTHENH	7	74E.35	10.10	Ì	Ì		İ		
TOTAL MARKET PROJECT	7	XANTHOMOMAS CALIPESTILIS	1	707.107			1				
		ERWINIA CAROTOVORA	10				1				
PCSOD ERWCH PROTEIN	PROTEIN D PRECURSOR	ERWINIA CHRYSANTHEAS	Т	367,977				-			
PGIFT STANDO GLUCOS	GLUCOSYLTIMASFERASE:I PRECURSOR	STREPTOCOCCUS DOWNEL	Т		7400-01/2	937-084					
KITTS STILLDO CALUCOS	INLTRANSFERASE ! PRECURSOR	STREPTOCOCCUS DOWNER	١,			_	_	1495-1529			
POTER STRAIN GLUCOS	SYLTRANSFERASE:S	STREPTOCOCCUS AILITANS		3	31-013	102:14	3.12			!	!
PGITE STRUKU GLUCOS	THE TRANSFERASE I PRECURSOR	STREPTOCOCCIICAGITANE	,								İ
PGTIC STRUM CLUCOS	I'M TRANSFERASE-SI PRECURSOR	STREPTOCOCCUS MITTANS	Ţ	10.13	161-118	199.246		592-627			
PGTFS STRDO GLUCOS	YLTRANSFERASE-S PRECURSOR		Т		792.50	-	614.613			-	
PGTACK METTE POSSIBLE	POSSIBLE G-T MISMATCHES REPAIR ENZYME	T	J	90.0	<u> </u>					Ī	
POUAA BACSU GAIP SYNTHASE	MTHASE	BACILLUS SUDTILIS	0	7				İ			Ī
POUAA_ECOL! GMP SYNTHASE	MTHASE	T	T	07.4.4	10.10						
PGUB BACCI BETA-GL	BETA-GLUCANASE PRECURSOR	92									
POUR BACK BETA-GL	LUCANASE PRECURSOR			1							Ī
PGUB BACKA BETA-CIL	UCANASE PRECURSOR		8 5								
PGUNI BACSA ENDOGE	ENDOG! UCANASE A		800	1							
CON! BACSU ENDOGLI	UCANASE PRECURSOR	BACILLUS SUBTILIS	Ţ,							-	
POUNI BUTFI ENDOCL	UCANASE 1	-	Т								
CUM BACSU ENDOCE!	UCANASE PRECURSOR		Τ		1						
PCUNI THEFU ENDOGLI	ENDOGLUCANASE E.2 PRECURSOR	POSPORA FUSCA	201.33			1					
CALINI BACSA ENDOGLI	UCANASE C PRECURSOR		7	141.3%	19.64	İ	1	1			
ACINI FIREI ENDOGE	UCANASE PRECUTSOR		T	Т			\dagger	1	1		
COM THEFT ENDOLL	ENDOCH UNANA E E A BA EN BARON	5	342-516				\dagger	Ť	1	1	T
POUNT THEFT ENDOG!	ICANAGE CASECINSON		304-342				1	\dagger	1	1	
PGUNA BACLA ENDOCAL	UCANASE A PRECIPISOR	BACH FILE AND SPORA FUSCA	П			I		Ť		1	
PGUNA CLOTH ENDOGLL	UCAWASE A PRECURSOR	NOCE III	T	454-481			l	1	\dagger	\dagger	
PGUNA PSEFL ENDOGLU	ENDOGLUCANASE A PRECURSOR							-		\dagger	T
GUNA RUMAL ENDOGLI	UCANASE A		687.70						T	\dagger	T
GUNA RUMON CELLODE	XTHINASEA	FACIENC	176-76								Ī
PGUNB BACKA ENDOGLU	ENDOGLUCANASE & PRECURSOR		9776	†	1						Ī
CUM CALSA ENDOGLI	UCANASE B	CAL DOCELLUM SACCHAROLYTICUM	Ť		1	1					
DOOR INTO BARRIO	ENDOGLUCANASE B PRECURSOR		T		1	1		1			
TOWN CLOCK ENDOCLU	UCANASE B PRECURSOR	2	Т	266.300	\dagger	1	1	1	1		
CINC CELET CANCEL	CANAMACANAS B PRECURSOR	OCELLUM	314.541	T	T	1	1	1		1	
GUNC PEER ENDOGE	LANA SECTION OF THE CO.		106-188	T	T	\dagger	\dagger	1	1	+	
GUND CLOTE ENDOG!			21-25			1	\dagger	1	\dagger	+	1
PGUND CLOCK ENDOGEU	PETITION CONTRACTOR		157-200					\dagger	†	+	1
GUNE CLOTH BROCK!		¥	П	1			\dagger	\dagger	\dagger	\dagger	1
PGUNH CLOTH ENDOGLU	RECURSOR	CLOSIADIOM INCIMACELLUM	<u>-</u>	П	164-311		-	+	\dagger	\dagger	T
BUNS ERWCA ENDOGLU			T	23.452			-			\downarrow	T
PGUNK CLOTH PUTATIVE		711113	2 2 2	\$ 2					\dagger	-	T
מואב כרספור ובאסספרה		KARUAI	T	97.60	1						Γ
PGUN BACHO ENDOGLU	ENDOGLUCANASE	LWWXA	1		1	1	+				
PGIN BAFEK FAROCI II			331.348		T	\dagger	\dagger	1	1		
Wit some jureau		MACILLUS SP	П	\$01.528 62	199.03	\dagger	\dagger	\dagger	+	+	7
						1		1	1	1	7

П	Probaryode Sequences	П	П	П	1 1	Г-Т	г			
CITE NAME PROTEIN	FECHERICHIA COLL	43	4	3	4	1	6	4	Q Q	20100
	HALOBACTERUM HALOBIUM	3					ĺ	-	:	:
GAS VESICLE PROTEIN.	HALDBACTERIUM HALDBIUM			П						
PGVPA APHOL GAS VESICLE PROTEIN	APHAMIZOMENON FLOS-AQUAE		35.							
PGVPA FREDI GAS VESICLE PROTEIN	FREMYELLA DIPLOSIPHON	٦	88							
POVPA HALME GAS VESICLE PROTEIN	HALOBACTERIOM MEDITERRANEI	3				1				
POVPA MICHO GAS VESICLE PROTEIN	MICROCYSTIS SP	3				}		-	:	!
POYTA TORAN GAS VESICLE TROICIN	A PHANIZONEMON BLOC. A DITAG	T								
TOYAL AND THE TABLE TRUITING	MAI ORACTERINA HAI ONITAL	56.35			T					
TOTAL MALTA CAS VENEZE PROTEIN	MAI OBACTERINA MEDITERANE	130.169								
POVE HALVE GAS VESKLE TROTEIN	HALOBACTERITA HALOBUM	10.16								
CVPO PROTEIN	HALOBACTERIUM MEDITERRANEI	9						-	į	
PCVPF HAT HA COPF PROTEIN PLASMID	HALDBACTENINI HALDBIUN	Т	13:181							
WE PROTEIN	HALOBACTERIUM MEDITERRANEI	Τ								
PCVPE HALLSA COVE PROTEIN	HALOBACTERIUM SALINARIUM	8.49								
PGVPG HALHA GVPG PROTEIN, PLASMID	HALOBACTERUM HALOBIUM	20:05								
VPG PROTEIN	HALOBACTERIUM MEDITERRANEI	<u> </u>								
PGVPH HALHA GVPH PROTEIN	HALOBACTERUM HALOBIUM	0.60								
PGVPI_HALME_GVPI PROTEIN	HALOBACTERIUM MEDITERRANE!	15.12						.		
POVPK_HALHA GVPK PROTEIN	HALOBACTERIUM HALOBIUM	٦								
PGVPK_HALJAE GVPK PROTEIN	HALOBACTEMUMI NEDITERRANEI	Ţ	7.5							
PGVPK HALSA GVPK PROTEIN	HALOBACTENUM SALINARIUM	T	٤							
PGVPL HALAGE GVPL PROTEIN	HALOBACTERUM NEDITERIANE		Ī							
POVEN HALHA GVPN PROTEIN	HALOBACTEROM MALOBION									
POVEN HALME COVEN PROTEIN	HALOBACTERIOR MEDITERANE	90.00		\int			I			
POWER HALDE CONDITIONED AND AND AND AND AND AND AND AND AND AN	MACHER STREET	Ī	630.650							
POYTH CAMP DNA CYTASE SUBIDATA	CAMPYL OBACTER JEUNI	L	T	452.479	\$69.698					
POYTA FORT DNA OYLASE SUBUNITA	ESCHENCHIA COLI	Т	T	Т						
POYTA KLEPH DNA OYTASE SUBUNIT A	KLEBSIELLA PNEUNIONIAE	Т	441.4%	\$18.545						
POYTA MYCPH DNA GYRASE SUBUNIT A	MYCOPLASMA PNEUMONIAE	П	П							
PGYILA_STAAU (DNA GYRLASE SUBUNIT A	STAPHYLOCOCCUS AUREUS	П	146-373	430.479	647.674	112.639				
PGYND BACSU DNA GYRASE SUBUNIT B	BACILLUS SUBTILIS	196-239								
PGYRB BORBU DNA GYRASE SUBURIT B	BORRELIA BURGDORFERU	100								
PGYRB ECOLI DNA GYRASE SUBURIT B	ESCHENICHIA COLI	916-64)								
POYER HALSO DNA GYRASE SUBURIT B	MALUPERAX SP	770-737								
POTES MICH DIA CIRASE SUBURITOR	WEIGEBIA CONOBBIOGAS	Т	111	Ī	Ţ					
POYER PSEPUL DNA GYRASE SUBLINIT B	PSEUDOMONAS PUTIDA	Т	684.71							
POTAB SPICE DNA GYRASE SUBUNIT B	SPROPLASMA CITIU	Π	L	283-310	341-368	\$40.579				
DNA GYRASE SUBUNIT	STAPHYLOCOCCUS AUREUS	152-279	Г	Т	Г					
PIEHIA ECOLI 1-ALPHA-HYDROXYSTEROED DEHYDROGENASE	ESCHENICHIA COLI									
I HELICASE IV	ESCHENICHEA COLI	-	\$29.556							
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PIEMI ECOLI GLUTAMYL-TRNA REDUCTASE	ESCHENCHIA COLI	205-216								
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PIEM2 METSC DELTA-AMINOLEVULDNC ACID DEHYDIATASE	Т	<u> </u>								
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PHYTH ECOLI	SENSOR PROTEIN HYDH		112.339	360.387							
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MALIONALM PRECURSOR CLOSTRIDIUM THERMOCELLUM 117-159 FROD-1, I/O, BET ACTULANTS FRECURSOR CLOSTRIDIUM THERMOCELLUM 117-159 FROM SELE LEUCOCK A DANIUM TY PROTEIN ACTOCOCCIN A SECRETION PROTEIN L'EUCONOSTOC GELIDIUM ACTOCOCCIN A SECRETION PROTEIN L'EUC L'ACTOCOCCUS LACTIS 163-189	т	IATED PROTEIN 2		,					L		1	T
PODO-13(1) BETAGLICANASE PRECIASOR CLOSTRIDIOM THERMOCELLIAM 111-159 DIOLI SYNTHESIS PROTEIN LASI PSEUDOMONAS AERUGINOSA 111-159 TACTOCOCCIA A SECRETION PROTEIN LEUCONOSTOC GELIDIOM ACTOCOCCIA A SECRETION PROTEIN LCHC LACTOCOCCUS LACTIS 163-159	WALLUTON TO			1	2				L	-		T
AND SYNTHESIS PLOTEIN LAST *ROBABLE LEUCOCHA SECHETION PROTEIN LEUCONOSTOC GELIDUM ACTOCOCCHA SECHETION PROTEIN LCHC **LEUCHOSTOC GELIDUM **LEUCHOSTOC	M ENDO-1,3(4)-BE	ANASE PRECURSOR		2						1	1	1
PAUNITY PROTEIN LEUCONOSTOC GELIDUM (1-7) TION PROTEIN LCNC LACTOCCOCCUS LACTIS (162-189	E OHOL SYNTHE	IN LASI	2	13.159	-	-	1	1		1	1	
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LCND LALLA	CALIFORNIA STATE	FICA	133.149	491.318							
LCRU VEREN	DW CALCIUM ACSIONS		123-149	491.518							
PLC TO TENTE	LOW CALCIUM RESI DIN		23-49	157.184	240-267						
PLCKY YEAVE	7	DTUBERCULOSIS	37.49	140-167							
PLCKY TERS	7	BACILLUS CALDOTENAX	\$ T								
עררום פעררע	_	BACILLUS STEAROTHERNOPHILUS	<u></u>								
מונים ווארפו	+	LACTOBACILLUS PLANTARUM	===								
TOUR PACES	I ACTATE DESIVOROS		(4.5	241-272	319.306						
PI DILK RACES	L'EACTATE DELIYOROG		1-4)	241-275	279.306			1			
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2000	CLACTATE DEUVDROCENASE		341-766	179.313							
LIMI BACS	CACINE DENVIROGENASE		~~	140-267							
OCT NO.	L-LACIATE DEUVORGENACE	BIFIDOBACTERUM LONGUM	22:49								
31/12	C-LACIATE DESIGNACED AGE	I ACTORACILLUS PLANTARUM	197.231								
- 1	L-LALIA E DEN 10ACCENACE		43.69								
LON CISMO	L-CACIALE DENIENCEMANE	MYCOPI ASMA HYOPNETIMONIAE	176-310								
	LLACIALE DENTUROCENASE	TITE BLACK A CALLA THE LICE	٩								
LOH THEAD	L-LACIATE DENTUROSENASE	BACILLIC ANTICACIS	163-192	10.90	410.514	541.578	859-619	23:75			
PLEF BACAN	LETHAL FACTOR PRECURSOR	BEET TOLONAS EL LOBECTENS	8			Т					
PLEPA PSEFL	LEFA FROIEIN	BAFTILLIS SUBTILIS	ŝ								
LEF BACSU	STURME PER LIDASE I	ESCHERICHIA COLI	137464								
1	S-ISOTROPTION AND ATE S	LACTOCOCCUS LACTIS	65-22	179.414							
TEO CACEA	SCHOOL LANGE ATEN		35.15								
שנים פערנים	STOREGIST MAI ATE DELIVING CENASE	UANUNI	10.212								
EUJ CLOAN	1-SOFROFT LIMALATE DELITION OF TASE P	LACTOCOCCUS LACTIS	163-190								
2000	TRANSPIPEINAL REGILATORY PROTEIN LEVE	BACILLUS SUBTILIS	297-324	676-703	144.174	785-822					
PI FXA FRWCA	EXA REPRESSOR	ERWINIA CAROTOVORA	146-173								
PLIP1 MORSP			36.53								
PLIPE MORSP	LIPASE 2		136.1								
PLIPB ECOLI	LIPS PROTEIN	SCHEMEN COL	134.301								
PLIP BURCE	LIPASE PRECURSOR	JEN6	1								
IP PSEFL	LIPASE PRECURSOR		176-203								
1253	LIPAGE PAECINGOR	STAPHYLOCOCCUS AUREUS	80-146	\$12.546							
VI IVE CALTY	I FINI EVAL/THR-BINDING PROTEIN PRECURSOR	SALMONELLA TYPHIMURIUM	193-220								
INC SALTY	יוי	SALMONELLA TYPHIMURIUM	195-222								
PLIVE SALIY		SALMONELLA TYPHIMURIUM	121-146								
PLIVE ECOLI	AMINO ACID TRANSPORT PROTEIN LIVE	ESCHENCHIA COLI	3.50								
PLIVI CITER		CITROBACTER FREUNDII	195.222								
PLIVI ECOU	LEUMENAL-BINDING PROTEIN PRECURSOR	ESCHENCHIA COLI	32.22								
PLIVK ECOU		ESCHERICHIA COL	227-66								
PLIVM ECOLI	_	CARDENCIN COLI			104 441	117 157	601.430	1100			
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PLK 10 PASHA	TO BECTEIN	ETENCOMITANS		9							
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TO THE STATE OF	I KTD PROTEIN	ACTINOBACILLUS ACTINOMYCETENICOMITANS	201-201	205.242	278.305	164.391					L
H KTD PASHA	LKTD PROTEDY	PASTEURELLA HAEMOLYTICA	184-389								-
TON ECOL	ATP. DEPENDENT PROT		131-148								
וויא מלוו	UDP-N-ACETYLGLUCOS		229-256								
MSPA ECOLI	LIPOPROTEIN SIGNAL	ESCHENCHIA COLI	10:17								
MSPA STAAU	LIPOPROTEIN SIGNAL	STAMINLOCUCCUS AURILIA			!						
HINE STAN	LINGOUNA SUBINIT PRICUASOR	MARITICA CALLOS ALBERTOS	101	İ	•	İ					
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ALKANAL MONOOKY	THUTOBACTERIUM PHOSPHOREUM	18.27	157-291							
ACAT COLDENIUM	VIBIOHANVEYI	173-400								
	PIOTOBACTERUM LEIOGNATHI	\$- -						Ī		
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	VIDEO MARCES	66.1	21-243							
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OHOR SYNTHESIS PRO	VIBROFISCHERI	ž.							T	
O LUMAZINE PROTEIN	VIBRO FISCHER	20.5								
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MEMBRANE-BOUND P		Т	239.303							
PAIN ATREE IN PROJECT SERVING THE 12 PRECURSOR	STREPTOCOCCUS PYOGENES		14.156	191.300	305-342	183-417	436-494	Ī	Ī	
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PAICED AGTVO	REDIXTASE OPERON PROTEIN D	VOLTAE	\$4.91							
7	JALATE DEHYDAOGEN		127-154							
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		EPIDERWIDIS & AUREUS								
PMEMI METCA	CETHANE MONOOXYG		214-248							
PAIE MOD METTR	METHANE MONDOXYGENASE COMPONENT A	UCHOSPORIUM	321-348							
PAGEND ECOLI	HCHC SYNTHASE		113.367			1				
-	PROBABLE HG TRANSPORT PROTEIN	CES LIVIDANS	159.186		1	1				
Ē	MERCURIC REDUCTASE		146-180			1				
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PMETB ECOLI	CYSTATHIONINE GAMPIA-SYNTHASE		36.30			+	+	+		
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PMFD ECOL	TRANSCRIPTION-REPAI					1	1			
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PMINC BACSU	SEPTUM SITE-DETERMI		07.130							
_	MICC PROTEIN	CHI AMYDIA TRACHOMATIS	2:35	T	T					
THE LEGAL	OLTER MEMBRANE PROTEIN MIP PRECURSOR	LEGIONELLA MICDADEI	106-133							
PAGES! ENTRA	RENA ADENINE N.4-ME		(-3)	120-154						
1	RRNA ADENINE N-G-METHYLTRANSFERASE		5			1			1	
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TACEV STAFF	ABA BROTER	ESCHERICHIA COLI	136-163		l	t		 -		
A AVEN	PENTAPEPTIDE.TRANSFERASE	BACILLUS SUBTILIS	Τ.	247.211		T				L
PHOLEB BACCE	ROD SHAPE-DETERMINING PROTEIN MIREB	BACILLUS CEAEUS	16-213							
PHOLEC BACSU	KOD SHAPE DETERMIN		21159							
PHOKE KLEPH	CHAPERONE PROTEIN MOUSE PRECURSON	KLEBSTELLA PYEUMONIAE	~	{_{1}}		1	+			
PACINC KLEPN	PHAKC RLEPH MAKC PROTEIN PRECURSOR			432.489	282-622	1	1	$\frac{1}{1}$		

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IBRINOGEN. / 10-BIN	STREPTOCOCCUS PYOGENES	Г	99-310							
PHOP STRSU MUNAMIDASE-RELEASED PROTEIN PRECURSOR	T	2	19.13	361.301	877 147					
PROB ATP-BINDING T			412-449		Т	100	Т	8	1058-1085	
PMSKA STAEP ERYTHROMYCIN RESISTANCE PROTEIN	STAPHYLOCOCCUS EPIDERANDIS	Т	33.350							
PAISYB ECOL! ACIDIC PROTEIN MSYB	ESCHERICIIIA COLI	Т								
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SODIFICATION METH	BACILLUS AMYLOLIQUEFACIENS	15-62								
PMTB1 BACAR MODIFICATION METHYLASE BANIII	BACILLUS ANEUNINOLYTICUS	Tr		Ī						
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	TB STRUM NETH TENDENCY ILLEGY FIGURE MOUTL	ESCHENCIA COLI	10.00					1	+	1	
	TO THE THE MISMATCH AFPAIR PROTEIN ANDTE	SALMONELLA TYPHINIURIUM	20.1					1	İ		
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TANDON PRECINSOR	CYCOLYSIN PRECURS	STREPTONIYCES CACADI	100-132						1		
	CATC BROTTE IN PRECIN	•	210-237						1	T	
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13.02 13.03 13.0	TA AVECTOR PRIONAL REC	-	133-260						1		
	JACK BROTER	ESCHERICHIA COLI	15-102						1		
STATE PRECURS STEERMEHT COLI 11-13 13-319 13-31	UVAL TROBOGI LICOSA)	CLOSTALDIUM PERFAINGENS	48-75	990-1017					1		
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PPIOK STRPA	IS KD PROTEIN IN FIMA S'REGION	STREPTOCOCCUS PARASANGUIS	115-149					-			
PPIBK_STRSA		STREPTOCOCCUS SANGUIS	10-37	114-148					İ	Ī	
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PPBP4 BACSU			136-363								
PBP4 ECOL	PENICILLIN-BINDING		145:172			-					
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PPRP STANU	PEMICITEN BINDING P	EUS	╗	176-203	261.124	502-529	1	1	1	1	
PPCAB PSEPU	CYCLOISOMERASE		П	28.33	-	1	1	†	+	1	
PPELI ERWCA	PECTATE LYASE III PA		9			†	†	+	+	1	
PPELA ERWCA		ERWINIA CAROTOVORA				†	1	†	\dagger	1	
PPELB ERWCA	PECTATE LYASE B PRECURSOR					+	\dagger	1	+	Ť	
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PPERT BORBA	PERIODIN PRECURSOR		628-655						-	l	
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PPCS AGTAN		UM BRYANTII	16-63								
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PPGTE SALTY	OUTER MEMBRANE PRO	ועטא	(6-99								
PPHAI FREDI	C-PHYCOCYANIN-I ALPHA CHAIN		11-12						1	Ì	Ì
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PPHAB ANACY	ALLOPHYCOCYANIN B	ANABAENA CYLINDIACA				†	\dagger	1	\dagger	Ì	
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PILAC SYNP6	ALLOPHYCOCYANIN A		33-60								
PPING FREDI	ALLOPHYCOCYANIN GAMONA CHAIN ;		12-59								
PPHB3 FREDI	т		29.56			1	1	1		1	
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PPHEA ERWHE	CHONSMATE MUTASE	Υ.	10-37	159.116	352-286						
PMEA PSESP	PHENOL 1-MONOOXYG		171-201	282-314	437-464						
PPIED MASLA	PHYCOERYTHROCYAN	LAMINOSUS	21-62								
PPILED PSESP			26.51			1	1				
PPHEG SYMPY	LINKER POLYPEPTIDE	3.6	151-165			1	1	1	1	1	+
PPHEP ECOLI			36-31		_	1	†	1	†	1	
PPIFT CLOSA	PENDLASMIC [PE] HY	TEUNIAMUNI	77.			1	†	1	1	T	-
PPIC BACKE	SPHUNCOMPLELINASE		92.			1	1				
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PPILC LISMO	PHOSPI10LIPASE C PR	LISTERIA MONOCYTOGENES	13:174						г	Т	
PPIC PSEAE	HEMOLYTIC PHOSPIIC	PSEUDOMIONAS AERUGINOSA	615-712								
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PPHLD BACCE	PHOSPHOLIPASE C PR	BACILLUS CEREUS	8								
PPFUL LEPIN	SPHINCOMYELINASE C PRECURSOR	LEPTOSPIRA INTERROGANS		394-428							
PPIND ECOLI	-	ESCHERICHIA COLI	196-126								
PPINK ECOLI		ESCHERICHIA COLI	178-205								
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PPHOE CLIFE	OUTER MENIDIKANE PO	CITROBACTER FREUNDII		47-105	_						
PPHOE ECOLI	OUTER MENIBRANE PO	ESCHENCHIA COLI	13-40	64-105	\$61-19	126-153					
PPHOE KLEOX	OUTER MENDRANE PO	KLEBSIELLA OXYTOCA		16-19							
PINOE KLEPN	OUTER MEMBRANE PO	KLEBSIELLA PNEUMONIAE	13-40	54-105							
PPHOE SALTY	OUTER MEMBRANE PO	INTURURI	63-104	130-347							Ī
PPHOP BACSU		8	115-219	Ī	Ī	İ					
PPHOO ECOL!	SENSOR PROTEIN PHO		244-278						Ī		Ī
PPHOO SALTY	VIRULENCE SENSOR P	INURIUNI	326-260	Γ							
PPHOR_BACSU		BACILLUS SUBTILIS	Т	317-425							T
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11.5 KD LINKER POLYPETIDE FRENYELLA DIPLOSIPHON 12-64 11.5 KD LINKER POLYPETIDE FRENYELLA DIPLOSIPHON 106-14] 10.1 KD LINKER POLYPETIDE FRENYELLA DIPLOSIPHON 106-14] 10.1 KD LINKER POLYPETIDE PARMYELLA DIPLOSIPHON 43-70 1.3 KSPATIATE CALBAMONT TILANSFEALSE SERMATIA MARCESCENS 10-91 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.142 11.143 11.142 11.143 11.142 11.144 11.142 11.144 11.142 11.145 11.142 11.		A KO I MYER POLYPEPTIDE	INCOMINA NON	75.7	\dagger	_	1	†	1	Ī	-
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Т	OREDUCTASE		180-213			+		Ţ	
POUEA ECOLI QUEDIOSINE BIOSYNTH	DSYNTHESIS PROTEIN QUEA		107-17	1	-	+			T
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PLACK BACSU PROBABLE AMINO ACT	TOSIDASE		911.68						
Т		ESCIERICHIA COLI	348-375						
PROFILE FOR BIRDSE TRANSPORT ST	PORT SYSTEM COMPONENT	ESCHERICHIA COCI	65-99 195-222	111					
		ESCHEWCHIA COLI	100-219						
PRUSE COUL MEDICAL RESTROPERON	OPERON REPRESSOR	KLEDSIELLA AEROGENES	6.47						
PACCA ECOL MICKWITHESIS	ACTIVATION PROTEIN A	ESCHENCHIA COLI	170.197						
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PACSA KLEAF IBIOSYNTHESIS ACTIVA	ACTIVATION PROTEIN A	KLEBSIELLA AEROGENES	<u>_</u>				1		
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		AGROBACTERIUM TUMEFACIENS	3.30	159 281-301		1	1		
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PRECA_AQUPY RECA PROTEIN		AQUIFEX PYROPHILUS	04-10		1				I
PRECA BACFR RECA PROTEIN		BACTERONDES FAMILIE	70. 100						
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PRECA BRUAB RECA PROTEIN		BRUCELLA ABUNTUS	,	Т	-				
PRECA BURCE RECAPIOSEIN		FRWINIA CAROTOVORA	384.331	-					
PRECA ERWCA RELA FROIEIN		I ACTORACILLUS DELBRUECKII	20-47	-					
PRECA LACUE MECA PROTEIN		LACTOBACILLUS HELVE TICUS	10-47						
PRECA LACTA MECA PROTEIN	-	LACTOCOCCUS LACTIS	135,162 233-369	369 218-315					
PRECA LETCH MECA PROTEIN		METHYLORIONAS CLAKA	166-303						
PRECA METEL MECA PROTEIN		METHYLOBACILLUS FLAGELLATUM	176-303						
PRECA MYCPU RECA PROTEIN		MYCOPLASMA PULAIOMIS	10-57				-		
PRECA MYCTU RECA PROTEIN		MYCOBACTERIUM TUBERCULOSIS	149-776						
PRECA NEIGO RECA PROTEIN	•	NEISSEAJA CONDRUJIOEAE	261-310			1			
		PROTEUS MIKABILIS	016.167	1		1			I
PRECA PSEAE RECAPROTEIN		TOCOCOMOTAS AEROGIACOS	1.10	158 250.307					
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		RHODOBACTER SPHAEROIDES	Т						
PRECA STRPN RECA PROTEIN		STREPTOCOCCUS PHEUNIONIAE	134-161 293-327	127					
-		SYNECHOCOCCUS SP	151-121						
PRECA VIBCH RECAPROTEIN		VIBRIO CHOLERAE	190-317						
		BACILLUS SUBTILIS	П	See			-		
PRECE ECOLI RECE PROTEIN		ESCHERICILIA COLI	12.109 147.174	174					
+-		PROTEUS MINABILIS	16-113				-		
PAECF PSETU RECF PROTEIN		PSEUDOMONAS PUTIDA	111-11						
•		SALMONELLA TYPHINIURIUNI	147.174				+		-
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S	ON PROTEIN	BACILLUS SUNTILIS	11-48 156-184	184 192-247	299.336	344.378			
	E NECO.	ESCHENCHIA COLI	461.495	+	_				I
PRELA_ECOLI GTP PYROPHOSPHOKIN	SPHOKINASE	ESCHENCHIA COLI	اء						
PREMA BACSU REPLICATION AND MA	AND MAINTENANCE PROTEIN	BACILLUS SUBTILIS	20.10	8 1	1	+	+	\downarrow	
PREMA STAAU REPLICATION AND MA	AND MAINTENANCE PROTITION	STAPHYLOCOLCUS AUREUS		1		$\frac{1}{2}$	1		

PUCCENT	1105.170.4	Prokacyotic Sequences	1				_		П	\prod
FILEPANE	PROTEIN		4	T VIET	ABEAL AREAS	A4 AREAS	AS ANEAS	AREA?	AREAI	AREAS
PREMA STAEP	REPLICATION AND MAINTENANCE PROTEIN		6.13	2.8		$\frac{1}{1}$	_			
LYEN ECOL	REPLICATION FAULER	2	٦		-	l	-	L		
TALLY BALSO	-		Т	231.355						
PREPA NEICO	REMICATION PROTEIN	UIDEAE	Π	116.172	-					
PREPBILACH.	REPLICATION PROTEIN RETO	LACTOBACILLUS PLANTARUMI	184-211							
PREPM STAAU	•	STAPHYLOCOCCUS AUREUS	24-284			1				
PREPIN STAND	-	STAPHYLOCOCCUS AUREUS	226-285		+	+	+	-		
PREPR STANG	AEPR PROTEIN	A.	2000		1	+	1			
PREPS STRPY	REPS PROTEIN	STAPLICICACION PROCENES	91711	917:710	-	+	+	-		
PRETA STAND	REF PROTEIN	FICHERICHIA COLI	311.11			-		-		
1000	REPLICATION PROTEIN	CLOST NDIUM PENFINGENS	164-195	297.524	343.378			L		
PREP ECOLI	REP HELICASE		Т	205-243						
PREP LACEL	REP PROTEIN	M		260-287		H				
PRESP CLOPE		UNGENS	68-102	151-185						
PLES BACSU	EPTIDE CI	2	34-68							
PAG ECOLI	PEPTIDE CHAIN RELEASE FACTOR 2	ESCIENCHIA COU	29 -113	163.204		1				
PAEL SALTY	PEPTIDE CHAIN RELEASE FACTOR 2	SALMONELLA TYPHINURUM	2	63.50	1	$\frac{1}{1}$				
PRS ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	ESCHERICHIA COLI	00.210	(/2/)	1	+	1	\downarrow		
LAN ECOL	ILEGALACTOSYLIKANSPERASE	ESCHERICHIA COLI	18.212			1	+	+		
TATA ECOL	BIOSTRIPESIS FACILIA MANO	ESCHERICHIA COLI	96	233-768		$\frac{1}{1}$		-		
PIEAL SALTY	1 2-CLUCOSYLTRANSFERASE	SALMONELLA TYPHINURIUM	64.93	145-172	136-263					
PILTAE SALTY	1 2-N-ACETYLGLUCOS	SALMONELLA TYPHIMURUM	135.369			L				
PINTAL ECOLI	O.ANTIGEN LIGASE	ESCHENICHIA COLI	366-393							
PIUAL SALTY	O-ANTIGEN LIGASE	SALMONELLA TYPHINURIUNI	326-360							
PRFAP ECOLI	BIOSYNTHESIS PROTE	ESCHERICHIA COLI	3			+				
PREAS ECOLI	BIOSYNTHESIS PROTE	ESCIENCIIIA COLI	67:10	94.240	-	+	1			
PREAY ECOLI	BIOSYNTIESIS PROTEIN RIAT	ESCHENCIIIA COLI	9	23152	1	$\frac{1}{1}$	-	-		
AL VALUE OF LAND	DITTO CHINCOSE A C.DE	SALMONELLA TYPHINGURIUM	130-159					 -		
PRUBIN SALTY			113/361							
PRFBS SALTI	-	SALMONELLA TYPHI	22-56	205-232						
PIVEA VIBAN	-	VIBRIO ANGUILLARURI	349.376							
PRFH ECOU	PEPTIDE CHAIN RELEASE FACTOR HOMOLOG	ESCHENCHIA COLI	9			+				
PRG12 BACTU	PUTATIVE GIZ SITE. SPECIFIC RECOMBINASE	BACILLUS INUMNIENSIS	13.08	190-262	310-313	+	+	1		
PROM ECOL	RHAMMULOKINASE	CAL MONE I A TYPING BUILD	207.50		+	+	1	+		
PERME FOR		ESCIENCIA COLI	0.0			+	+	+		
PRUIAS ECOLI	L. PULAMNOSE OPERON	ESCHENCHIA COLI	152-179		-		-			
PRHIT RHILV	RHIR REGULATORY PR	RHIZOBIUM LEGUMINOSARUM	206-233			Н				
PRHALB ECOLI	RNA HELICASE IMLBANDRA	ESCIÆNCIIIA COLI	19:165							
PLHO BORBU	TRANS TERM FACTOR INO	BORRELIA BURGOOMERI	77.5	327.369	1	+	1	+		
PRIOR BACSU		ESCUEDIOUS CONTRACTOR	W		+	+	+			
PRHSA ECOLI	MASA PROTEIN PARCURSOR	ESCHENCHIA COLI	107.00		+	+	+	\downarrow		
TANS ECO.	PAINT PROTEIN PRECINSOR	ESCIENCIA COLI	10414	667.694	1010-101	+	+	-		
200	_	ESCHENICINA COLI	671.712	1001-1001		+	-	+		
THE ECO.	RHSE PROTEIN	ESCHEDICHIA COLI	345.372		+		-	-		-
PRING ECOLI	ACETYL TRANSFERASE	ESCHEAUCHIA COLI	93.127			L				ŀ
PRINT ECOLI	NUBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	ESCHENCHIA COLI	167.194			-		L		
PRUSA PHOLE	RIBOFLAVIN SYNTHASE ALPHA CHAIN	PHOTOBACTERIUM LEIDGNATIII	3-43	131.158		H				
PRISE BAGSU	RIBOFLAVIN SYNTHASE BETA CHAIN	BACILLUS SUBTILIS	<u>:</u>			1				
PRISB PHOLE	AUBORLAVIN SYNTHASE BETA CHAIN	PHOTOBACTERUM LEIOGNATHI	7				1			
PALIO STRAT	- 1:	SINE IONITCES ANIMIDICOS	2	6		+		+		
PALES SYNYS	105 KIROSOMAL PROTEIN LIZ	STRECHOCTSHISSE			1	1	1	$\frac{1}{2}$		

		107:170:4		AREAL	73157	ARCAJ A	7 FVIEV	25.0	1000	d		
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STEROGOLAL POTENT STELLING COCCUS LATER STEROGOLAL POTENT		SOS RUBOSOMAL PROTEIN LIA	MICROCOCCOS COTECOS	26:15								
STEEDGOLAL POTEIN 1		SOS RIBOSONIAL PROTEIN LIA	MICULASAIACAMOCOCOM	1717								
100 100		SOS NIBOSONIAL PROTEIN LIS		94.134								
SER INDOCOMAL PROTEIN STATULOS TOLIN STATULOS STREET	1	SOS NIBOSONIAL PROTEIN LIS		66.5								
SST BROGONAL POTENT SCHANTON STATE	SBACSU	SOS RIBOSOMAL PROTEIN LIS										
STATE	15 P.O.	SOS RIBOSONIAL PROTEIN L15	CITLAMYDIA TRACIIONIATIS									
	2	SOS BIROSOMAL PROTEIN LIS	ESCHERICHIA COLI									
19 19 19 19 19 19 19 19		SAC PERSONAL PROPERTY.	LACTOCOCCUS LACTIN	5.5								
MINOSTALL FORTILLY MINOSTALLY 1911 1	5	NO PRINCIPAL PROPERTY OF	METHANOCOCCUS VANNILLI	64.102								
ACCOLLAND IN TOTAL IN TOTAL IN TOTAL IN TOTAL IN TOTAL IN TOTAL FOLIAN IN TOTAL IN	METVA	MOS RIBOSCINIAL PROTECTION	NACORI ACUA CAPRICOLUM	\$1.13								
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19 19 19 19 19 19 19 19		CON BIRDADAIAL PROTEIN LIS	HALDARCULA MARIKMORTI	27:10								
STATEMENT STAT		PROTEIN	METHANDCOCCUS VANNIFILII	45.72								
MINOSONAL PROTEIN 19.17 FOUNDS TOLAR ARTICLS 19.17 14-21 14-	N.E. V.	TRUBARIE VOI MINOSO	PROTEUS VIJ.GARIS									
VOID STATE VOI	PROVU	SOS RUMOSONIAL PROTESSA CI	PIN POLITIC COL SAFABICE C	3	184-211			_				
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STATE STAT		SOS RIBOSONIAL PROTEIN L'10	ESCHERICHIA COCI									L
SATERIORS SUMPLIES 18-15	٢	SOC BIRDSONIAL PROTEIN L'70	MIYCOPLASMIA FERMENTANS									
10.00 10.1	Т	STATE OF STA	BACILLUS SUNTILIS	•								
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VIEW VIEW		SOS AUBOSONIAL PROTEIN L22	EXPENSION	5								
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150 150	7	CAC PIROCONIAL PROTEIN L'33	MYCOPLASMA CAPNICOLUM	32-39								
15.00	_	AND PROPERTY OF THE PARTY OF TH	HALOARCULA MANISMORTUI	48-75								1
15 15 15 15 15 15 15 15	\neg	NO KINGSOMINE PROPERTY SA	METHANOCOCCUS VANNIELII	61.90								
15.50 15.5	METVA	105 IUBOSONIAL PROTEIN LA	MICEOCOCCUSTUTEUS	16.63								
STATE STAT	אוכנע	SOS RIBOSOMIAL PROTEIN LA	CHI ANYDIA TRACIONATIS	19.66								
150 150		SOS AIBOSOMIAL PROTEIN LAV	CHANGE COMPANY	16.61								
STATE STAT		SOS RIBOSONIAL PROTEIN LIFE	EXCHENCIAL								L	L
100 100	4	SOS RIBOSONIAL PROTEIN L29	MITCURLASMA CACRICOLORI								L	L
144-174 144-	1	SOS RUBOSONIAL PROTEIN LA	BACILLUS STEAKUTHERATORIHLUS	8								
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19 19 19 19 19 19 19 19		ASSESSMENT OF THE STATE OF THE	THERMUS AQUATICUS	31-65								
19-46 19-4	L L	A LANGUAGE TO THE PARTY OF THE	IBACILLIS STEAROTHERAKOMILUS	79.106								
150-150 150-	BACST	SOS ICIBOSCHAL PROTECTA LO	ESCHEDICHIA COLI	19.46								
STATE STAT	ECOLI		PARTITION OF THE VANNET II	130.150								
SACRECUS AND PROTEIN L9 BACRECUS AND PRODUCED 122-149	METVA		ME INANCOCCO CANADA									L
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ACIDIC NIBOSOMAL PROTEIN PORGOCOUS MAINTENED STATEMENT 15-16 1-19	O HALMA	ACIDIC AIBOSOMAL PROTEIN PO HUMULUO	TOTAL CONTROL OF THE PARTIES IN	187.331								L
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100 100	ALIVITY		_	67.2	İ							1
METHANOCOCCUS VANNIELII 1-19 1-			_	5.29								
785 RIBOSOMAL PROTEIN HAT MICROCOCCUS LUTEUS 15-32 90-117	1	_	METHANOCOCCUS VANNIELII	2.29								4
13 TO FEL XX TION PROTEIN SALMONELLA TYPHINTRUIM 136-160 102-131 171-210	X	MINDUSOMAL PROJECT	MICROCOCCUS LUTEUS	2	8-17		L					-
11. X PROTEIN 1.1. STAPHYLOCOCCUS AUREUS 1.50 102-133 171-218 12. X PROTEIN 1.2. X PROTEIN 1.2. X PROTEIN 1.50 102-133 171-218 12. X PROTEIN 1.2. X PROTEIN 1.50 102-133 101-301 102-3	A MICEO	TO KIBUSOMOL TAN	SALMONELLA TYPHINUNUM	176-160	L	-		L				
12 KD RELAXTION PROTEIN SALMONELLA TYPHIBAURIUM 19-33 ALX PROTEIN STAPHYLOCOCCUS AUREUS 3-30 103-133 ALX PROTEIN STAPHYLOCOCCUS AUREUS 3-30 146-216 ALX PROTEIN STAPHYLOCOCCUS AUREUS 3-30 146-216 ASS RIBOSOMAL PROTEIN LX 1 SALFARICUS 3-30 146-216	X1 54-11	S V PROVER	STAPITY OCOCCUS AUREUS	0:1	102-133	177.218	266.300					4
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PRINS ECOLI	REGULATORY PROTEIN RNS		116-160								
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PRPS4 ALCEU	RNA POLYMERASE SIGMA-54 FACTOR		229.266								
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PRPIO MYXXA	RNA POLYMERASE SIGNA-80 FACTOR 6		T	Т	39.106					Ī	Ī
PRINCE SYNDY	BILIN BIOSYNTHESIS PROTEIN RPCF		180-207				-			Ī	
PIUDA BACSU	DNA.DIRECTED RNA POLYNERASE ALPHA CHAIN		\$5.107								
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	SUCROSE PORIN PRECURSOR			240-267		-					
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	PREPROTEIN TRANSLOCASE SECA SUBUNIT	2	П	336-360							
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7	PROTEIN EXPORT MEMBRANE PROTEIN SECF		174-201								
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PSECY METVA PR	EPROTEIN TRANSLOCASE SECY SUBUNIT		131-161	196-423							
PSECY STACA PR	PREPROTEIN TRANSLOCASE SECY SUBUNIT	STAPHYLOCOCCUS CARNOSUS	161-61			_					T
7	FC PROTEIN PRECURSOR	Atibis	137-164	475-535							
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┱	CELL SUMFACE PROTEIN PRECURSOR	5	Ţ	282-309	113.433	451-419 5	\$17.544	361.593	\$19-170	136.735	
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	SOMB PROTEIN PRECURSOR	Ī	T	10.01	27.10	+	1	Ì	1	1	
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	STAGE II SPORULATION PROTEIN AA	KIUM	19.53			T	T	T	Ì	Ī	
FSZZA BACSU SIA	STAGE II SPORULATION PROTEIN AA		21.55			-		T	Ī		
	CTACE II SPORTE ATTOM PROTEIN AN	BACILLUS LICHENIFORMIS	43-69								
ATT BATTER	STACE II SOCIETA ATION PROTECTION		19:13								Ī
_	POSSIBLE ASPARTY PROTERSE		≣								
7	CTACE II COOMIN ATTOM PROTEIN			17.144							
•	STAGE III SPORTE ATION PROTEIN D	BACILLOS SUBTILIS	Ī	463.500							
PSP31 RACOU STA	STAGE III SPORULATION PROTEIN I PRECURSOR		26	32-86		1					
+	STAGE IV SPORULATION PROTEIN A						1				
+	STAGE IV SPORULATION PROTEIN B			1	+		1				
PSP4G BAUSU STA			241.278	1	+	\dagger	1				
SPSA BACSU STA	STAGE V SPORULATION PROTEIN AF		9.36		\dagger	†	1	+	1	1	1
PSPAA_STRDO AN	ANTIGENI	WINEI	114-211	\dagger	+	\dagger	\dagger	\dagger	1	1	
SPAB BACSU SUE	SUBTILIN BIOSYNTHESIS 117 KD PROTEIN		191-200	r	\mid	\dagger	l	t	\dagger	1	
PSPAC BACSU SUB	SUBTILIN BIOSYNTHESIS PROTEIN SPAC	BACILLUS SUDTILIS	311-338	F	t	+	\dagger	t	T	T	T
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	PROTEIN SPAT			226-267		1				1	
	CURSOR	STREPTOCOCCUS PYOGENES								1	
Т		SPIROPLASNIA CITRU	13:109	185-182							
T		IFERUNI	195-222								
STIN STIME	A IOSOLIOCA T. PYBORIOCERIO! YOROLA		637-664			ľ					
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Т	PARTICLE PROTEIN	ESCHENCHIA COLI	301-328							1	
Ъ		COIDES	21-65	107-141	194-428						
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		ESCHERICHIA COLL	\$6-19							-	
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T	E PRECURSOR		611.06	172-199	310.311						
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	NSC CONTROL PROTEIN			Ī						1	
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Г	OSPHATE AMIDINOTRANSFERASE I									1	
1	CURSOR			281-308						1	
Т	ECURSOR	STREPTOCOCCUS PYOGENES	209-236								
Т	ECURSOR /		209-236	10(-117							
1-	AR PROTEASE EPR PREC		415-462	522-563	603-639						
7	PRECIPECOR.	BACILLUS SUBTILLIS	40.67	9.116	121-141	554-597				H	
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PSUBT BACST		HERMOPHILUS	197.234		-						
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PCIMY PACELL			\$5.108	959-519	741.768						
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PEYE THETH	GLUTAKIYL. TRNA SYNTHETASE	Sr	165-432		•					~	į
PEYSA RACKLI			7.34								
SYFR BACSU	PIENYLALANYL. TANA SYNTHETASE BETA CHAIN		340-367	107-441							
FCOL	PHENYLALAWYL-TRNA SYNTHETASE BETA CHAIN		546-573	607-634	144.771						
CVCB ECOL		ESCHENICHIA COLI		487.514							
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TO SAN	PROLYTERA SYNTHETASE		\$41-568					T	Ī	Ī	T
PSYO ECOL	GLUTAMINYL-TRMA SYNTHETASE		18776								
PSYRD PSESY	SYAD PROTEIN	RINGAE	449-483								
PSYR ECOLI	ARGINYL-TRNA SYN		\$40.534								
PSYTI_BACSU				6(9:509							
PSYV BACST	VALYL-TRNA SYNTHETASE	THERMOPHILUS									
PSYV ECOLI	VALYL-TRNA SYNTHETASE				924-951						
PSYW BACST		HERNOLIHI.US		139-266							
PSYYL BACSU	TYROSYL. TRNA SYNT		Ž	175.409							
PSYY2 BACSU	TYROSYL-TRNA SYNT										
PSYY BACCA	TYROSYL-TIMA SYNTHETASE		7	177-416							
PSYY BACST	┪	THERMOPHICUS	7	7							
LIMI ECOL	ENZYME ECORI247		-	П	485-512	\neg	П				
FTIRI ECOLI	ENZYNE ECORI24/3 P		П	159-979	302-736	161.793	643.670	0001-996			
PTIR ECOLI	ENZYME ECOK I R PROTEIN		38-363								
	ENZYME ECONIZAS I SPECIFICITY PROTEIN		2					1		1	
FISA ECOL	ENZYME ELUA I SPELIFICAT FROTEIN	ESCHENCHIA COLI	8						1		
L SB ECOL	ENZYME ECON I SPECIFICATY PROJEIN							1			
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277		101	Т	704 766	100						
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PIZA ACICA	TYPE II RESTRICTION ENZYME ACCI	ALCOACETICUS	Т	Т		Т	Т	*			
	TYPE II RESTRUCTION ENZYNCE BSUF!		T	13.23	236.210						
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l 1	TYPE II RESTRICTION ENZYME CTAB!		П	П	П						
PT2C1 HERAU	TYPE II RESTRICTION ENZYME HGICL		176-215								
PT2C2 HERAU	TYPE II RESTRICTION		10,473								
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PIZOI SINCE	TYPE II RESTRICTION	STALFTOCOCCUS PREUNIONIAE	P								
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	AN A PRECURSOR R.	501			195-119 195-119 195-119 115-24) 115-24) 115-219 196-119			199		
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	URSOR PROTEIN B PREC THESIS PROTEIN C THESIS PROTEIN C THESIS PROTEIN F THESIS PROTEIN T T THESIS PROTEIN T T T T T T T T T T T T T T T T T T T	501			40-470 115-243 175-403 175-403 179-106			199-416		
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	HESIS PROTEIN E THESIS PROTEIN E ENGELNI I PRECURSOR SALATORY PROTEIN TCDT COC PRECURSOR TOC TOC PROTEIN TOC PROTEIN	HOEAE IETTII IMURUUN HERNOPHILUS AUREUS			195-21 115-42 115-42 199-21 179-106			159-186		
	THESIS PROTEIN F PROTEIN I PRECURSOR PRASE SULATOR PROTEIN TOT CPC PRECURSOR SIS PROTEIN TOTE STROTEIN TOTE STROTEIN TOTO CE PROTEIN ANCE PROTEIN ANCE PROTEIN	HOEAE ETTII IMURUM HERNOFIIILUS AUREUS	0 0 0 0 0 0 0		196-213 199-213 179-106			987-		
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	EASSE SILATORY PROTEIN TCDT TCO PRECURSOR ROTEIN TCP ROTEIN TCP ROTEIN TCP ROTEIN TCP RECULATORY PROTEIN	IIILUS			175-401			987		
	ULATORY PROTEIN TOD CPC PRECURSOR ROTEIN TOP ROTEIN TOP IS PROTEIN TOP REGULATORY PROTEIN REGULATORY PROTEIN REGULATORY PROTEIN REGULATORY PROTEIN ANCE PROTEIN ANCE PROTEIN	IIILUS			279-106			917-19		
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	REGILATORY PROTEIN SIS ROTEIN 1 CPV SIS ROTEIN 1 CPV SIS ROTEIN 1 CPV ANCE PROTEIN ANCE PROTEIN ANCE PROTEIN ANCE PROTEIN		48.75 710-257 121-148 44.85 404-434 422-451 404-431							$\frac{1}{1}$
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	SIS PROTEIN TCPY SIS PROTEIN TCP2 ANCE PROTEIN ANCE PROTEIN ANCE PROTEIN ANCE PROTEIN	VIBRIO CHOLERAE VIBRIO CHOLERAE BACILLUS SUBTILIS BACILLUS STERADTIERASIOPIILUS STAPHYLOCOCCUS AUREUS	121-148 44-83 404-434 422-431							
	SIS PROTEIN TCP2, ANCE PROTEIN P ANCE PROTEIN FANCE PROTEIN FANCE PROTEIN	VIBRIO CHOLERAE BACILLUS SUBTILIS BACILLUS STEAROTHENJOHILUS STAPHYLOCOCCUS ÁUREUS	44-85 404-434 422-453 404-431							
	ANCE PROTEIN FANCE PROTEIN FANCE PROTEIN	BACILLUS SUBTILIS BACILLUS STEAROTHE RAIOPHILUS STAPHYLOCOCCUS AUREUS	404-434							
	TANCE PROTEIN TANCE PROTEIN TANCE PROTEIN	BACKILUS STEAROTHERMOPHILUS STAPHYLOCOCCUS AUREUS	404-431							
	TANCE PROTEIN	STAPHYLOCOCCUS AUREUS	164-431						+	$\frac{1}{1}$
	ANCE PROTEIN			֡						\prod
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	ANCE PROTEIN	STREPTOCOCCUS PNEUNIONIAE	37.53						+	
_	IN TRANSCRIPTIONAL ACTIVATOR	ESCHENCINA COLI	210.230						1	
7		ESCHERICIIIA COLI		161 191	117				+	-
PTEES STAPY TRYPSIN	T	STREPTOCOCCUS PYDOLINES	7	car-lor						
_	TETRACYCLINE REPRESSOR PROTEIN CLASS B	ESCREDICITA COLI	27.0							
П	TETRACYCLINE REPRESSOR PROTEIN CLASS U	ALCAL CENTRAL	9							
-	IUM MESISTANCE PROTEIN 1CAN	ECHERICAL COLI	T							
PTESB ECOLI ACTICO	ACTUACON INDESTERASE IL	ENTEROCOCCUS FARCALIS	Γ	10-130	79.206	217.244				
-		ENTEROCOCCUS FAECALIS	Г	130-139	217.344	260-287				
-		ESCHENCHIA COLI		116-131						
1		STREPTONIYCES LIVIDANS	83-109						-	
12	TETRACYCLINE RESISTANCE PROTEIN TETM	UREAPLASMA UREALYTICUM	П	130-139	217.244	265-217			1	+
		CANIPYLOBACTER COLI	2.29						-	1
	TETRACYCLINE RESISTANCE PROTEIN 1610	CAMPYLOBACTER JEDNI	2						1	+
		STREPTOCOCCUS MUTANS	2.29							
		BACTEROIDES FRAGILIS	┪						-	1
	TETANUS TOXIN PRECURSOR	CLOSTRIDIUM TETANI	1	26.267	615.642	692.719	785-1012	1240-1277		+
•		PYROCOCCUS WOESE!	218-258						+	+
	CHLOROCATECHOL I,3-DIOXYGENASE	ALCALICENES EUTROPHUS	2							
PIGT ECOCI QUEUTA		ESCHENCHIA COLI	13.200						+	+
	THOLEONINE DEITYDRATASE BIOSYNTHETIC	LACTOCOCCUS LACTIS	267.303							1
PINDS ECOLI TIPLEON	THUE ONINE DEHYDRATASE CATABOLIC	ESCHENCHIA COLI	293-320							1
PRIDE BACSU FURANCE	FURAN OXIDATION PROTEIN THUF	BACILLUS SUBTILIS	7	92-26	365.718	200				
PTIIDE ECOLI FURAN	FURAN OXIDATION PROTEIN TILD?	ESCHENICHIA COLI	Т	25					+	
	FURAN OXIDATION PROTEIN THUF	PSEUDOMONAS PUTIDA	3	270 070					\dagger	+
PTHER BACCE THERMAC		BACILLUS CELEUS	T	197-067						1
PTHER BACST THERMO	THERMOLYSIN PRECURSOR	BACILLUS STEAKOTHERMOPHILUS	77.6							

	PCGENE 107s178s4	Prakaryotic Sequences		-1		_		_	1		
	FILE MAME PROTEIN	ORGANISM	N N	т		_	48543		4	AREAL	AKEA!
	PINER BACTH THERMOLYSIN	BACILLUS INERMORROI EULT III.US				T			1		
		THERMOACTINOMYCES VULGARUS	131-161								
	Į	ESCHENCHIA COLI	237-763	301-328							
INCOMES SYNTHASE INCOMES SYN	THIG PROTEIN	ESCHENCHIA COLI	131-163	_	1						
Integrated State S	THERMOPSIN PRECURS	SULFOLOBUS ACIDOCAL DARIUS	135-172	199-233							
The Profest, M. Standard, Profest, Pr	THIREONINE SYNTHASE		238-315								
Indicate Note	PUTATIVE THIOSULFAT	Г	96-69								
TEPOSTELLA, LEGARIANE ROLLER N. P.	•	ESCHENCHIA COLI	144-171								
TEPOSECIAL GEORGIANE ROLLEGY INFORMAL PALLIDAN (14.1) 11.10 11.1	TREPONENAL MENBRA	•	336-266								
Transitional programmer Transitional pro	TREPONEMAL MENGEL	_	44.78								
This STORY AND TRANSPORTED BY THE STATEMENT OF THE STAT	TREPONEMIAL MEMBER		41-61								
Interview Inte	OTEVET VINCENTAL	-	74.108								
MANSON INTEGRACION NOTES 1747 1	┱	ESCHENCHIA COLI		37.							
Interviged Act		STAPHTLUCCUS AUREUS	27:76	A (-) / (-)							
INVARDAGE STANTOCCCCUS ALABLES 111-11 11		ENTEROCOCCUS FAECALIS	19.97	111-13							
INTENTIONAGE STANITOCOCCUS ALABELS 142 11-10	_	STAPHYLOCOCCUS AUREUS	151-171								
Part Person Part		STAPHYLOCOCCUS AUREUS	\$19-625								
TANSPORDER IN LANSFORLION PAGE IN 1942 1943 1944 1943 1943 1944 1		BACILLUS THURINGIENSIS	7-62	65.92	174-201						
TANGENGON TRIL LASSESCENCE TO 19-26 10-27 10-2	THANKPOSON TNI TRAP	+-	99.126	\$10.537							
TAMESPOCION IN TAMESPOCIION ROTEIN TASS	TO ANCEDICAN THE TRANS	+-	32.59	114.341							
TOTALDER 1.2 DOING TOTAL SEE STORMEN STEELS 19-10 TOTALDER 1.2 DOING TOTAL SEE STORMEN SEE STORMEN STEELS 19-10 TOTALDER 1.2 DOING TOTAL SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEE STORMEN SEED SEED SEED SEED SEED SEED SEED SE	THE LAND SOUTH THE TANK	+	110.144								
TOURSE 1, 2000/TGEMASE ALPHA SUBURIT FISTEDOMONAS PUTIDA 19-11	7	-	197			Ī					
OLLOWER 12-BIONYCERALS STATES PREDOMONAS PULBA 19-31	_	-									
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YATO GERMASE 1909-101 1909-	XYLULOSE KINASE	US		311-238	260-287						
VATORE REPRESSOR PACILLUS SUBTUS 15-102 160-181 11-215	XYLULOSE KINASE			Π	209.236	246-273					
VALORE REPLETATION LACTORACILLUM SECTION 19-23 19-135 19	XYLOSE REPRESSOR		75-102	260-287							
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ELECTRON TAXASSER COMPONENT PSEUDOMONAS PUTIDA 191-319 191	XYLOSE REPRESSOR			101-138	181-218	331-388	274-301				
PATATIVE ENDO-1, DE TAYNAMASE CALDOCELLUM SACCIANOLYTICUM 19-233 13-30	ELECTRON TRANSFER COMPONENT .		╗	2							
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ENDO-1.4 BETA-XYLANASE PECURSON PSEUDONIONAS FLUORESCENS 13-13 11-34 14-34	ENDO-1, 4-BETA-XYLANASE PRECURSUR, 3		+	3,6,3,6				T			
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INTERPOLITE CALDOCELLUM SACCIARULYTICUM 440-77 171.344	BETA-XYI OSIDASE		59-416								
ALPHALLARABINOURANSE PRECURSOR 915-310 131-314 1	DETA: XYLOSIDANE	CHAROLYTICUM	140-474								
ALTHANIA AND BINDER CRANGURSON PSEUDOMONAS FLUORESCENS 11-38 151-319	ENDO-1 4-BETA-XYLANASE PRECURSOR 'S		T	311.378	317.344	475-502					
HYPOTHETICAL 31 N. DPAOTEIN 1. STREPTONYCGE LIVIDANS 19.110	ALPHA-L-ARABINOFURANOSIDASE C PRICURSOR		Г	181-278							
INTOTITETICAL 14 9 ED PROTEIN 1	ENDO-1,4-BETA-XYLANASE C PRECURSOR.		103-210								
INFOTITETICAL 31) R.D.PROTEEN	HYPOTHETICAL 14.9 KD PROTEIN ;		19.61								
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HYPOTHETICAL 15 % DO PROTEIN ESCHERACHIA COLL 171-259	HYPOTHETICAL 36.7 KD PROTEIN '.		128-162	172-218							
HYPOTHETICAL 31 9 KO PAOTEIN SECUEDAMONAS FLUORESCENS 21-20	HYPOTHETICAL 14 & KD PROTEIN		171-298								
HYPOTHETICAL 16 & RO PROTEIN ESCHENCHIA COLI 153-72 153-15 154-15 155-15	HYPOTHETICAL 33 9 KD PROTEIN	JORESCENS	24-30								
HYPOTHETICAL 15 & R.O. PROTEIN SECIENCHIA COLL 135-139	HYPOTHETICAL SO I KO PROTEIN		27.5								
INTOTILETICAL 28 S. D. PROTEIN INTOTILETICAL 28 S. D. PROTEIN INTOTILETICAL 19 S. D. PROTEIN	HYPOTHETICAL S6 KD PROTEIN 1		52.33								
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170 12 12 12 13 13 13 13 13	HYPOTIGETICAL 63 9 KD PROTEIN				•]						
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	HYPOTHETICAL 21 6 KD PROTEIN		П	14.144							
IYPOTIGETICAL PROTEIN , CLOSTALDIUM ACETORULY LICLNI 21-55 NVÁSIN PRECURSOR 1 YERSÍNIA ENTEROCOLITICA 196-319 141-214 NVÁSIN PRECURSOR 3 YERSÍNIA PSEUDOTUMERCULONIS 155-312 191-340	INPOTITETICAL 16 9 KD PROTEIN		13.159	961-591	210.237						
YERSINJA ENTEROCOLITICA 196-219 141-214 YERSINJA PSEUDOTUMERCULONIS 135-212 191-360	IYPOTHETICAL PROTEIN										
YERSINIA PSEUDOTUMERCULOSIS 1255-282	_				118.381						
	į			207.360							

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PYAEA RICKI	17 KD FROTEIN	TISII	107:134					Ī			T
т			221-248								T
	HYPOTHETICAL 29 1 KD PROTEIN		14:31								
Т			22-22		1						
_	HYPOTHETICAL PROTEIN	ESCRIBIGION PENCONOMI	3 3					1			
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PYAIR BACH	HYPOL ATP-BINDING TRANSPORT PROTEIN		=	Т			T			T	T
PYATS MYCGA	HYPOTHETICAL PROTEIN		=			Ī	Ī				
		MYCOPLASMA GALLISEPTICUMI	39.56	2.8							
	HYPOTHETICAL SO KD AVIAULENCE PROTEIN	NIPESTRIS	Γ	199.116				•			
			49:39								
	HYPOTIETICAL ABC TRANSPORTER		69-9		П						
_,,	HYPOTHETICAL 9 1 KD PROTEIN	ESCHERUCHIA COLI	2:2								
	HYPOTHETICAL I4 I KD PROTEIN		97.124								
	IVPOTICETICAL 24 5 KD PROTEIN		14-61								
PYCBA ECOLI	HYPOTHETICAL PROTEIN		2								
PYCBL BACKY	AVPOTHETICAL 173 KD PROTEIN	OKNIS	8								
PYCEA BACLA	APPOINE TICAL PROTEIN				1						
TCIC ECOCI	HYPORIETICAL 23 VIO PROTEIN	ESCHENCIAIN COLI	*		1		1		Ì		
COLUMN ALCON	MACHINE SICKLE OF PROPERTY						1		1		
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	HYPOTICE TICAL PROTECT		Ţ		1		T	1			T
	TYPOTHETICAL 43 1 KD PROTEIN					T	T				T
PYCPS SYNPY H	HYPOTIGETICAL 19 1 KD PROTEIN	SP	194-331				T				Ī
	IYPOTHETICAL 18 0 KD PROTEIN			20:134				Ī			T
PYCPS SYNYS II	INPOTITETICAL 19 S KD PROTEIN		117.304								
7	HYPOTHETICAL PROTEIN	MINOSUS	£.								
_	IYPO PHYCOCYANIN OPERON PROTEIN Y	PSEUDANABAENA SP									
PYCHA BACTA	HYPOTHETICAL MITTORIES		2.2	2		1	1	1			
TE	HYPOTHETICAL PROTEIN		T	N. S.	1				1		
-	YPOTHETICAL 61 4 KD PROTEIN	JRANTIACUS	I	Ŀ	360.416		T	1	1	1	
	HYPOTIETICAL PROTEIN		T	Т	Т	133.367	295.339	458-485	676-717	136-1161	400.1410
PYDDD ECOL! H	IYPOTHETICAL PROTEIN		10-101		Т	Т	Т	Т	1	-	
	HYPOTHETICAL 16 1 KD PROTEIN		П		126-753						
- 1	YPOTIETICAL 10 1 KD PROTEIN	ESCHENCHIA COLI	П	421-452	621-648						
	HAPOTHETICAL 40 KD PROTEIN		27.55		1				1		
PYDEJ ECOLI	HYPOTHETICAL IS I KD PROTEIN		5		1	T	1				
_	HYPOTHETICAL 65 5 KD PROTEIN		3	28.55	\$65.592	T	T		1	1	Ì
Ξ	HYPOTHETICAL II 3 KD PROTEIN		Т	Т			T	Ī	T		
PYDOL SULSO H	MYPOTHETICAL 14 7 KD PROTEIN (17.58	16.10				Ī	T	T	
PYDOJ SULSO H	HYPOTHETICAL 169 KD PROTEIN	ATANCUS	Γ				Ī		T	T	
PYEBA ECOLI H	HYPOTHETICAL PROTEIN .		91:18						Ī	Ī	T
	IYPOTHETICAL 18 7 KD PROTEIN		50.77				T	T	T		
	HYPOTHETICAL 18 I KD PROTEIN		43-70		-						-
	TYPO 49 I KD TRANSPORT PROTEIN		147-174		-	[Γ	Ī	Ī	T	T
	HYPOTHETICAL IN DCD J'REGION		145-172		ŀ				T	T	-
PYEN ECOLI H	HYPOTHETICAL 369 KD PROTEIN		69.106	283-310							T
_	HTPOTIETICAL 92 1 KD PROTEIN			501-545					T		
┱	HYPOTHETICAL 191 KD PROTEIN		8-133								
TYEN ECOC	HATOIRE II CAL MICKOTRIN	ESCHEACHIA COLI	٥					Ī			
1	HOME TO THE PROPERTY.		25.78	102-179				1			

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FILE MAME			I	र्मे रुप्रम	ABEAL ABEAL	7 7 7	AREA	45.64	ABEA 4	ABEAL
PYENU ECOLI	HYPOTHETICAL 62 1 KD PROTEIN		326-359	1	4	+				
PYEIC ECOL!	HYPOTHETICAL 33 6 KD PROTEIN		46.80	-						
PYEIF ECOLI	HYPOTHETICAL PROTEIN		81-19							
PYEU ECOLI	HYPOTHETICAL 43 4 KD PROTEIN		275	-						
PYEJA ECOLI	HYPOTHETICAL ABC TRANSPORTER		9-110	1	1					
PYEJF ECOLI			453-480	-	-	-				
PYCIO FCOLI	HYPOTHETICAL 91 2 KIS PROTEIN		199.433							
ryilio (col.)	INTUILIEFICAL 40 6 KI) PROTEIN		135-203							
PYTUS DACST	HYPOTHETICAL 30 6 KD PROTEIN	ros	091.((1							
PYTYR BRAIA		AICUM	109.150		L				l	
2000	HVPOTIETICAL 17 7 KF		40-67		_	-				
200	NAME OF TAXABLE PARTY.		214.241							
100	MYNOTHE ILAL IN AND TROITING		116.36						İ	T
1,000	HYPOTHE LICAL, JO V K.D PROJEIN						-		İ	I
PYCCC ECOL!	HYPOTIETICAL 31 B KD PROTEIN		907-607						1	
PYGIZ BACTU	HYPOTHETICAL 22 BKD PROTEIN	SIS	10-01		1				1	
PYGI3 PSEPU	HYPOTHETICAL 32 4 KD PROTEIN	IIDA	7/1/2							
PYGIF ECOL	HYPOTHETICAL 48 4 KD PROTEIN		223-264							
PYGL & BACST	HYPOTHETICAL 35 5 KD PROTEIN		6-33	_						
PVCI C BACKT	HYPOTHETICAL PROTEIN		183-209	-						
SACI E BACKE	HAPOTHETICAL IS NO		79.124	-	H					Ī
	AVECTOR IN PROTE		20.47	-	-	-			T	
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DE DALSO	THE PART OF THE PROPERTY	MICH STILL	016,000		<u> </u>		-		T	
LYCE CLOAD	HYPOTHE I KAL 18 8 KD PROTEIN			Т		1			1	
PYGT2 STRAN		CIANS	7	797-567	707	+			1	
PYINE ECOLI			20-02	1	1				1	
PYHAC ECOL!			1		+					
PYNIAF ECOLI			7	136-165	$\frac{1}{1}$				1	
PYING ECOLI	PROBABLE ABC TRANSPORTER .		_	┪						
PYNIBG PSEPU	PROBABLE ABC TRANSPORTER .		┪	106-133	147.174					
PYING THIFE	PROBABLE ABC TRANSPORTER	GOOXIDANS	113-140							
PYING ECOL!			267-297							
PYHEM BACSU		171(.13	122-253							
PYHET ANASP			11.99	-						
PYHIIA ECOLI	HIYPOTHETICAL 16 6 KD PROTEIN		\$6-84]						
PYHHG ECOLI	HYPOTHETICAL IS I KD PROTEIN		43.77							
PYHIIM ECOLI	HYPOTHETICAL 14 5 KD PROTEIN		(1.1)		L			_		
ACIA LACIA	HYPOTHETICAL PROTEIN	LACTOCOCCUS LACTIS	167.194		-			-		Γ
PYTHE LACTA	HYPOTHETICAL 38 0 KD PROTEIN		90-134	133-159	-	-				
PYIII LACLA	HYPOTHETICAL 30 7 KD PROTEIN .		Г		-		_			
PYTHE LACEA	HYPOTHETICAL 30 7 KD PROTEIN		77.104	156-183		 -		-		
LYIN NIAAL	HYPOTHETH'AL PROFIEN	STAPHYLOCOCCOS AURIEUS	191	<u>!</u>	1				T	
FYIR N VIDCII	HIYPOTHETICAL IS NO PROTEIN		99.136		-	-			T	Ī
PYNAG METSE	HYPOTHETICAL 33 2 KE	METHAMOTHERMUS FERVIDUS	106-133							
PYHSI CLOAB		3	41:83	-	<u> </u>				T	
PYHEA CLOAD	-		91-125						Ī	
IVII CLOAN	HYPATHETICAL 42 4 K		Γ	201.253	176-110				T	
PYHYL I ACIM	III POTITION PROTISIN		93.120	Ť					T	Ī
PYLIVA PYECH	HYPOTHETICAL PROTEIN		1_	-	-				T	
AN IN INC.		HALOBIUM	265-272	ł		-			T	T
DAY STAN	ISSUE HYPOTHETICAL 6 6 KD PROTEIN	OSIS	19-46							
PYIAT PSEAY	HYPOTHETICAL 42 6 KD PROTEIN		9.76	-						T
PY143 ME	ISMI HYPOTHETICAL 48.3 KD PROTEIN	HIII	١	134-114 331-365	200	L			T	T
PY153 HALMA	HYPOTHETICAL 31 KD PROTEIN IL	HALOBACTERUM HALOBIUM	86-113						-	
PYIDD ECOLI	HYPOTHETICAL 14 0 KD PROTEIN I		102-239							
PYIDD ECOLI	IIYPOTIIETICAL PROTEIN		(7-6			Н				
PYIBE ECOL	HYPOTHETICAL 22 6 KD PROTEIN	ESCHENCHIA COLI	121.151							
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Т	NATIONAL IN THE PROTECT		141.140			1			
1			113.140		1	-			
TOUR BLAN	HVPOTHETICAL AND ROTEIN		717-707	$\frac{1}{1}$			1		1
PYICI ECOLI			132.149			+			
PYICH ECOLI	HYPOTHETICAL 11 2 KD PROTEIN		76-103						
PYICO ECOLI	HYPOTHETICAL 49 9 KD PROTEIN	ESCIENCHIA COLI	330-343						
	HYPOTHETICAL IS RED PROTEIN	1	П	П			-		-
PYIDE ECOLI	HYPOTHETICAL ST 9 KD PROTEIN		103-203	111.104					
	HYPOTHETICAL 15 7 KD PROTEIN		56-83						
_ ł	HYPOTHETICAL 63 I KD PROTEIN		2.39						
	HYPOTHETICAL 27 3 KD PROTEIN		63.97						
PYIEA ECOLI	HYPOTHETICAL 49 2 KD PROTEIN		_						
PYIEC ECOLI	HYPOTHETICAL 60 6 KD PROTEIN		20.51 270.797						
PVIEC ERWCH	HYPOTHETICAL PROTEIN	NTHENI	22.67						
THEO ECOL	HAPOTHE FICAL AS RED PROJEIN		16-120						
- 1	HAPOINE HICKLES OF ALD PROJECT		293-327						
- 1	INTO THE INCAL 24 TAU PROTEIN		51.78						
[HYPOTHETICAL IS 0 KD PROTEIN		╗						Γ
1	HYPOTHETICAL 31 3 KD PROTEIN	ESCRERICHIA COLI	201-242 380-407						
	THE HEALTH IN THE PROPERTY		173-202						
Т	HYPOTHE HEAL IN THE PROTEIN	ESCREMINING COLI	21.92						
NO.	WHO THE TICK I AT 3 PO PROTEIN		20.071						
Т	MACHINETICAL 38 1 EC PROTECA		*(2./07						
PYIGF ECOLI	HYPOTIETICAL 12 1 KD PROTEIN		133.300	\downarrow		-			
Т	HYPOTHETICAL 27 B KD PROTEIN		13.160						
т-	HYPOTHETICAL 21 2 KD PROTEIN		13-40			1			1
Т	HYPOTHETICAL 10 3 KD PROTEIN .		11.55						
PYNG ECOL	HYPOTHETICAL S4 1 KD PROTEIN (172.306				-		
П	HYPOTHETICAL 19 I KD PROTEIN		112-139						T
_	HYPOTHETICAL 65 4 KD PROTEIN		16.3						
_1	HYPOTHETICAL 36 9 KD PROTEIN		13-110 120-154	197.324					
1	HYPOTHETICAL II.S KD PROTEIN		612-646						
THE ECO.	NYTOTHE HIGH ST. IND PROJECT	ESCHENCHIA COLI	357-384						
_	HYPOTHETICAL 31 4 KD PROTEIN		73.99						
PYTHY ECOL	HYPOTHETICAL IS OND PROTEIN		9:30						
_	INFOTHETICAL 32 9 KD PROTEIN		100			1			
ECOLI						+			1
П	HYPOTHETICAL 26 6 KD PROTEIN 7		136-163			-	-		
	HYPOTHETICAL 78 3 KD PROTEIN . 1		115-263						Ť
	HYPOTHETICAL II 2 KD PROTEIN		26-53						T
							-		T
1	ITYFOLIETICAL 66 6 KD FROTEIN		110-137 419-446		_	_			
_		TOGENES	7.34			L			T
SHISO	INSERTION ELEMENT 19800		62-19						
+		SUPERIORITES COELICOLOR	13-152						
۲			96-100						
PVIAG FCO I	HYPOTHETICAL 22 6 KD PROTEIN	1 703	112-119	3					
+	HYPOTHETICAL 20 4 KD PROTEIN		31-78			-			
TO THE A	Protectical 2s sko protein		11-122						
7	INPOTHETICAL 9.7 KD PROTEIN		77-170	1					
1	PPOTHETICAL 16.1 KD PROTEIN		112.140			1			
П	HYPOTHETICAL IS:1 KD PROTEIN		3:39						
PYICC ECOL! H	INPOTHETICAL 60 & KD PROTEIN		33-65 414-441	451.492	-				
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7	Z		AREAL AREAL	Z AREAZ	1414	र रुप्त	10 ST	AREA AREA	т	1
	HYPOTHETICAL 60 3 KD PROTEIN		137.00			1	\dagger	1	\dagger	T
	HETICAL 39 2 KD PROTEIN	ESCHENCIAA COLI	175.6				\dagger	$\frac{1}{1}$	\dagger	I
_	HYPOTHETICAL 25 I KD PROTEIN		911-118	$\frac{1}{1}$		+	1	1	+	
	HYPOTHETICAL STAND PROTEIN		497-707					1	+	T
	HYPOTHETICAL 73.7 KD PROTEIN		266-006			1	1		1	I
PYICW ECOLI HYPOTH	HYPOTHETICAL ADC TRANSPORTER								+	Ī
١.	ETICAL B42 KD PROTEIN		(1) (4) (1) (1) (1) (1) (1) (1)				+	+	+	
PYIDE ECOLI HYPOTH	HETICAL PROTEIN	ESCIEDICHIA COLI	Ţ			1	1		+	
П	HYPOTHETICAL 17.5 KD PROTEIN PRECURSOR		13-69 88-129				1		1	
_	HETICAL 48.8 KD PROTEIN		321-355						1	
PYLAI LACAC HYPOTH	HETICAL PROTEIN	LACTOBACTILUS ACIDOPHILUS	47-14					1	_	
PY A1 LACAC HYPOTH	HETICAL 14 S KD PROTEIN		13-43							
TOTAL ACAC HANDE	EVI AT 1 ACAC MANDOTAGETICAL 14 4 KD PROTEIN		47.74						r	
TOWN OF THE PARTY	CTATAL 34 AND PROTEIN		23.50					ŀ	H	Γ
אווער אחוש	ACTION AT THE BROTER		116-213 314-34					-		
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PILTA TENEM TLYAL	TOTAL STATE OF SOM		133.100		I		T		\dagger	
LIFT WAY HILD	THE STATE OF THE PROPERTY	I ACTOCOCCIR I ACTIS	15.70					-	T	
PYLUD LACLA HYPOIL	TELICAL (9) AD PADIEIR		97.53	+				-	\dagger	
PYME BACSU HYPOTI	PYMET BACSU HYPOTHETICAL IN IKU FROIEIN		140,101	377067	1001		\dagger		\dagger	T
PYMG2 MYCGE HYPOTI	HEILCAL HIS SAN PROTEIN TRELONSON		Ţ,	Т		1	Ì	1	\dagger	
PYNGA CLOPE HYPCINETICAL PROTEIN	HETICAL PROTEIN	CLOSI MOION TEN MINOCENS	13 40	1]	\dagger	t		+	
PYNGS CLOPE HYPOTI	HETICAL 31 2 KD PROTEIN	CLUS I MUIUM PEN MINGENS	Ţ	7,7		1	t	1	t	
PYNII METTL HYPOTI	HYPOTHETICAL PROTEIN	Т	4			1	1	+	\dagger	
PYNO! PAIDE HYPOTH	IETICAL 9.3 KD PROTEIN	DEMINICANS	97.70			1	1		\dagger	
PYNTS ANASP HYPOTH	ETICAL 28 I KD PROTEIN		161-161					1	1	
PYNTS ANASP HYPOTI	RETICAL PROTEIN		17.165	+				1	1	
PYOND ECOL! HYPOTH	HETICAL 21 4 KD PROTEIN	ESCHENCHIA COLI	┪				1		1	
PYOHG ECOLI HYPOTH	I HYPOTHETICAL 43 3 KD PROTEIN	ESCHENCKIA COU	104-171 289-316			1	1		1	
PYOIA_ECOL! HYPOTH	KETICAL 150 KD PROTERM	ESCHENCHIA COLI	7:40				1	$\frac{1}{1}$	1	Ī
PYONE ECOLI HYPOTH	DLI HYPOTHETICAL 93.5 KD PROTEIN	ESCHERICHIA COLI	221:24				1	1	\dagger	1
PYOJE ECOLI NYPOTH	HETICAL 9 S KD PROTEIN	ESCHENCHIA COLI	70:10				1	1	1	
PYON ECOLI HYPOTI	HETICAL SASKD PROTEIN	ESCHEMUNIA COCI	143-173			1		$\frac{1}{1}$	\dagger	
PYOU ECOLI HYPOTA	ETICAL 16 2 KD PROTEIN		171.74	-			\dagger	+	+	
PYONG PHOSE HYPOTH	RETICAL PROTEIN IN UMUM JULIMON	× 2013.	201	1		Ì	1	+	†	T
PYOPH YEAEN PROTE	N-TYROSINE PHOSPHATASE YORK	2000	501-00			1	1	$\frac{1}{1}$	†	
PYOPH YERPS PROTER	PROTEIN-TYROSINE PHOSPHATASE TOPI		Т				1	+	1	T
		TERSINIA EN IEROCOCITICA	0.17	707-507			1	1	1	
	OUTER MEMBRANE PROTEIN YORN	-	8.67	707-572			1	+	†	Ī
	YORG PROTEIN PRECURSOR			 					1	
	HYPOTHETICAL 31 3 KD PRUIEIN ,	MACMOTALUS INTLUENCAS	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	+			1			
PYORA LISMO HYPOT	HYPOTHETICAL 15.6 KD PROTEIN	LISTENA MONOCT I DUENES						1	†	
	HETICAL 24 7 KD PROTEIN		012:001				1		1	
PYORD HAEIN HYPOTI	. 19 E		39-66	1						
PYORC MAEIN INTPOTHETICAL	HYPOTHETICAL 199 KD PROTEIN	HAEMOPHILUS INTLUENZAE	٦					-	1	
PYORE ILLEIN BKD FI	ROTEIN	IIAEMOPIIILUS INTLUENZAE	47-74 12-100						1	
PYONE HAEIN 16 8 KD	z	HAEMOPHILUS INFLUENZAE	199-229							
PYORH HAEIN HYPOTI	HYPOTHETICAL I) ? KD PROTEIN	HAEMOPHILUS INFLUENZAE								
PYOR! HAEIN 95 4 KD	95 4 KD PROTEIN	HAEMOPHILUS INFLUENZAE	416-450 688-723	2						
PYONG BACSU HYPOT	HETICAL 14 KD PROTEIN	BACILLUS SUBTILIS	148-175							
PYORX PYRWO HYPOTHETICAL PROTE	HETICAL PROTEIN	PYROCOCCUS WOESE!	(6-9)					-		F
PYORZ LISKO HYPOT	HETICAL 16 9 KD PROTEIN	LISTENIA MONOCYTOGENES	П						ľ	Γ
	HYPOTHETICAL 15.5 KD PROTEIN	STAPHYLOCOCCUS AUREUS	11.91 110.137	-				-	F	F
	HETICAL 22.5 KD PROTEIN	BACILLUS SUBTILIS	57-84					-		
PYP23 STAND	HYPOTIETICAL 33.2 KD PROTEIN	STAPHYLOCOCCUS AUREUS	19-70				-			
	HYPOTHETICAL 16 9 KD PROTEIN	STAPHYLOCOCCUS AUREUS	14.104						r	
т-	HYPOTHETICAL 27.0 KD PROTEIN	STAPHYLOCOCCUS AUREUS		179.106						
Г	HYPOTHETICAL 11.1 KD PROTEIN	STAPHYLOCOCCUS AUREUS	13-13					_		
1										

Г	10741314									
Ι	PROTEIN	ODC ANEX	Т	Т	┰	٦	┑	П		
PYP) AGRT4	HYPOTHETICAL PROTEIN 7	AGROBACTERITM TIMEFACIENS	9,	70320	7	V V V	AREA AR	AREA ABEA?	N. ABEAL	AREA?
	HYPOTHETICAL PROTEIN	LEGIONELLA PNEUMOPHILA	25.35	T	T	1	1	1		
PYPAS ENTEA IN	HYPOTHETICAL 13 KD PROTEIN	ENTEROCOCCUS PAECALIS	8	T	T	1	1	1		
PYPA BACAN	HYPOTHETICAL 11 6 KD PROTEIN	BACILLUS ANTHUACIS	T	115.162		1	1			
PYPCI ECOLI	HYPOTIETICAL 27 6 KD PROTEIN	ESCHERICHIA COLJ	Ī		T	\dagger		1		
PYPDA BACSU H	HYPOTHETICAL 17.1 KD PROTEIN	BACILLUS SUBTILIS	164-332	T	T	T		+	1	
PYPT ECOLI		ESCHENCHIA COLI	16-43					1		Ţ
TITLE STATE	HYPOTHETICAL IS IND PROTEIN	SYNECHOCOCCUS SP	19.6				-	-		
7	HYPOTHETICAL 19 7 KD PROTEIN	CLOSTRIDIUM PERFRINGENS		41.11	83.149			 		T
Т	HIVEOTIETICAL 14 3 AD PROTEIN	CLOSTRIDIUM PERFRINGENS	П	П				-		
7	UNDOTHER TOTAL SECTION OF THE PROPERTY	CLUS I KIDIUM PENT KINGENS	=	261-290	303-340		-		-	
PYPE BACK	MYPOTHETICAL DE SECTION DE CHE A CE	PSEUDOMONAS AERUGINOSA	22.22					-		
7	VACTURE ICAL PROCESSING PROTECTS	BACILLUS SUBILLIS	329-356					-	L	
_	AVECTUE TICAL TAN PROTEIN	ALEBSIELLA PREUMONIAE	23.52							
_	HVPOTIETICAL AS PER PROTEIN	FLECTUREMA BORYANUM	٦							
+	HAPOTHETICAL 33 CKD PROTEIN	ME I HANDBACI ENIUM I HERNIOFORNICICUM		33						
-	HYPOTHETICAL 17 1 KD PROTEIN	Т	9.							
+-	HYPOTIETICAL 404 KD PROTEIN	METHAMOBACTERION THERMOPORALICICUM	┪							
PYPYR BACSU H	HYPOTIETICAL 22 4 KD PROTEIN	Т	7	64.9						
PYPZI METTE HI	HYPOTIETICAL 40 6 KD PROTEIN	METHANORACTER IN THE BANGE OF WILLIAM	979.70							
PYP23 METTE HI	HYPOTHETICAL 33 I KD PROTEIN	METHANDRACTER IN THE MODE OF MICHOR	T	66.33			-			
PYP25 METTE HI	HYPOTHETICAL 54.1 KD PROTEIN	METHANOBACTERITM THERMOFORMICICIAL	Ę	100.00	20, 100	1				
	IIYPOTIETICAL 9.7 KD PROTEIN	METHANOBACTERUM THERMOFORMICICUM	Т	Т	5		1			
	YPOTHETICAL IS 7 KD PROTEIN	THERMOFILUM PENDENS	12.100	T	1	T		1		
	HYPOTHETICAL 40 KD GTP-BINDING PROTEIN	HALOBACTERIUM CUTIRUBRUM	20.00	T	T	T	-	+	+	
PYZEC SYND? HY	HYPOTHETICAL 28.7 KD PROTEIN 14		49.76		T	T				
	POTIETICAL 40 6 KD PROTEIN	SALMONELLA TYPHIMURUM	143-190	Ī	T	T		+	+	
	HITOTHE HICAL STURIO PROTEIN	SALMONELLA TYPHIMURUM	428.455							
PVEEK CALTY HIV	POTITE ILAL 10 & KD PROTEIN	SALMONELLA TYPHIMURIUM	39.56						 	I
PYRG2 LACIA HV	HYPOTHETICAL PROTEIN	ACTOCICE TERMONOR	130-157							
_	HYPOTHETICAL PROTEIN									
PYRP2 METVA HY	POTHETICAL II 6 KD PROTEIN			29-130						
	HYPOTHETICAL 11.5 KD PROTEIN .	25			1	1				
PYRPI SULAC HY	HYPOTIETICAL 14 S KD PROTEIN		17.1	T	1	\dagger	+			
PYRTP BACSU HY	POTHETICAL 25.3 KD PROTEIN		35.5	1	\dagger	\dagger	+	+	1	
PYRTS BACSU HY	PYRTS BACSU HYPOTHETICAL 11.4 KD PROTEIN 1;	BACILLUS SUBTILIS	Γ	1	T	1			+	
BVECT VEHEN VE	PONE DICAL TSC OPERON PROTEIN BY								1	
PVSCD VERFN VI	COPERON PROTEIN O	VERSINIA ENTEROCOLITICA		962-390			-			
PYSCH YEREN YS	PYSCH YEREN YSC OPERON PROTEIN H		207.769							
PYSCII YEARS YS	C OPERON PROTEIN H	0516		1	1	1				
PYSCI YEREN YS	C OPERON PROTEIN I		, is	†	1	1				
PYSCI YEMPS YS	C OPERON PROTEIN I	YERSIMIA PSEUDOTUBERCULOSIS	2,6		1	1		+		
PYSCI YEREN YS	YSC OPERON LIPOPROTEIN ! PRECURSOR,		99.136	T	\dagger	\dagger	+	1		
YSO YEUS YS	C OPERON LIPOPROTEIN I PRECURSOR '	rosis	95.126	T		\dagger	-	+	1	
Т	YSC OPERON PROTEIN L		99-					1		
		CULOSIS	41.68			T	-			
PYSMA SELMA HY	HYPOTHETICAL 9.3 KD PROTEIN		02:11		F	\dagger		+		Ī
TYSOL DESIGN	HYPOTHETICAL 21.3 KD PROTEIN		68-109	r	+	t	+	+	$\frac{1}{1}$	$\frac{1}{1}$
	PUREITAL PROJEIN	LENS	63-155			1	-	-		
200	HANDELINAL PROJECT	15	6-33	7.3	l	\dagger		1		
PYSY1 BACKLI HV	POTHETICAL 18 AND PROTEIN	ODES	П	105-227 30	100-327	f	-	-		
PYSYN METER 11Y	POTHETICAL PROTEIN		22.99				F			
PYT37 STAGR HY	HYPOTHETICAL 33.1 KD PROTEIN	CLEEPTONYCES SO ANIAG	201-12						-	T
			246-277	1	1			H		T

					ŀ			
	Probate Seasones							
	200 A 21684	AREA I AREA	AREA 1 AREA 2	AREA	AREAS A	BEA 6 AB	AREA A AREAS AREAS AREA! AREA!	AREAS
FILE NAME PROTEIN	MONOWA					-		
SYTHE BACK! LIVERTHEAL 35 & KD PROTEIN	BACILLUS SUBTILIS	1						
14 CE 14 OLL MILE CONT.	I EPTOSPILA BIFLEXA	===						
THE LEVEL MITCHEST AND PROPERTY	L ACTOCOCCUS LACTIS	2113						
PTIC LACLA HITOTHERICAL IS NOT PROTECT	BACILLUS SUBTILIS	17.62						
PTIST BACSO MITOINELICAL TO AD INCIDENT	CPIROPLASMA CITAL	102-149						
PYTSF SPICE MYPOLICE HOAL TO SAU PROTEIN	BACILLUS SUBTILIS	17-64 68-95						
VED THE PICAL PLO	BACILLUS SUBTILIS	143-169						
TOTAL SECTION	DACILLUS SUMTILIS	13.51					_	
PTAIL BACSO THE POLICE AND	BACH LUS SUBTILIS	165-207 262-289						
TENETICAL OF	BACILLIS SUBTILIS	1.10	94.143					
PTXIS DALSO SITTO SIETATA SI SEDENCIENA	BACILLUS SUMTILIS	\$6.03 15-112						
	BACILLUS SUBTILIS	34.58						
LVEOTIE TICAL 18 0	ANABAENA SP	17.104						
	CALDOCELLUM SACCITAROL YTICUM	9.39					1	
.12	CALDOCELLUM SACCHAROLYTICUM	96-19						
TATE CALS ALTONOMIC TO SECURITION OF THE PROPERTY OF THE PROPE	F SCHENICHIA COLI	41.78						
PYZE ECO. HYDIREIKALINA NOTROTES								

TABLE D

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

PCGENE	1871 1785 d Mailf Search on All Homan Praisin Sequences	П	()								
FILENAME	PROTEIN	Т	AUGA AUGA	2	2000	S S S S S S S S S S S S S S S S S S S	o de la composition della	+	-	1	
PIAS HOMAN	14-3-3 PROTEIN HOMOLOG STRATIFIN	700		$\frac{1}{1}$	-	+		-			
PIOT HOMAN	14.3.3 PROTEIN THETA (14.3.3 PROTEIN 1-CELL) (113) PROTEIN)				1	-					
	IA-1-1 PROTEIN ZETA (PROTEIN KINASE C. INIUBITOR PROTEIN-1) (ACIT-1)			$\frac{1}{1}$	1						
PIASS HEMAN	HELA CLASS I HISTOCOMPATIBILITY ANTIGEM, A-28(AW-19) A-2801 ALPITA CHAIM		-	$\frac{1}{1}$	1	+					
PIAS HUMAN	HELA CLASS I HISTOCONDATIBILITY ANTIGEN, A-14 AW-19) A' TWI ALTHA LILAIN			1		+	-				
PIBOS HOMAN	THE A CLASS I HAS OCCUMENTED IN ANTICEN. B. 11 BOLLO ALENA CHAIN		41.112	-		-	1				
TANGE HOLD IN	THE CLASS TO COMPATIBILITY ANTICEN BY 1/8 13 801502 ALPITA CHAIN	1		-		-					
NAME I I I I I	IN A CLASS HISTOCOMPATIBILITY ANTIGEN, DW. 72(BW.70) B. 150) ALPHA	3		-	-						
NAMA WIND	IN A CLASS HISTOCOMPATIBILITY ANTIGEN, B-62 B-1504 ALPITA CHAIN	76-107		_		_					
PIRIT HIMAAN	SELACLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B-1101 ALPITA CHAIN	20:00		-							
PIRZI HIMAN	HELA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B-3501 ALPHA CHAIN	¥:115									
PIB22 HIMAN	PILA CLASS I JUSTOCOMPATIBILITY ANTIGEN, B-35 B-3502 ALPHA CHAIN	14-115		L							
PIBIS HUMAN	ILLA CLASS I HISTOCOMPATIBILITY ANTIGEN. B-35 B-3503 ALPHA CHAIN	\$11.5									
PIB24 HUMAN	ILLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B-3504 ALPITA CHAIN	76-107						-			
PIB25 HUMAN	ILLA CLASS I HISTOCONDATIBILITY ANTIGEN. B-35 B-3505 ALPHA CIIAIN	86-115									
PIB26 HUMAN	ILLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B.35 0"3506 ALPHA CHAIN	1113						-			
PIB27 HUMAN	INC. A CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B-3507 ALPIVA CHAIN	14-115									
PIB28 HUMAN	FILA CLASS I IUSTOCOMPATIBILITY ANTIGEN, B-35 B-3508 ALPHA CHAIN	25.13		-							
PIB29 HUMAN	HELA CLASS I HISTOCOMPATIBILITY ANTIGEN. B-37 B-3701 ALPHA CILAIN	11:13									
PIB32 HUMAN	FILA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B-3903 ALPHA CHAIN	17:114			_						
PIB33 HUMAN	HEA CLASS I HISTOCOMPATIBILITY ANTICEN, BW-40(B-40) B*4001 ALPHA CIIAIN	16.09		-	_						
PIBM HUMAN	HEA CLASS I HISTOCOND ATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN	2 = 2		1	-	$\frac{1}{1}$		-			
PIBJS HUMAN	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4003 ALPHA CHAIN			1	+	1		-			
PIBJE HUMAN	INTA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN	=			1	1		-			
PIBJE HUMAN	INTA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN	<u> </u>		1	-	1		1			
PIBJ9 HUPLON	MLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN			1	1	1	-				
PIB40 HUNAN	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-4(B-13) B-4401 ALPHA CHAIN			$\frac{1}{1}$	+						
PIB41 HUMAN	HELA CLASS I HOSTOCOMPATIBILITY ANTICEN, BW 44(B-12) B-4402 ALTHA CHAIN			ł	1	1	-	ļ	I		
PIB42 HUMAN	HEA CLASS I RISTOCOMPATIBLE IT ANTICEN BULLED IN BOARD AT BULL OF				1	+		<u>-</u>			
A HOME	THE A CLASS I HIS LOW A LIBRARY AND LOCK, BW-260-1416 - 5501 ALPHA CHAIN	1	-		+	+	+				
NAME AND A	IN A CHASS HACTOCOMPATIBILITY ANTIGEN BW-47 B*4701 ALPHA CIMIN	=				-	-	L			
PIRAS HUMAN	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, B 48 B-4801 ALPHA CHAIN	F 13									
PIBAT HUMAN	HEACLASS I HISTOCOMPATIBILITY ANTIGEN, BANG. 21) B-4901 ALPHA CHAIN	17:114									
PIBE HUMAN	HOLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B"5001 ALPHA CHAIN	14-115									
FIBSS HUMAN	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53(B-5) B-5201 ALPHA CHAIN	87-114									
PIBSS HUMAN	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54(BW-22) B*5401 ALPHA	===		1	-		-				
PIBSE HUMAN	HEA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-15/BW-22) B*5501 ALPHA	¥		1	-	+					
PIBST HUMAN	I	-		1	1	-					
PIBS HUMAN	_	*		1	1	-					
PIBS HUMAN	MA CLASS I HISTOCOMPATIBILITY ANTIGEN, BWOOGBW-221 B-3802 ALFITA			+	+	1					
PICE HOMAN	HIA CLASS HOSTOCOMPATIBILITY ANTICEN, CW. I CW. 1010 ALTERA CHAIN		1	$\frac{1}{1}$	+	$\frac{1}{1}$					
A HOME	THE CLASS I PUSIOUS WAY A IDENTITY OF THE CHAIN CALLS OF THE CHAIN			†	ł	+					
	-	27.17		<u> </u>	+	+					
A HOMAN	_	1		+	<u> </u> 	+	1				
		87.114		ļ	<u> </u> 	<u> </u>		L			
NOTE HOLD	_	13.114		+		-					
PICIA HIDAAN	+=	17-114		\vdash		 -					
PICIO HUMAN	+-	17.114		-							
P15A6 HUMAN	+=	103-620									
PAKA HUMAN			П	-					i		
PZAAB HUMAN		┱	41.68 79.106	x	+	+					
PZABA HUMAN	PROTEIN PROSPHATASE PEZA, 35 KD REGULATORT SUBURIT, ALPIA 150FORM	12.5	+	+	+	$\frac{1}{1}$	+		I		
PAIL HUMAN	EXTINATE INCIDENCE OF THE PROPERTY.			1	$\left \right $	$\left\{ \right.$					

PCGENE	107217814 Motif Search on All Human Pratein Sequences		П							
ELLENAME	PROLING PROPERTY AND	185	7	AREAL	AHEA4	SEA3	AKA	AREA?	ARK-	AREAS
P42 HUMAN	FRYTHROCYTE MEMBRANE PROTEIN \$1	8	58:35			T			T	
P4F2 HUMAN	4F3 CELL-SUNFACE ANTIGEN HEAVY CHAIN (472HC) (LYMPHOCYTE ACTIVATION	1							-	
PSHIE HUMAN		311-336								
PSHIF HUMAN	S-HYDROXYTR YPTAMONE IF RECEPTOR (S-HT-IF) (SEROTONIN RECEPTOR)	122-253								
PSHZA HUMAN		% ∶≈								
SHT HONE	S-HYDROXYTRYPTALINE TRECEPTOR (S-HT-X) (S-HT-X) (SEROTONIN RECEPTOR)	Ť	-			1				
TAIAC BUMAR	ALTHA-I-ANIICHT MUINTPSIN PAECUASUR (ALI)	201.04	130-131		1					
PAIN MUMAN	ALTHAS : AUTHOR CASCURAGE IN COME (AT 1990 TE ACE CASCURATION) (CASCURATION AT 1990 TE ACE CASCURATION	1 1 1		1	T	1	Ţ			Ī
NAME OF THE PERSON OF THE PERS	AT BUT I ANTITUDE OF THE ATENDED THE DESCRIPTION		I	1		1	Ī		·	
PATAP HILLAN	ALPHA-3-ANTIDI ASAMPHECUSOR (ALPHA-3-PLASMIN INHIBITOR) (ALPHA-3-	7	165-195		T	T				
PANCE MEMAN	LEUCINE RUCH AL PHA-3-CE Y COPROTEIN (LRG).	+								Ī
PANA HIMAN	AL PHA.3. MACHOCA CONTROL PERCHASOR (AL PHA.3.M)	Ť	110.140	1045.1113	1403.1430					
PA HOUSE	ALZHEIMERYS DISEASE AMYLOID AFPROTEIN PRECURSOR (PROTEASE NEXIN-II)								1	
PAACT ROMAN	ALMA-ACTION (F.ACTIO CROSS LINKING PROTEIN)	911.6	720-747						-	
PAATH HUBELD	_	96-136								
PABP2 HUMAN	ENDOTHELLAL ACTIN-BINDING PROTEIN (ABP-310) (NONMUSCLE FILANIN)	10-19	119-147	2604-2633						
PACI2 HEMAN		306-333								
PACIS HEDAM		Ī	182-209	968-700					•	
PACE HONAN	ACYL. COA DEMORDGEDASE PRECURSOR, LONG-CHAIN SPECIFIC (EC.) 99 (1)	20.02	1	97:140		1				
	ANCIOTENEM CONVENTING ENGINEER PACCONSON, 183113-37 ECT (16.) 4 13 11	٦.	100.00	201 016		1				
TALE AUTOM	ANGIOLENSIN-CONTENTING EACHER PACCONSOL, ANNA HILLECT VILLIANCE	Ť	3							
STATE STATE	ALEITICHACAME ACCEPTOR PROJEIN, ALPRA LAGIN PACCURSOR	2		T					•	
TACHE HUMAN	ACET FLOWER RECEPTOR PROTEIN, EXSLED CHAIN PRECINCIO	T	10.50							
NYWH DUY	NEURONAL ACETY COOL NE RECEPTOR PROTEIN BETA CHAIN (FRACKIENT)	T	16.91	1		1			1	T
PACE O HUMAN	ACROSIN PRECURSOR (EC.) 4.21 (9)	-								
PACYM HUBA	ACYLMOSPHATASE, MUSCLE TYPE ISOZYME (EC 16.1.7) (ACYLMOSPHATE	25.5				Ī			-	
PADT2 HUDAN		163:119							,	
PADTI HOMEN		┪							₩.	
PAKTO HUMAN		_	71716							
PALFA HUMAN	FRUCTOSE BISPHOSPHATE ALDOLASE (EC 4 1 2 1)) A (ANUSCLE)	(9-6)								
	FRUCTOSE-BISPHOSPHATE ALLOCIASE (EC. 4.1.2.1.) B (LIVER)	1								
TANK IN ALL	AND DEALINASE 1 (EL 12 4 6) (MI DO EN LA SE DEALINASE (CALL DEALINASE)	76 07	Ī			1				
PANEN HUMAN	ANIMOPEPTIDASE N. (C. 1.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CP150)	_	604-648	926.964			Î			
PANOR HUMAN	AMPHINEGULIN PRECURSOR (AR)	Т	T			Ī				
PALOU HUBLAN	ALPHA-3-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR	173-236	263-290							
PANTE HOLVE	BRAIN NATINUMETIC PEPTIDE PNECUNSOR	T	_							
PANK! HOKAN	ANKYNIN R (ANKYNINS 1.1 AND 1.2) (EXTINACETIE ANKYNIN)	- 1.	100.1031	1617-1644						
PANCE PROPERTY	APPLICATE BRAND VARIANT O CANY VERLES (ANY VERLES MONTH VONTRATIONS)	2	1			1				
PANEA MILLAN	ATRIAL MATERIALITIC PEPTIDE RECEPTOR A PRECITION A JANE AND ALANDRALICE. AL	. 1	135.153							
NAME HOLA	ATHIAL NATHUMETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B)	T		Ī						Ī
PANTS HUMAN	ANTITUDIOMBID-LII PRECURSOR (ATIII).	162-196				T				Ī
PANCE HUMAN	ANNEXON II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 1)	40-67	106-333							
PANCO HUMAN	ANNEXON III (LIPOCONTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III)	-								
PANCE HUMAN	ANNEXTH VI (LIPOCORTIN VI) (P64) (P70) (PROTEIN III) (CHROMOBINDIN 20)	П	626-653							
PAND HUMAN	ANNEXIN, INTESTINE SPECIFIC (ISA).	П	137.164							
PAOFA HUMAN	AMINE OXIDASE (FLAVIN-CONTAINING) A (EC 1.4.) () (MONOAMINE OXIDASE)		74.104							
PAOFE HUMAN	AMONE OXIDASE (FLAVIN-CONTAINING) B (EC 1.4) 4) (MONOAMINE OXIDASE)	84.98								
PAPAI HUMAN	APOLIDOPROTEIN A-I PRECURSOR (APO-AI)	┪								
PAPB HUMAN	APOUNDPROTEIN B-100 PALCUASON (APO B-100APO B-11)	383-619	0011-001	1353-1360 1524-1584 2074-2113	1324-1584	2074-2113		2181-2215	1240-1271	2360-2389
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PANC HUMAN ADENOMATOUS POLYPOSIS COLIPROTEIN (APC PROTEIN)	145.172	617-651	134-86	1795-1822 2172-2212 2572-2609	1122-2212	1372-2609			
-	41-11	247.274						-	
Ī	4448-4475								
PAGP! HIMAN AQUAPORIN-CHIP (WATER CHANNEL PROTEIN FOR RED BLOOD CELLS AND KIDNEY 19-7)	739.73	ŀ			1	Ì		I	
PAIK! HUMAN BELA-ALMENEKUK MELETIUR MIMASE LIEU Z. L. 1.100 (BELA-ALM-1)	10.00								
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	203-230							-	
PATEL HUMAN (FRANSCRIPTION FACTOR ATF.) (FRAGMENT)	155-183								
-	10-01							:	
	14.68								
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PBASO MUMAN BASONUCLIN	101-07	110-337	13:80					-	
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PBNOT HUMAN BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-1) (OSTEOGENIC PROTEIN I)	192-219								
	284-311								
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PRIFE HIDAAN BASIC TRANSCRIPTION FACTOR 62 KD SUBLIMIT (P62).	128-162	ž							
PBTGI KUMAN BTGI PROTEIN (B-CELL TRANSLOCATION GENE I PROTEIN).	36.53								
KITC HUKKN CITETANT DROPOLATE STRIPLASE, CYTOTAS PACTOR PROTECTION CONTINUES OF THE STRIPLAS O	9			1					
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PCATS HOBLAN CALPADY PM, LANGE (CATALYTIC) SUBUNIT (EC 2.4.2217) (CALCIUM-	674.701								
PCAN, HUMAN PLACENTAL CALCHAN-BRODNO PROTEIN.	9			1		1			
INCA HUMAN (ADENILLIC LICENSEASSOCIALIS) PROTEINING) i	66-176	1	1	1	1		
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PCASB HUMAN BETA CASEIN PRECURSOR.	17								
	422-456							-	
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	41.68								
PCATE HUMAN CATHERSIN LIPRECURSOR (EC.) 4 22 15) (NIAJOR EXCRETED PROTEIN) (NIEP)	278.305	ŀ							
PCATS, MUMCATHEPSIN S PRECUNSOR (EC 3.4.22.27)	36.55	147.168							
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PCCI HUMAN CDC21 HOMOLOG (PI-CDC31) (FRAGMENT)	1							1	
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PCDK3 HUMAN (CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1) (KINASE PSSALRE)	5.32			ŀ		T			
PCEBB_HIMAN CCAATIENHANCER BRIDING PROTEIN BETA (CEBP BETA) (NUCLEAR FACTOR	296-130							F	
PCEMB HUMAN MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENT-B)	368-395							-	
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PLENE HUMAN (CENTROMERIC PROTEIN E (CENPLE PROTEIN)	177.199	493.520	\$33-607	215-212	767-825	110.051	20.00	963.005	1080.1107
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	MINORE PASS VII (CROLES) ENOL I ALFITA MUNOCATI GENASE)	Т							-	
Š	CYTOCHROME P450 IIC17 (EC 1 14 14 1) (P450-234C) (PRACMENT).	911-61	T	Ī					1	
	CYTOCHDOME PASSILEI (EC 1.14.14.1) (PASS-1) (ETHANOL INDUCIBLE)	7								
I	CARBAMOTIL PHOSPHATE SYNTHASE (ANIMONIA) MITOCHONDINAL PRECURSOR	Ì	į							
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-	HIOME PASS XIXA! (AROMATASE) (EC!!4 i4 !) (ESTROGEN	134-271								
PCIU HUMAN COMPL	COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (CR1) (COMPLEMENT C1D RECEPTOR) 916-1013									
PCACA HUMAN COLOR	COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).		379-420	119-619	124-754	163-790				
PCREA HEMAN CAND R	CAMP RESPONSE ELEMENT BINDING PROTEINS A AND B (CREB-A AND CREB-B)	<u>2</u> :32								
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-	CLEAVAGE SKUNAL-I PROTEIN (C3-1)								1	
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_	ALPHA-CATENIN (CADMENIN-ASSOCIATED PROTEIN)	11.11								
_	ALPHA-CATENIN RELATED PROTEIN (CATENIN ALPHA-1)	1000			-					
_	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 26) (CX16)								1	
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-	CYTOCHROME 55.	7	Т							
_	GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4 6 1 2) (10 KD CHAIN)	101-00		2						
_	GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4 6 I 1)	108							-	
	RETINAL GUANYLYL CYCLASE PRECURSOR (EC + 6 1.2)	150.05								
PCYRO MUMAN CYTOX	CYTOKINE RECEPTOR COMMON GANMA CHAIN PRECURSOR (GANDIA-C)	203-320								
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	ONCOCENE DBL PRECURSOR (CONTAINS MCF2)	T		8						
			211.711							
PDESP HUMAN DESNO	DESMOPLAKIN I AND 11 (DPI AND DPII) (FRAGAIENT)	7		71.744	269-317	20.2	47.467	25.52	20.59	630-674
			A	1436-144	1308-1333				*	
POHAP HUMAN ALDEM	PDHAP, HÜMAN ALDEHYDE DEIYDROGENASE, DINERIC NADP-PREFERUNG (EC 1 2 1 5)	7	Т							
POND HUMAN DYSTR) PAGN	_	200		753-780	976-1003		1201-1228	104-1394	200
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	DYAJ PROTEIN HOMOLOG		100							
	DEAL LUCKS (18C + 3.1.1) (FOLT DEOX TABONOCLEO) DE 31 FINASE (A17.)		7	100.1137					1	
POTON MUNICAN DIVA PO	DIA POLITICA DE LA CATALITA CITARNI (EC. 2.3.7.7)	29.78								
THE PARTY OF THE PARTY	DIRECTION PEPTIDAGE IV ISC 14 14 ST MPP IN IT CELL ACTIVATION	29.77	2							
PORNI HIMAN DEDXY	DEDXYEIDONICLEASE PRECINSOR (EC.) 21) (DNASE))	14.3								
POSCS HUMAN DESMO	DESMOCOLLIN JAJB PRECURSOR (DESMOSOMAL CLYCOPROTEIN II AND III)	101-0	155-398							
POSOI HEMAN DESMO	DESMOCLEIN I PRECURSOR (DESMOSOMAL GLYCOPROTEIN I) (DGI).	275	271.298	497.531						
	DESMOCLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARUS ANTIGEN) (PVA)	211-241	335-352							
POUG HUMAN DIVERG	DIVEACENT UPSTILEAM PROTEIN (DUP)	584-611								
PEAR! HUMAN V-EABA	V-ERBA RELATED PROTEIN EAR-I.	523-550								
PEBLY HUMAN EBV-DR	ENV.DIDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2)	44.78								
PEFIB HUMAN ELONG	ELONGATION FACTOR I-BETA (EF-I-BETA).	105-132								
PEFID HUMAN ELONG.	ELONGATION FACTOR 1-DELTA (EF-1-DELTA).	84-118								
PEGFIT HIDAM EPIDER	EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	16-31	440-467							
_	EPIDENMAL GAOWTH FACTOR PRECURSOR, KIDNEY (EGF) (UROGASTRONE)	47.74								
	ETSRELATED TRANSCUPTION FACTOR ELF-1.	351-588								
	ENDOPLASMEN PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GP96	47.74	246-273							
	RETROVINUS RELATED ENV POLYTROTEIN	383-430								
PEPC HUNAN IG EPSO	IG EVSILON CHAIN C REGION.	_								
_		T	26.70	249-211						
PERT HIDAN PROTE	PERTY HOLD PROTEIN DISULTIDE ISOMERASE HELATED PROTEIN PRECURSOR (EXP. 2)	346.376	A91-701	91483						
PERCI HUMAN IDNA E	(CISION REPAIR TRUIBIN ERCC+1.	786.675]							
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CHACOLATION FACTOR IX PRECURSOR (EC 3.4.2) (CIBUSTMAS FACTOR)	11.298					Ī	Ī		
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COACULATION FACTOR RY PRECURSOR (EC.) 31131 (CIRCISTNAS FACT FATTY ACRD-BINDUNG PROTEIN, INTESTINAL LADOT 10515-MEDIA TING SURFACE ANTICEN FACE FOR A CAPICAL AND LOW AFRITY DEALWOOLDELINE PRICURSOR (EC.) 1.1131 FIRENDECEN ALPHA CHAIN PRECURSOR. FIRENDECEN ALPHA CHAIN PRECURSOR. FIRENDECEN ALPHA CHAIN PRECURSOR. FIRENDECEN ALPHA CHAIN PRECURSOR. FIRENDECEN GAMBAL & CHAIN FIRENDER. FOUNDE THALLATURE BECKNESSOR (EC.) 11 SI (ALPHA.F. THO) FIRENDECEN GAMBAL & CHAIN FIRENDER. FOLLATE MONOCACE FROTEIN. FOLLATE AND ANTICEN I. FOLLATE AND ANTICEN I. FERNINGEN CONCOCEN FROTEIN. FOLLATE AND ANTICEN INCOMEN AND ANTICEN I. FOLLATION INCLEDING BENDOND PROTEIN GIS, ALPHA SUBURIT (ALPA GUANDE NUCLEDING BENDOND PROTEIN GIS, ALPHA SUBURIT (ALP GUANDE NUCLEDING BENDOND PROTEIN GIS, ALPHA SUBURIT (ALP GUANDE NUCLEDING BENDOND PROTEIN GISTOR (GC.) I & 101 (GC.) I GUANDE NUCLEOTING BENDOND PROTEIN GISTOR (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.) I & 101 (GC.	AASE AASE AASE AASE AASE AASE AASE AASE	(FEEN) (19-13) (FEEN) (19-13) (FEEN) (19-13) (FEEN) (19-13) (FEEN) (19-13) (FEEN) (19-13) (FEEN) (19-13) (FEEN) (F	10 111.39 10.000 10.00	11-159 11-159 16-111 11-159 16-111 16-111 16-111 16-111 16-111 16-111 16-111 16-111 16-111 16-110 1	N	11-159 11-159 16-111 11-159 16-111 16-111 16-111 16-111 16-111 16-111 16-111 16-111 16-111 16-110 1	N	N	N

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FILENAME	٦	J	AREA! OBL	ONIA CAMA	7	2	1	50300	1	
POLYT HUMAN	SERINE HYDROXYNETHYLTRANSFERASE, MITOCHONDILAL (EC. 2.1.2.1) (SEMINE		101 436	+	t	T			T	
PORTE HUMAN	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GIV 78) (IMMILINGGLOUDLIN	Т	141.168	1	\dagger	†			ŀ	
PGRAZ HUMAN		100	1	-	\dagger	T	Ī			
PORAV HUMAN	GRAVIN (FRAGMENT).	1			t	İ	I			
PORTA HUMAN	GROWTH HORMONE. RELEASING HORMONE RELEVIOR PRECURSOR (GROWTHEE)		-	1	T					
POTHE HUMAN	GLUTATHIONE S-TIMMSFERASE HA SUBURIL 2 (EL 2.3 1.18) (OLIVATOR)	١	1012.1043		1					
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POTRI HUMAN	GLICOSE TRANSPORTER TYPE I, EATTINGE, T. EURAIN.				ì	İ				!
POTEL HUMAN	GLUCOSE TRANSPORTER TYPE J. BILAIN.	47.777		1	\dagger	ĺ				
POTRA HUMAN	GLUCOSE TRANSPORTER TYPE 4, INSULIN-NESPONSIVE.	280-312		-	1		1			
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PHID HOMAN	HISTONE HID (HILZ)	101	1		t	İ				
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PH2BO MUMAN	MISTONE HZB 1.	20.47	-	-	1	Ì			-	
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MALAN DAVIS	MICTONE HUB (MUB I A)	20-47			-					
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TO COMPANY	TA A CARE IN CONTRACT THE ITY ANTICEN DE. WEI BETA CHAIN PRECURSOR	\$6.83	-	-						
PUBLIC HUMAN		15.95								
PHBZP HUMAN	HIA CLASS II TUSIOCOMO NI CHELLI NATIONEL DEVAN BETA CHAIN PRECINCOR	10.73	$\frac{1}{1}$	-						
PHB20 HUMAN	HIA CLASS II NUSIOCUMA SIMELI I ANTIOCIA, COLATA CLASS CONTROLLA	1	-	-	T	T	T		-	
MESS HUNCH		96.1		+	Ì	Ī			-	
PHBGI HUMAN			+		Ť	Ì				
PHEBOT HUMAN	DIT-1 PROTO-ONCOGENE PROTEIN PRECURSOR (MBGF-1).	1			1				-	
PHONOS HUDSAN	FIBROBLÁST GROWTH FACTOR 4 PRECÍRSOR (FGF 4) (HBGF-4) (HST-2)	7	159.116	-	1				1	
PHINI HUBARAN	PSO PROTEIN (HSP BINDING DAMINOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL	264-312		1	1	1				
PHENE HINAN	TROPORTHYNDAGGEN-UI SYNTHASE (EC 4.2.1.75) (UROPORPHYNDAGGEN-III)	34-118		_					•	
PLEED IN LANK	HEPARIN COFACTOR II PRECURSOR (HC-II) (PROTEASE DAUBITOR LEUSEAPIN 1)	961-691								
PIESE LEINAN		67-22							7	
PLACYA LITTAAN	RETALIFYON ALIMIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N.ACETYL	136-313							-	
MANAN HINAN	RETALIFICACION MAGE BETA CHAIN PRECURSOR (EC 3.2.1.53) (N-ACETYL-BETA-	311-111	_							
A PARTY IN INVAN	LANGE CHOT PROTEIN MIX. I MOX.71	178-212								
PUNCTA LIBRAN	HEPATICYTE MICI EAR FACTOR I ALTHA (POF-1A) (LIVER SPECIFIC	2-29	L						.	
777.5	HEVE DYYCENACE (EC. 14.99.3) (HO.1).	197-224	-	\mid						
2000	-	106-313	-	L	r			_		
NYPULL AUTO	_	\$21-548	914.974 163	1637-1666 2215-2286	\$-2286 2	2289-2316	3317-3344	3448-3475		
MACH INDIAN	HEMATOPOETIC LINEAGE CELL SPECIFIC PROTEIN.	02-64		_						
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NALES TO MAN	-	\$11.545		-						
MANAGE STREET	_	113-140	166-209							
MAIN HE CANA	HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (NEAT SHOCK TRANSCRUPTION FACTOR	117-190								
NAME OF TAXABLE	7	101-69								
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SCAL HOLEN	_	7	907.641	-	T	Ī				
ACT TO ACT	INSULANDEDING FOR THE CENTRAL INC.	Т	322-349	-	T	Ī				
FIG. HOMON	т	۲	406-433		T					
NO HOME	7	Т		1	T					
2000	INTEREST BITCH. I ALPHA PRECURSOR (IL. I ALPHA) (AEXATOPOETIN-1)	Г	183-210	H						
24765	INTEREST FUNDAL RECEPTOR TYPE I PRECURSOR (IL. IRI) (P80)	Γ	172.199	-						
THE STREET		-5								

PCCFNF										
ELE NAME	17	. 7.26		Т		$\overline{}$	$\overline{}$		-	
TEIR HOMAN	7			1	1000	3	1	3	ABEAL	ARIA S
PILIS HOMAN	╗	10.184							-	
PESE HOAV	7					1				
PILS HUMAN										
PENAL HUMAN	INTERFERON ALPHA I PRECURSOR									
PINAR HUMAN	INTERFERONALPHA RECEPTOR PRECURSOR (IFN.ALPHA.BEC)			7						
PDB HUMAN	INTERFERON BETA PRECURSOR (FIBROBLAST)		(M-10)	ž Ž	28.55					Ι
PDE HONAN	INTERFERON DIDICIO IT KD PROTEIN (CONTAINS, INTERFERON PRINCES	2								
AND ROLL	INTERFERON MINISTER A KIN PROTECTION (KIN)	2								
PENSE HIMAN	NSID DE PETERTON PRECIDENT POR SELECTION CONTRACTOR	51-78	216-245	393-430			Ī	Ī	T	
PDWO HIMAN	NVM INTERIOR	\$63-619					T	T		
PIPIK MINAAN	-	961-611	279-273	326-363	316-450		T	T	1	
PIPE UNIVERSITY	A ASSAULT TRUSTHOSTHATE J-KINASE A (EC 2.7.1.127) (INDSITOL	121-162		т		T	T		-	
2000	PLASSES SELUNE PROTEASE (PROTEIN C) INHIBITOR PRECURSOR (PCI)	90-113	100.30	Ī			1	1	1	
TABLE HUMA	INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN PRECURSOR (IRBP)	670.697				1	1			
PIG2 HUMAN	INTERFERON REGULATORY FACTOR 3 (IRF-3)	6		-	*	!		-	7	
PITSP HUMAN	13 KD INOSITOL 1,4,5-TRUSPHOSPHATE 5-PHOSPHATASE PRECIPEOR			1						
PITA2 HUMAN		Т							-	
PITAS HUMAN	П	7	26.00						-	
PITAS HUMAN	INTEGRINAL PRECURSOR INT. A.A. (INTEGRINAL) BUA EL COLORES	Т	037-605	165-792						Ī
PITAL HUMAN	EUXOCYTE ADMESTING OF VICTORIAL IN ALL PARK CHARLES	Т				-		Ī		Ī
PITAM HUMAN	THE STREAM CONCORDING MACHAINED STREAM CHAIR PRECURSOR (LEUKOC	╗	10-341	795-822				T	†	T
PITAV HIMAN	THE CASE CITY SECRETOR AS MAKEN FACTOR SUBURING PRECURSOR (CR.) ALPHA	1044-1078					T	T		
MANA SERVICE	FIRECARCITY RECEIVED ALTER SUBURIL FRECURSOR (INTEGRUN ALPHA-V)						Ì	Ť	1	
No.	TEACHER IN RECEIVE BEING SUBURIT PRECURSOR (INTEGRIN BETA-1) (CD29)	П	34.399				T	1	1	
	LELL SUM ACE ADMESION GLYCOPROTEINS LFA-1, CRU AND P150,95, BETA-	319.366	705-732	Ť	T	l	1			
	PLATELET MEMORANG CL YCOPROTEIN HIA PRECURSOR (GPHIA) (INTEGRIN BETA.	150.35	İ	Ť	T	\dagger	1		-	
7111	MI ECHUM BETA- SUBURIT PRECURSOR (GP150)	307:20			T	T	1	1		
100	WIEWAN BEIAS SUBUNIT PRECURSOR	124-751	Ī	Ì	T		1	1	1	
27/2/17	INTEGRAL BEING SUBURIT PRECURSOR	Г	152.393	T	T	\dagger	\dagger	1	1	
OTTAIN SELEC		363.399	17.35	T	T	\dagger		1	1	
7477171	INTER-ALTHA THE THE THE HOUSE CONDITION CONDITION IN PRECURSOR	Г	Γ	772.810	†	\dagger	\dagger	1		
NAME OF STREET	KENATIN TYPE CYTOSKELETAL 10 (CYTOKERATIN 10) (K10)	154-187	Г	Т	428-462	İ	1	\dagger	†	
AVINE ADIA	MENAITY (MITTER CONTROLLE) AL 13 (CYTOMERATIN 13) (MIS)	13:142		Т			\dagger	\dagger	7	
PKICO HABAAN	CENTRAL TYPE I CYTOSEELE IAL 14 (CYTOSELATIN 14) (KI4)	H	38-135	193-424	İ		\dagger	1	†	
NY PULL SUITA	CENTRAL TITE CONTENT OF CONTENT O	113-143			T	İ	\dagger	1	1	1
PKICO HUMAN	CEASIN TYPE I CYTOSKEE FALL 18 (CYTOKEATIN 16) (R16)	Н			T			\dagger	1	T
PRICE HUMAN	CRAID IVE CYTOKETETAL INCOMPRESSION IN CO.			163-431			t	T	\dagger	Ī
PKICS HUMAN	KEINTIN TYPE I CYTOSKEI ETAL 10 CYTOKERATIN 10 (A 10)	7	┪	337.365					T	T
PK2CI HUMAN	KERATER, TYPE I CYTOSKEL ETAL I (CYTOKERATIN II ALI) CYTOKKEI ETAL A		7	370-397			-			Ī
PRZCZ HUMAN	KENATON, TYPE II CYTOSKELETAL 63 KD.	Ť	7	190-467						T
PRINCE HEINAN	KENATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (FRACKENT)	Ή	(0)	101-411						Γ
PK2CS HUMAN	KERATUL TYPE II CYTOSKELETAL S (CYTOKERATIN S) (KS) (SI KD	Ĭ,	T	107-248					-	
PICTOS HEBADAN	KERATIN, TYPE II CYTOSKELETAL 6 (CYTOKERATIN 6) (K6B KERATIN)	7	T.		1					
NY HOWAN	KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN II) (KS)	T	Т		†	1				
AZCA HUMAN	KERATOV, TYPE II CYTOSKELETAL 56 KD (K6A KERATOV) (FRAGMENT)	t	20.161	217.344	1	1	+			
TAN HUMAN	4-PHOSPHOFAUCTOKINASE, MUSCLE TYPE (EC 27.1.11) (PHOSPHOFAUCTOKINASE	5	Т		1	1	1	1		
TAPL HOME	F-PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 27.1.11) (PHOSPHOFRUCTOKINASE	97	28-159		\dagger	+	1	1		
TALE HUKA	PROTO-CINCOCENE TYROSINE-PROTEIN KINASE ABL (EC 2.7.1.112) (P150)	_		\dagger	1	1	1			
PKAC HUMAN	IG KAPPA CHAIN C REGION.	200	\dagger	1	t	1	1			
TALK HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (ADMESTON MOLECULE LIKE X.LINK	1101	T	\dagger	\dagger	\dagger		1		
TANK HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY CHAIN	39-306		+	\dagger	1	\dagger	1	1	
WANT HUMAN	CAMP-DEPENDENT PROTEIN KINASE TYPE L'BETA REGULATORY CHAIN	177-204	t	\dagger	\dagger	+	+	1	1	
PERSONAL PROPERTY	CAMP-DETENDENT FROI EIN KINASE TYPE ILALPHA REGULATORY CHAIN	1	280.317	t	t	+	+	+		
NAME OF STREET		529-570		\mid	\dagger	\dagger	1		1	T
KECK HUMAN		101-128			I	1	+	\dagger	\dagger	
KFER HUMAN	PKFEK HUMAN PROTO-ONCOCENE TYROSINE-PROTEIN KINASE FER (EC. 2.3.1.113/PMLEER)	466-491	1		Н		\vdash	+	\dagger	Τ
	1	7	<u> </u>	1			\vdash	\mid	f	T
								1	1	1

PCGENE	107117816 Mail Search on All Human Protiin Sequences	П			1		77.17	Aut 3	12/10/	ARFA
THENAME	PROTEIN		┰		2000	1			-	1
PKPES HUMAN		7-	318-351	T						
PECKS HOLDEN	MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-I-R)	293-320							.	
PICTURE HUMAN		199-233								
PKCPE HUMAN		¥.		1						
PKHEK HUDAN			57.50	(3)-(4)	411.680	619.716	037-650		T	I
PKDA HOKA	KINESIN HEAVY CHAPE.	Т	Т	Т						
PENET HIMAN	-	828-928								
PKNY KUKA	KININGGEN, HAW PRECURSOR (ALPHA-3-THIOL PROTEINASE INHIBITOR)	505-532								
PKPSE HEDAN	GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE PSINGTA (EC 2.7.1)	10i-18							~	
PKT-GB HEJBANN	INTERFERON INDUCED, DOUBLE STRANDED RNA-ACTIVATED PROTEIN KINASE	П	191-225	218-312						
PKPTE HEBLAN	PUTATIVE SEADIE/HIRECHINE-PROTEIN KINASE P78 (EC 17.1)	28.60							-	
PKPCL HUMAN	PROTEIN KINASE C, ETA TYPE (EC 2.7.1) (NPKC-ETA) (PKC-L)	7							1	
PKPTI HUMAN	SEAINE/THUEONINE-PROTEIN KINASE PCTAINE-I (EC 17 1)			1					-	I
PKPY1 HUMAN	PYTUVATE KINASE, MI (MUSCLE) ISOZYME (EC 27.11.49) (CT1050CRC 1HTROID	241.300	T						-	
PKPY3 HOKAN	PYRUVATE KINASE, FIZ ISOZYME (E.C. 7.7.1.40).		T	T					-	
PICYTE HOMON		117:111							-	
PICHET HUBIAN		59-703	T	Ī					 	
POCOS HUMAN	FOR PACIFICATION OF THE PROTEIN KINASE SAC (EC. 2.7.) (12) (160-SRC)	0. 1-19								
PRIT HIMAN	LIPUS KU AUTOANTIGEN PROTEIN P10 (10 KD SUBUNIT OF KU ANTIGEN)	135.239								
PKUR HUMAN		158.291								
PKYES HUMAN	PROTO-CHICOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES)	109-243		П					}	
PLAN! MUMAN		32-66	Т	Т	214-241	197.424	10.20	\$10.539		
PLANA HUMAN	(LAMIN A (10 KD LAMIN)		7	297.343	+				1	I
PLAMC HUMAN LAMIN C.	ILAMIN C.	13-26	(al-	202:343					-	
TAN HOUSE	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIOEN RELATED) (EL 3.1.3.40)	101.101	143						-	
TA HOMAN	LUPUS LA PROTEIN (NOCAREN STRUKUMIS LITE B ANTIOLIN (1979).	T		Ī						
MAN KINAN		100	102-329						₩.	
PLDION HUMAN	4LLACTATE DEHYDROGENASE M CHADI (EC 1.1.1.17) (LDIHA)	125-252								
PLDLE HUMAN	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR.	413-510	1							
PLECH HIDANN	ASSALOGLYCOPROTEIN RECEPTOR I (HEPATIC LECTIN HI) (ASSAR).	T								
HEND HUMAN	P-SELECTIN PRECURSOR (MANULE MEMBRONE FAULE) (WAY 199) (MANULE MEMBRONE FAULE) (MANULE FAULE FAULE) (MANULE FAULE) (MANULE FAULE) (MANULE FAULE FAULE) (MANULE FAULE	T								
MAN THE	I FINARMA DIMINITIONY FACTOR PRECURSOR (LIF) (DIFFERENTIATION-	121.56								
PLDY! HUDAN		П	132-261	198.398	869-119	106-118	9901-9101			
PLIPO HUMAN	_	21-12		Ī						
PLD'S HUNGAN	HORMONE SENSTTIVE LIPANE (EC. J. I. I.) (HNL.)	13.61	300.134							
HUA HOMAN		3	ī	1705-1812	1024-1851	1884-1921	1965-1999	2026-2059	2091-2118	
MANA MANAN	+-	1267-1314	1364-1394	1597-1631	1631-1714	1722-1781				
PLAB2 HUMAN		S	1513-1547							
PLIADZ HUMAN		135-182								
PLOX2 HUMAN		34:36								
PLOXS HUMAN	I ANACHEDONATE S-LIFOXTGENASE (EC. 1.13.11.36) (3-LIFOXTGENASE) (3-LIFO).	776-803	T							
MAN HOMAN	-	140-167	119-615							
PLING HOMAN		1061-1108								
PLUZ HUMAN	_	183-583	三	1973-2000						
PLSHR HUMAN		711-99	441-430							
PLV2B HUMAN	I IG LAMBDA CHAIN V. II REGION (NEI)	10.10	1							
PLYAD HUMAN	LYSOSOMAL ALPHA-GLUCOSIDASE PRECURSON (EC.) 2 30) (ACID MALTASE)	\$6.71	T							Ī
PACON HUMA	PROOM HUMA INCHONDRUAL 3 OXUGLUTAKA 11 MALATE CAKAKIA YAULEN UKACI 1 MALAMI GATA AMINGHA MALAMI GATA AMINGHA MALAMI GATA AMINGHA MALAMI GATA AMINGHA MALAMI GATA MALAMI MALAMI GATA	Ī								
TAKE TOWN	NIKANIOLAL PHA MANNOKIDASE (IC 121.)	414-441								

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PHANA HEAM HANNINGE SHOULD HATE ICOMPEASE FOR CIT BY PUNCHANGE FOR FEET	ABEA1	AREA?	ABEA	AREA 4	ARCA S	AREA	AREA 2	ARCAL	AREA?
_	_	1147.1102						+	
-	434-478							-	Ī
	400-449								
PHAX HUMAN MAX PROTEIN.	117.144						L		I
PADMG_HUMA_MDMQ PROTEIN (P33-ASSOCIATED PROTEIN).	235-288								
PACK! HUMAN MULTIDALIO RESISTANCE PROTEIN! (P-GLYCOPROTEIN!)	\$65-195								
	377-407	\$32-366							
PACKO NOMAN MERUSIM NEAVY CHAIN (LAMININ CHAIN AZ) (FIAGMENT).	71.105	138-13	431-438	111116				ŀ	
PACKET BY THE ALL WAS THE PROPERTY OF THE PROPERTY PACKET FOR THE STERASE (EC. 2.1.1.6.1) (6-0-	┪								
	207-234	319-346	\$10.537	209-675				-	
	1.35						L		
-	130-157	331-346			L	L			
	193-430	L			L				
	119.146	151-403						1	
=	286-313							-	
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_	05:61	L							
	MAN-6-1569-1596	2437-2478							
	396.423							+	
	N 38-65							\cdot	
Ī	YLATEDITY-204	230-260							
	387-414	60.628							
PMTF1_HIMAN MITOCHONDRIAL_TRANSCRIPTION FACTOR 1 PRECURSOR (ACTTF1)	_							Ī	
Z	_								
								•	
	ATED 451-489	670-697						Ī	
								-	T
-	11:117							F	T
	263-300	197							
	191-422							-	
	119.146							1	Ī
PMY73 HUMAN IMPOGENIC FACTOR MYF-3.	121-148						Ī		T
MAYAZ HUMAN MATELIN PA PROTEIN.	10-110								
PMYPR, KUMAN MYELIN PROTEOLIPID PROTEIN (PLP) (LIPOPHILIN) (CONTAINS: MYELIN	43.30							1	Ī
	38.75	111-98	171.70	236-324	38435	460-415		T	T
PMISS HUMAN MIOSIN HEAVY CHAIN, CAUDIAC MUSCLE BETA ISOFORM.	48-75	186-156	997-1044	1088-1122	1192-1234	1266-1332	1360-1401	1442.1479	1411-1532
PACYSE HIMAN LAYORIN HEAVY CHAIN FACT CYCLETAL MIRCHE BARREYOME	1941-1582	1640-1681	=	1001-1838					
THE PROPERTY OF THE PROPERTY O	40-73	100-001	22-012	119-1146	22.23	1267-1340	1193-1235 1267-1340 1364-1411	1483-1597 1641-1675	641-1675
PAYSP HUMAN MYOSIN HEAVY CHAIN PERINATAL CARDIAC MIRCI F ISBACAGEMEN	1/0/-1/34	201.77	7		٦				
	131.003	27-173	141-166	213-2112	24.00	507-552	516-624	615-736	784-818
PMYSS, HUMAN MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT).	113.160	191.280	P	977 1.17	,,,,		┪	╗	
		146-171	Т		Т	80	80.08	10.79	101-135
	840-678			T				1	T
	1 492-519	594-621	35.735	Ī	Ī			T	
	OUM 255-282						1	1	
	134-361	310-337							Ī
	5-32							T	
MARY MARKAN DRA-BINDING TAUTEN NEW PRECURSOR	75-77	11.112	343-395						
Ť	1	644-671						T	
Т	(T) 1165-1172	1386-1422	1639-1666						
7	7	R							
		10.10	215.310	116.119	77.	_			
	+		Т		Т	97	(16.7)	1	
PNKA HUMAN INATURAL KILLER CTILS PROTITIN & PRICURKUR	166-193			Ī		T	Ì	Ť	
						1			7

PCGENE	1973 17824 Moulf Sepreb on All Homon Protein Seguences	П	П	П						
THEMME	MI IIMO LOCAL DE LA COLORADA INC.	A SECOND	10 10 10 10 10 10 10 10 10 10 10 10 10 1	45.59	100	3		1000	ST ST ST ST ST ST ST ST ST ST ST ST ST S	d
PNKCR HIBKAN	Ì	1	T	1	!		i		•	
PACK HELLAN		389.416	1116-1146 1292-1319	2.1319					-	
	HOS) (NOS,	389-416								T
		131-158								
-		2.5		1					Ī	1
	RTER)(5)(TT)	F.	1	†				-	i	
1		9		i	Ī	-				
	HADH-UBIQUINONE ÖXIDOREDUCTASE CHAIN 2 (EC 1 6 5.1)	207.740		1						
		2	175.377						·	
		6.73	180-381	1					1	
		462.50		1						
PNYJA HUBAAN	١	≅				į	:			
	OXO.	91.128								
Τ.		139.173								
-		37.78							-	
									-	
	CIIA	121-001	375-402							
		11.99	-							
-		00-65								
MANAN MANAN		120-247								
NAME OF STREET	J.	Г	239.266							
NAME OF THE PARKET	Γ	20.00	239.266							
-	TONE PROTEIN)	139-266							-	
		170-204							-	
1.	14-40)	133.207			,					
		18-133	190-217 290	290-317	377-604				-	
POYON HOMAN	OXYTOCIN RECEPTOR (OT A)									
PPIG? MINAM		•	433-449							
1	DNA POLYNŒRASE ALPHA HOLOENZYNŒ-ASSOCIATED PROTEIN PI.	09-61	637-664							
_	PLECKSTRIN (P41).	38.33	1	1					•	
1	╗			1					-	
	7	٦	<u>.</u> ■	٦						
	┪	•	120-476 586	2003 2003	\$8.715					
PAPI HUMAN	ANCILEATITIS ASSOCIATED PROTEIN I PRECURSOR.	3		1						
PPAXS HUMAN	AURED BOX PROTEIN PAX-S (B-CELL SPECIFIC TRANSCIUPTION FACTOR)			1						
PPDGA HUMAN	PLATELET DELUYED GROWTH FACTOR, A CROWN PACCUROUS (PLOY A-CHAIN)	66.314		†						
WECH HOMON	LATELE MOUNTAIN CALL MILLION FOR COLLEGE	142.176				Ī				
PPENE HUMAN	CANADAM PERCENTIAN PERCENTION (ECT II. 1) (EPO) (FRAGARIT)	306.335								
	(PFP)	11-11								
	MATELET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS: CONNECTIVE-TISSUE	21.55								
		13-100								
POC HUMAN		8-3	1300-1417 155	1333-1380						
PCDH HUNAN	15-HYDROXYPROSTAGLANDIN DEHYDROGENASE (NAD(+)) (EC 1.1.1.141) (PGDH)	2.5	╗							
PPCDR HUMAN	BETA PLATELET-DELIVED GROWTH FACTOR RECEPTOR PRECURSOR (EC 2 7 L 112)	3 4. 32	7	╗						
PPGDS HUMAN	ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR	3	147.395 46	=======================================	224-551	916-1038				
PPGHS HUMAN	PROSTAGLANDIN OM SYNTHASE PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE)	<u> </u>		1						
	BONE/CARTILAGE PROTEOGLYCAN PRECURSOR (BIGLYCAN) (PG-S1)	28		1						
	PHENYLALANDKE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4-	39.76								
		9		1		-				
1-	PHOSDUCIN (13 KD PHOTOTIKANSDUCING PROTEIN) (MEKA PROTEIN)	£73		1						
PPHSI HUMAN	GLYCOGEN PHOSPHORYLASE, LIVER FORM (EC 2 41.1)	Ş	1	1						
	GLYCOGEN PHOSPHORYLASE, MUSCLE FORM (EC 2 4 1 1)		1	1						
PPHS3 HUMAN	CLYCOGEN PHOSPHONYLASE, BRAIN FORM (EC.1 4.1.1).	33.58	+	\dagger						I
PPIP4 HUMAN	I.PHOSPHATDYLINGSTIUL-1.3-813FHU3FIIA IE FIIUSFRUUIES IERASE BEIN 4	77.00	1	1]					

PCGENE	1071/7014 Moulf Search on All Humon Protein Sequences									
FILL KAME	PROTEIN	П	ARA	AREAL	AREA 4	AREAS	AREAS	AREA?	AREAI	AREA
PPLAK HIMAN		Т	87.56	Ì					+	
PPLSL HIMAN		300		1						
100 CT 100 CT		107.700								
NOW THE PARTY OF T		10.561								
LL HOMAN	PENTREMAL MYELIN PROTEIN 22 (PAP-22)	1.33								
PENGE HUMAN		11111								
ACM HONE	PHOSPHOGLYCE LATE MUTASE, MUSCLE FORM (EC 5 4 2 1) (PGAM.NI)	11-115			İ					
THE RUNAN		581-585								
A HOAV	PROBABLE TRANSCRIPTION FACTOR PML.X	\$81:188		Ì						
PPMSC HUMAN	AUTOANTIGEN PM-SCL.	103-130								
PPOCA HIGHAN	DNA-BINDING PROTEIN PO-GA.	14.51	13.300	410.433	907 600		Ī			
PPOLI_HUMAN		274.904	Т	Т		Ì	Ī		1	
PPOL3 HUMAN		T	300	Ì			1			
PPORT HUMAN		Ţ	507:17							
VALUE LANGE	-	7	97.716						•	
200	-	235-269								
2	-		-						-	
TION TOWN	-	•	972-1003	-					-	T
PPRC2 HUMAN	-	19-66							1	
PKC ROMAN		19-96						Ī	Ī	
PRO HOME		197-101	Ī		Ī		Ī		Ŧ	
PAGA HUMAN		146-190		İ					Ī	Ī
PPRIS HOMAN		111.711					T		Ī	
PPRTZ HUPCAN		29.56	l		T			T	Ī	
PISOR HUMAN		26-59		T					-	
PPSPD HUMAN		224-251	T	İ				T	-	
PTHY HUMAN		111-93	Ī				T	T		
PPTINI HUMAN	I	136-177	T		Ī		T		1	Ī
PPTN2 HUMAN	ı	T	1		T	1	T		1	1
PPTING HUMAN	PROTEIN-TYROSINE PHOSPHATASE IC (EC 3 I.3 48) (PTP-IC) (NEMATOPOLETIC	L	\$12.580		T	İ			Ī	
PPTNB HUMAN	PROTECH-TYROSINE PHOSPHATASE 2C (EC 3.1.3 41) (PTP-2C) (PTP-1D)	T	318.346	1	1	1	1			1
PPINC HUMAN	PROTECULTYROSDIE PHOSPHATASE GI (EC.3.1.3.48) (P.1PG1).	Ŀ	695-722	T	1	1	1	1	7	1
PPTRA HUMAN	DNE-RELATED PEPTIDE	Τ		T		1	1	1	7	
NAMON EXTEN	Π	4-10	\dagger	T		T		1		
PPUTZ HUMAN	36	103-630		T					ĺ	
PPURE HUMAN	MULTIFUNCTIONAL PROTEIN ADE2HI (PHOSPHORIBOSYLANGNOIMDAZOLE.	391-418		T	T		1		-	
PPURE HUMAN	ADENTLOSUCCEMATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL)	10.40	T	T	T	1		1		
PYTE HUMAN		20-150			T		1	1	1	
PPYRO_HUMAN	CTP SYNTHASE (EC 6.3.4.1) (UTP-ANOMONIA LIGASE) (CTP SYNTHETASE).	Т	700	T	T	1		1		
PPZP HUMAN			L	1162.111911	1405.1413	T		Ī	Ī	
PRATE HOKEN	LPHA SUBUNIT (TFIIF, ALPHA SUBUNIT)	434-501	+			T	T	T	1	7
PADA HUMAN		38-85			T		†		1	T
PAADO HUMAN	ATED PROTEIN IMB-6.						T	T	Ì	Ī
TADE HUMAN		П	414-463 5	\$10.537			T			
PAGE HUMAN		151-178				-	İ	T		
PARTY MANAGE	ACTION SINDING PROTEIN J (RBBP-J) (PAB-BINDING PROTEIN EJF-J)	2	(22.19					T		
PPEN AMENAN		3	1							
PREST MINAN	BESTALCOTOR A STACE DAYER BOOTEN IN ALMIN STACE TO THE STACE OF THE ST	٦	┪							
		_	200	272	11-619 7	144.771	784-652	1023-1050	1011-1139	1137.1184
PREAL MINISTER	BEN ICATION PROTEIN A 19 PO DAY SPOND SIBING OF A 19 A 19 A 1	श्र								
WALANT WARAN		I	433-433							
MANAN HEA		25.6							Ī	
PERS HADAAN		_								
PAGE HOMA		101-101	06.3		•					
PRICK! HUDAAN	T	Т	207.02.	1		1				·
	(EPSTEIN-BARR VIRUS SMALL RNA ASSOCIATED			\dagger	1	1	1			
PILZ6 HUMAN		Γ	10)-137	t	\dagger	+	\dagger	†		T
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FILE NAME CR PRLAO HUMAN 60 PROS HUMAN 33 PROS HUMAN 60	ROTEIN 408 NIBOSONAL PROTEIN L9. 408 ACIDIC RIBOSOMAL PROTEIN PO (LIDE)	16149								
z	S MBOSOMAL PROTEIN PO (LIDE)				_		_		-	
	S ACIDIC RIBUSOWAL TRUILIN TO LIVE!									
	THE RESERVE TO A PROPERTY OF THE PARTY OF TH	Т	318.364						-	
7	ST KO ROPRUIEIN (SKOCKEN STRUKOME LITTE A ANTIGEN (33-A))	т							1	
	60 KD ROTEIN (STOCKEN SYNDRONE LYPE A ANTICEM (33-A)).									
	HETEROGENEOUS MYCLEAR RIBONUCLEOPROTEINS CIACS (HARAP CLAND HARAP	Ŝ								
PROL HUMAN HE	TEROGENEOUS NIBONUCLEOPROTEIN L (HRNPL)	501-528								
PROU HUMAN HE	TEROGENOUS AURONICLEOPROTEIN U.	7								
T	DNA-DALECTED POVA FOL YAKERASE II 215 KD POL YPEPTIDE		665-720	30.00	1314-1341	1371-1391				
-			1001.1015							
+	TANA PARICTED BAYA POR VARIENCE II 13 KO POR YPEPTIDE	343.374	!	i						
-	PATISTICAL ACID DECEMBER 1 VB. AT 10 ALA	111.352							-	
	RETINGIC ALID RELEFTOR RAN-ALTHA	107.74								
	TINDIC ACID RECEPTOR MAR-BETA ISONORM I			:	:		1	-	:	
=	RETINOIC ACID RECEPTOR ICXA-UETA ISOLURMIZ									
PRS12 HUMAN 40	405 RIBOSOMAL PROTEIN SII	8						Ī		!
PASIG HUMAN 40	40S RIBOSOMAL PROTEIN S16	<u>د</u> .							•	
•	405 RIBOSULIAL PRUTEIN S13	5.4							-	
-	40S RIBOSONIAL PROTEIN \$27A	7								
۰	10S RIBOSOMAL PROTEIN \$7 (50)	13.100							:	
T	ANG RIBOSON/AL PROTEIN SI	146-161							-	j
1,	NAS-LIKE PROTEIN TCJI	133-130							•••	
PETTE HOMAN	LII SALALL MUCLEAR RIBONUCLEOPROTEIN A (UI SNRNP A PROTEIN)	13-43								
ELIZE HUDAAN	112 SASALL MUCLEAR RESONUCLEOPROTEIN D'	13-44					1			
PEVAN INTAKE	BY ANDRING RECEPTOR, SKELETAL MUSCLE	154-111	148.522	100.89	\$140.2777	2810-2847	1304-3331	1529-1556	3013-3010	4921-4941
NATURE OF THE PERSON	C.IM PROTEIN ALPHA CHAIN	12:54							•	
TO THE PARTY OF TH	LIMPORTED RETAIN	8.5				L	L			
7777	Library People DA	2:3								
	DEMOST MOMENTERNASE (EC.)) 1 (15. ADENOSTI, L. HONIOCYSTEINE	119.416					L		•	
	DNA-BRODING PROTEIN SATE	709.736								
PECCA HABLAN SO	COUMNOUS CELL CARCINOMA ANTIGEN (SCCA) (PROTEIN T4-A)	78-105								
	STEM CELL FACTOR PRECURSOR (SCF)	74-101								
	SEMENOCELIN I PROTEIN PRECURSOR (SGI) (CONTAINS SEMINAL BASIC	2	10.270	2					•	
	SUENOCELIN II PRECURSOR (SGII)	2.1.	977-1	6		66.66				
_	SET PROTEDY	76-03			\rfloor					
PSGI HEMAN SE	SECRETOGRAMN I PRECURSOR (CHRONIOGRAMIN B)	200	300.113	27.5						
7	SECRETOGRAMM II FALL UNSUR (CHAUMOUNAMEN C)		138-193	136.20						
-	BONE SIMILATING THE MACABOTION ACTIVATOR (NEV.)	231.238	33.53							
PSW2L HUMAN	CONTROL ATEN CACOCENE SNOW	414.441		L						
DEPCA LIPLAN	SECTION ALPHA CHAIN	193-220	129.015	655.712	1099.1126	6 1461-1502	1813-1909	1988-2022	2120-2154 2223-2250	223-222
		2346-2373								
PSPCB HUMAN ST	SPECTION BETA CHAIN, EXYTHROCYTE	150-177	316-350	486.520	648.675	1201-186	1027-1013	1287-1324	1347.1374	1834-1861
	SEPIGNTEUN REDUCTASE (EC 1 1 1 15) (SFR)	80.124								
	SERUM RESPONSE FACTOR (SAJ)	7.18	480-507							
	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPITA SUBUNIT (SR. ALPITA)	26-110								
PSSA1 HUMAN S	SONATOSTATIN RECEPTOR TYPE I.	289.310								
PSTHOM INDIALANS	STATION (PHOSPHOPROTEIN P19) (ONCOPROTEIN P11) (LEUREMIA-ASSOCIATED	17-74								
PSUIS KUNCAN SI	SUCILASE-ISOMALTASE, INTESTINAL (EC 17 1 41)/(EC 17 1 10)									
PSYBI HUMAN S	SYNAPTOBREVIN I.			1	1	1	1			
PSYD2 HUMAN	ASPARTMENTA SYMPRETASE ALPHA-2 SUBUNIT (EC. 0.1.1.14) (ASPARTME-	174.301	140.771							
_1	IN THURSTRONAL AMENDACTIC IN THE INSECTION AND SECOND		5			1				
_	HISTIDYLTHAN SYNTHETASE (EC 6 1.1 21) (113) IDIME-11AN LIGASE)	141	360.301							
PSYTI MUMAN	SYNAPTOTAGMENT (POS)	697.534	658-685			-				
_	THEONIE THE TANK STATES OF THE TANK THE TRINK LICASED (VALES)	1230-257	413-440			-				
TALL STATE	THE VATIONAL TRING SYNTHETASE (EC 6.1.1.2) (TRYPTOPHAN-TRING LIGASE)	93-127	136.23			L				
TYPER HUMAN	THANSCRIPTION BUTLATION FACTOR IE-BETA CIKAN (TRIE-BETA).	14-64								
TANK HANGEN	PTAPA HIMAN ITANSCHIPTION FACTOR AP 4 (FRAGMENT)	169.196	245-272							

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		AREAL	AREAI	AREAL	AREA	AREA S	AREA 6	AREA? AREAS	AREAS	AREA 9
	TIANSCRIPTION FACTOR JUN-B			_					-	
-	INANSCRIPTION FACTOR JUN-D	101.111								
	MICROTUBULE: ASSOCIATED PROTEIN TAU	178-305							Γ.	
-	MICKOTUBULE.ASSOCIATED PROTEIN TAU, FETAL	311-238								
_	TRANSCOBALAMIN I PRECURSOR.	301-341	330-357						Ī	
-1	T-COMPLEX PROTEIN I (TCP-I)	16.34							Ī	
Т	DNA MUCLEOTIOY LEYOTRANSFERASE (EC 2 7.7 11) (TERMINAL ADOITION ENZYME)	61.93								
PIEK HUMAN RECE	PTOR TYROSINEIPROTEIN KINASE TEK PRECURSOR (EC 2 7 I 112) (III'K.6)	644.678	369.936	1007-1076					:	:
PTF28 HUNGAN TRAN	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)	135-162								
PIFE HURAN IRAN	TRANSCRIPTION FACTOR ES (FRAGNENT)	5.30	123.149	171.236	T		T		ŀ	
PTESS HUMAN TRAN		T			Ī		1			
PTF HUMAN TISSU	ATION FACTOR III)	7	I	Ì	1			1	-	
z	TRANSFORMING GROWTH PACTOR BETA I PRECISOR FICE BETA II									
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	PROTEIN CHITANAM CANAL CHITALOR ALTHA FALLERSON (TOF-ALPINA) (EGF-LIKE TCH	13:11								
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-			24.314						-	
_	٦	185-212								
	AINS SUBSTANCE P, NEUROKININ A	1:1							1	
- [*		626-653					İ		1.	
_		94-125								
_	7	26.33						Ī		
_	(9-6	503-532					T	1	
	C 5 99 1.3)	35.65	616-647	İ		İ			Ī	
		Ī	3.136		Ť	T		Ī		
PTPALA HUMAN TROPO	3	Ī	T	13.116	147.174	116.101	341.333	1	Ī	
PIPER HUMAN IROP			٥	T	Т	т		1	1	
PTPMC HUMAN TROPO		Ť		117.11	1	T			1	
PIPE HUMAN TROP	(PE (TAUS) (TME1)	3:116	10.240	8.5	T	T	T		1	
HUMAN	Ī	T	Ť	7	715.705	Ť	†			
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		L	E	1160-1117	1	1	1	1	Ì	
1	E (FRAGMENT)	t			T	1	1	1	1	
		٢	147.769		T	T	1	T	1	
	CMONE RECEPTOR (TRH-R) (THYROLIBERUN	_			Ť	\dagger			1	
	Γ	36-63	Ī	İ	T	T	1	1	†	
	KSOR (EC 2.7 (112)	T	117-161		T	\dagger	1	1		
	THANSFERRIN RECEPTOR PROTEIN (TR) (ANTIGEN CD31) (T9)	111.215	366-193			T		T	1	
$\overline{}$		211.7	130-417		T	T	\dagger			Ī
		170-197	124.359	\$10.544	\$49.583		T		T	
	EC 2.7.1.812)	150-173			T		İ		T	Ī
-		448-475						\mid	T	
	<u>:</u>	227-254							T	
STORY NOWN COL	UDITACIONOMOSTILIMAMSI ENASE PRECUNSIM MICROSOMAL (EC 2 4 1 17)	227-254								
7		488-522			-	l				
-	UNSINEAN SIMULATURE FACIOR I	2						T	T	
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PULL HUMAN VILLIN				17.744				T		
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		3.13 13.13					İ			
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PXPAC HUMAN DNA.R	(XERODERMA PICHENTOSIN	31.0	1							
PXPCC HUMAN DNA.R.	EPAIN PROTEIN COMPLEMENTING XP-C CELLS (XEXODERMA PIGNENTOSIM)	_	101.77	†	1	†	1	1		
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JAN DNA REPAIR PROTEIN COMPLEMENTING XX-D CELLS (XEXUDEXMA	316.744	047.1081						
THE PARTY PROTECTION CONCUENCENTING XP-G CELLS (CERODERAL PICKEN I USUM	t							
TO SECURITION OF THE PARTY OF T		_						
PXRCC HUMAN DNA. REPAR PROTEIN ANCHI:								
ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN AUX	107.114	1071-1078 1469-1500 20	1407-1500	2013-2057	2013-2057 2146-21803			
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1-10	101-102							
N ZINC PINCER PROJEIN STONE IN								
PZWIE HUMAN JZRAC FINGER PROTEIJ 46 (ZINC PINGER TRO I EIN NOT.								

TABLE X

Search Results Summary for PCTLZIP, P1CTLZIP, and P2CTLZIP Motifs

PCTLZIP LIBRARY FILE		1							
LIBRARY FILE		1 MO AGY ETI 8		-		LIBRARY FILE	-		
700000		SELECTION CONTRACTOR	ANARO			PENV BIVOD	628-642		
PENV FOAMV	401-400	PENV BIVUS	200			PENV BIV27	664-671		
PENV HV1MA	439-463	PENV BIV27	40.4	000.000		PENV FENVI	3047	630-647	
PENV HVIMP	183-189	PENV FOAMV	000	200.500		PENV PIVPS	781-798		
PENV HVIRM	445-460	PENV HVIKB	/bZ-/68			PENY FIVED	770-706		
PENV HV18C	166-201	PENV HV1MA	437-463	-		PENV PIVT2	780-787		
PENV HV122	123-138	PENV HVIMP	183-188			PENY FLVC®	39-56	624-641	
PENV HV12H	439-463	PENV KVIRH	8			PENY FLVOL	605-622		
PENV HV2BE	760-766	PENV HVIST	/30-704			PENV FIVIS	625-642		
PENV HV2D1	741.768	PENV HV18C	186-201	+	-	PENV FLVBA	602-619		
PENV HV201	741.766	PENV HV122	123-138			DELIV COALIV	210.227	987.074	
PENV HV2NZ	742-767	PENV HV123	117-133		1	PENY FOUNT	A25.042		
PENV MV2RO	761-769	PENV HV1ZH	437-463			CDAGA LEAG	AAR 823		
DELLY UV388	743.760	PENV HV28E	750-768			FENV TOVOS	200.000		
PENY HVSET	745-760	PENV HV2D1	741-756			PENV FBVBM	000	1	
DENY 190V	104-119	PENV HV201	741-756			PENV HVIOV	200		
PENY SANGTVO	A18.A33	PENV HVZNZ	742-757			PENV HV122		1	
PENV MMINE	A18.411	PENV HV2RO	761-789			PENV HV123	171.40		
PENV MMI VO	730	PENV HV288	743-768			PENV HV2CA	/80-/8/		
PENV SIVMK	138-104	DEAN UVSAT	746.760			PENV MCFF	600-617		
PENV BINMIL	139-164	PENV NVEO!	104.110	641.557		PENV MCFF3	601-618		
PHEMA CVBLY	391-406	PENV JOHY				PENV MLVAV	630-647		
PHEMA CYBM	391-406	PENV MCP	200			PENV MLVCB	625-642		
PHEMA CVBO	391-406	PEND MCFF3	214-/85			PENV MIVES	039-656	_	
PHEMA CYMOC	391-406	PERV MLVAV	42/443			PENY MIVE	639-656		
PHEMA CYMAS	402-417	PENV MIVCB	422438			BELLY MI VED	819-056		
PUFMA CVMS	403-418	PENY MLYHO	423-430			PENY MENT	020-643		
OUEMA MRAA	286-310	PENV MLVMO	426-442			TENY MENT	107.184		
2000	303-318	PENV MLVRD	424-440	•		PENV MLVA	200		
PHEMA INDO	201.108	PENV MLVRK	424-440			PENV MIVMO	078-040		
PHEMA MEBO	44.5	DENY MMTVB	616-633			PENV MLVRD	024-041		
PHEMA INBEN	301:310	BENY MATTO	618-633			PENV MLVRK	624-641		
PHEMA INBFU	780-301	DENN SEVI	684-880			PENV MAVEB	170-167		
PHEMA NBOL	280-313	PENA BEVAL	861-877			PENV RMCFV	803-620		
PHEMA INDHK	283-308	DENN BROD	93-109			PENV SFV1	710-727	067-974	
PHEMA INBIB	288-303	PENY BRANK	110.184	802.010		PENV SPV3L	707-724	954-971	
PHEMA INBID	269-314	PEN BIVER	139.184	801.817		PENV BIVMS	766-783		
PHEMA INBLE	302-317	PENY DIVING	BOA 823			PENV SIVMK	765-782		
PHEMA INBMD	202-307	PENV BIVE	810.83			PENV BIVML	764-781		
PHEMA INDIME	286-311	PENY BIVOR	20.5		-	PENV BIVB4	760-786		
PHEMA INBNA	288-303	PHEMA COVO	20-05			DENV SIVAD	773-780		
PHEMA INBOR	301-318	PHEMA CVBLY	391-400			Deny analy	KIALKKI		
PHEMA INBB!	301-316	PHEMA CVBM	381.400			SELLY BILLBAY	42.50		-
CUENT MARL	208-313	PHEMA CVBQ	381-408			PENV BRIDAY		300.213	-
PHEMA HISTORY	204.308	PHEMA CVHOC	391-408			PHEMA COVO	30.02	77707	1
PARMA INDO	900 411	PHEMA CVMAS	402-417			PHEMA CVBLY	207		
PHEMA INDVI	915 505	PHEMA CVMB	403-418			PHEMA CVBM	391-408		
PHEMA INBVK	303-318	PENELLA LAATO	237-283	-		PHEMA CVBO	391-408		

MATERIAN 133-140	CHIPTON A ACCOUNT	***		TATEL TATEL	200 000		- 461 186	-
79 135140 FREMA, MACA 224-200 FREMA, MACA 234-200 FREMA, MACA 7 145-300 FREMA, MACA 231-237 FREMA, MACA FREMA, MACA 7 165-50 FREMA, MACA 232-240 FREMA, MACA 7 165-50 FREMA, MACA 232-240 FREMA, MACA 7 165-50 FREMA, MACA 232-240 FREMA, MACA 7 164-70 FREMA, MACA 232-240 FREMA, MACA 8 7-64 FREMA, MACA 221-237 FREMA, MACA 8 7-64 FREMA, MACA 221-237 FREMA, MACA 8 7-64 FREMA, MACA 221-237 FREMA, MACA 9 7-64 FREMA, MACA 221-237 FREMA, MACA 10-10 FREMA, MACA 221-237 FREMA, MACA 10-10 FREMA, MACA 221-237 FREMA, MACA 10-12 FREMA, MACA 220-240 FREMA, MACA 10-12 FREMA, MACA 220-240 FREMA, MACA	PHEMA MUMPIN	2 3		ביינוייי	741.437	STATE OF THE STATE	200 000	-
92 1135 140 PREMA LACKA 224-230 PREMA LACKA 7 135 140 PREMA LACKA 220-240 PREMA LACKA 8 105-100 PREMA LACKA 220-240 PREMA LACKA 10-100 PREMA LACKA 220-240 PREMA LACKA 10-10 PREMA LADIC 221-237 PREMA LACKA 10-10 PREMA LADIC 221-237 PREMA LACKA 10-10 PREMA LADIC 221-237 PREMA LACKA 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA LADIC 10-10 PREMA LADIC 221-237 PREMA	PHEMA MUMPA	133-140		FREMA LABOU	707-477	LUEMA IAAIC	344-038	
N. 546-500 FREMA LACKY 232-240 FREMA LACKY 7 06-50 FREMA LADAY 232-240 FREMA LACKY 8 06-50 FREMA LADAY 232-240 FREMA LACKY 1 06-50 FREMA LADAY 232-240 FREMA LACKY 1 06-50 FREMA LADAY 232-230 FREMA LACKY 1 06-50 FREMA LADAY 221-237 FREMA LACKY 1 06-50 FREMA LADAY 221-237 FREMA LADAY 1 06-50 FREMA LADAY 221-237 FREMA LADAY 2 06-50 FREMA LADAY 221-237 FREMA LADAY 3 06-50 FREMA LADAY 221-237 FREMA LADAY 4 06-50 FREMA LADAY 221-237 FREMA LADAY 5 06-50 FREMA LADAY 221-237 FREMA LADAY 6 06-50 FREMA LADAY 221-237 FREMA LADAY 7 06-50 FREMA LADAY 221-237 FREMA LADAY 8 06-50 FREMA LADAY 222-230 FREMA LADAY 8 06-50 FREMA LADAY 230-240 FREMA LADAY	PHEMA MUMPS	133-146		PHEMA IACKA	234-250	PHEMA LABAN	306-323	
(66-50) PHEMA, LACKY 23-240 PHEMA, LACK (67-50-50-50) PHEMA, LACKY 23-250-50 PHEMA, LACKO (67-50-50-50-50) PHEMA, LACKO 23-250-50 PHEMA, LACKO (67-50-50-50-50) PHEMA, LACKO 23-250-50 PHEMA, LACKO (7-64) PHEMA, LADIA 221-237 PHEMA, LACKO (8-6-50-50-50-50-50-50-50-50-50-50-50-50-50-	PHEMA PITHW	346-360		PHEMA IACKO .	231-247	PHEMA IABUD	320-337	
(66-50) PHERA, LADA (252-250) PHERA, LACK (252-250) PHERA, LA	PHEMA_PI2H	92-90		PHEMA IACKV	230-248	PHEMA LACKA	320-337	
X 366-263 PHEMA, LIANA 237-263 PHEMA, LIANG 7-94 PHEMA, LIANI 227-237 PHEMA, LIANG 8 7-94 PHEMA, LIANI 227-237 PHEMA, LIANG 8 7-94 PHEMA, LIANI 227-237 PHEMA, LIANG 10 7-2-3 PHEMA, LIANG 227-237 PHEMA, LIANG 10 7-2-3 PHEMA, LIANG 227-237 PHEMA, LIANG 10 7-2-3 PHEMA, LIANG 227-237 PHEMA, LIANG 10 7-2-3 PHEMA, LIANG 227-237 PHEMA, LIANG 10 7-2-3 PHEMA, LIANG 227-237 PHEMA, LIANG 10 10-10-1 PHEMA, LIANG 220-240 PHEMA, LIANG 10 10-10-2 PHEMA, LIANG 220-240 PHEMA, LIANG 10 10-10-2 PHEMA, LIANG 220-240 PHEMA, LIANG 10 10-10-2 PHEMA, LIANG 220-240 PHEMA, LIANG 10 10-10-2 PHEMA, LIANG 220-240 PHEMA, LIANG	PHEMA PIZHT	09-99		PHEMA IADA1	234-250	PHEMA SACKO	310-333	
1-84 PHEMA MUCZ 234-250 PHEMA MCCO	PHEMA RINDK	366-383		PHEMA IADAS	237-263	PHEMA IACKP	302-310	_
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20-36 PHEMA IANFO 230-262 PHEMA LAUGU 11-64 PHEMA IANFO 230-262 PHEMA LAUGU 12-37 PHEMA IANFO 230-240 PHEMA LAUGU 125-1206 PHEMA LAHLO 230-240 PHEMA LAUGU 22-37 PHEMA LAHLO 230-240 PHEMA LAUGU 22-37 PHEMA LAHLO 230-262 PHEMA LAUGU 20-203 PHEMA LAHLO 230-262 PHEMA LAHCO 20-203 PHEMA LAHRO 230-240 PHEMA LAHRO 20-204 PHEMA LAHRO 230-240 PHEMA LAHRO 20-205 PHEMA LAHRO 230-262 PHEMA LAHRO 20-206 PHEMA LAHRO 230-262 PHEMA LAHRO 20-206 PHEMA LAHRO 230-262 PHEMA LAHRO 20-206 PHEMA LAHRO 230-262 PHEMA LAHRO 20-207 PHEMA LAHRO 230-262 PHEMA LAHRO 20-208 PHEMA LAHRO 230-262 PHEMA LAHRO 20-209 PHEMA LAHRO 230-262 PHEMA LAHRO 20-209 <td>PV025 BPT4</td> <td>97-112</td> <td></td> <td>PHEMA IAHDE</td> <td>230-248</td> <td>PHEMA IAGRE</td> <td>320-337</td> <td></td>	PV025 BPT4	97-112		PHEMA IAHDE	230-248	PHEMA IAGRE	320-337	
11-94 PHEMA_LANKO 230-262 PHEMA_LANKO 230-262 PHEMA_LANKO 230-260 PHEMA_LANKO 230-260 PHEMA_LANKO 230-240 PHEMA_LANKO PHEMA_LANKO 230-240 PHEMA_LANKO PHEMA_LANKO 230-240 PHEMA_LANKO PHEMA_	PV029 HSVII	20-38	Ĩ	PHEMA IAHFO	236-262	PHEMA MOUZ	320-337	
106-123 PHEMA, IAHIT 230-240 PHEMA, LAHIT PHEMA, LAHIT 230-240 PHEMA, LAHIT <t< td=""><td>PVG30 BPPHB</td><td>11-04</td><td></td><td>PHEMA IAHKO</td><td>236-252</td><td>PHEMA LADUA</td><td>319-336</td><td></td></t<>	PVG30 BPPHB	11-04		PHEMA IAHKO	236-252	PHEMA LADUA	319-336	
108-123	PV036 BPOX2	22-37		PHEMA JAHK7	230-262	PHEMA INHAL	321-338	
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102-17 PHEMA LAHRO 230-262 PHEMA LAHRO 102-17 PHEMA LAHRO 230-282 PHEMA LAHRO 102-17 PHEMA LAHRO 230-246 PHEMA LAHRO 120-282 PHEMA LAHRO 120-246 PHEMA LAHRO 120-240 PHEMA LAHRO 120-240 PHEMA LAHRO 120-240 PHEMA LAHRO 120-240 PHEMA LAHRO 120-262 PHEMA LAHRO 120-262 PHEMA LAHRO 120-262 PHEMA LAHRO 120-262 PHEMA LAHRO 120-270 PHEMA LAHRO 120-261 PHEMA LAHRO 120-270 PHEMA LAHRO PHEMA LAHRO 120-270 PHEMA LAHRO 120-264 PHEMA LAHRO 120-270 PHEMA LAHRO 120-264 PHEMA LAHRO 120-270 PHEMA LAHRO 120-263 PHEMA LAHRO 120-270 PHEMA L	PVOB5 HBVII		_	PHEMA IAHNM	230-262	PHEMA LANDE	316-332	
102-117 PHEMA (AHGA 230-232 PHEMA (AHGA AHKG	PV050 HBVII	208-283		MEMA IAHRO	236-282	PHEMA LAHFO	321-338	
1 267-262 PHEMA IAHEP 230-246 PHEMA IAHK7 1 618-633 PHEMA IAHT 230-240 PHEMA IAHE 234-240 PHEMA IAHT 230-262 PHEMA IAHU 67-72 PHEMA IAHT 230-262 PHEMA IAHM 234-240 PHEMA IAH 230-262 PHEMA IAHM 24-270 PHEMA IAH 230-261 PHEMA IAHM 9 284-270 PHEMA IAHM 235-261 PHEMA IAHM 7 264-270 PHEMA IAHM 237-263 PHEMA IAHM 1 264-270 PHEMA IAHM 237-263 PHEMA IAHW 264-270 PHEMA IAHE 237-263 PHEMA IAHW 264-270 PHEMA IAHE 237-263 PHEMA IAHW 264-270 PHEMA IAHE 237-263 PHEMA IAHW 264-270 PHEMA IAHE 237-263 PHEMA IAHW	PV059 HBVII	102-117		PHEMA IAHBA	236-282	PHEMA WHKO	321-338	
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234-249 PHEMA IAHTE 236-252 PHEMA IAHLO 236-262 PHEMA IAHLO 236-262 PHEMA IAHMI PHEMA IAHMI 236-262 PHEMA IAHMI 234-249 PHEMA IAHMI 236-262 PHEMA IAHMI 236-262 PHEMA IAHMI 236-261 PHEMA IAHMI 236-261 PHEMA IAHMI 236-279 PHEMA IAHMI 236-264 PHEMA IAHMI 236-279 PHEM	PV065 HBVII	518-533		HEMA IAHBW	230-240	PHEMA LAHLE	316-332	
134-240 PHEMA (AHTO 230-222 PHEMA (AHMI 130-222 PHEMA (AHMI 130-222 PHEMA (AHMI 130-222 PHEMA (AHMI 130-222 PHEMA (AHMI 130-221 PHEMA (AHMI 130-221 PHEMA (AHMI 130-231 PHEMA (AHMI 130-	FVOD BPPH2	234-240		HEMA IAHTE	236-252	PHEMA IAHLO	316-332	
134-249 PHEMA IAHUR 236-262 PHEMA IAHUM 236-261 PHEMA IAHUM 236-261 PHEMA IAHUN 236-279 PHEMA IAHRA 235-261 PHEMA IAHRA 235-261 PHEMA IAHRA 235-261 PHEMA IAHRA 235-262 PHEMA IAHRA 235-262 PHEMA IAHRA 235-264 PHEMA IAHRA 236-279 PHEMA IAHRA 237-263 PHEMA IAHRA 236-279 PHEMA IAHRA 237-263 PHEMA IAHRA 236-279 PHEMA IAHRA 236-	PVOD BPPZA	234.240		HEMA IAHTO	230-252	PHEMA IAHMI	321-336	
234-246 PHEMA LAKE 226-251 PHEMA LAHNN	PV00 8PV1R	87.72		HEMA IAHUR	230-252	PHEMA IAHNM	321-338	
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0 284-270 PHEMA LAMAA 233-240 PHEMA LAHRO Y 284-270 PHEMA LAMAO 237-254 PHEMA LAHBA 1 264-270 PHEMA LAME 237-253 PHEMA LAHBA 284-270 PHEMA LAME 237-253 PHEMA LAHBA 284-270 PHEMA LAME 237-253 PHEMA LAHBA	PVOL2 CVBF	264-270	٦	HEMA IALEN	235-251	PHEMA IAHPR	316-332	
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264-279 PHEMA IAME2 237-253 PHEMA IAHTE	PYOL2 CVBO	264-278		HEMA IAMET	237-253	PHEMA JAHBW	315-332	
	PVOL2 CVBV	204-278		WEMA IAME2	237-253	PHEMA IAHTE	321-338	

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CAPES .	442.467		PHEMA IAMED	221-237			בוניין יייניין	221.238		
	440-466	604-618	PHEMA IAMIN	85-101	231-247		MICHA MAION	213.33		
	218-233		PHEMA IANTO	237-283	•		MEMA IAJAF	100-100		
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T	1066-1071		PHEMA MAND	234-250			PHEMA IAMAS	324-341		
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T	1056-1070		PHEMA IASTA	230-248			PHEMA JAMEZ	324-338		
	1056-1070		PHEMA IATA!	235-251			PHEMA IAMED	306-323		
T			PUEMA IATEM	234-250			PHEMA IAMIN	316-333		
	101-718		Dicesta tatyo	211.248			PHEMA IANTO	322.330		
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T	144.441		PHEMA IAUSS	236-261			PHEMA WBEZ	755-335		
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1	10.00			217.263			PHEMA IATKM	320-337		
	266-250		PINCHA MANA	221.217			PHEMA JAUDO	322-339	380-387	
	205-280		PHEMA INCH	211.27			PHEMA IAVIT	323-340		
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PYOUR HRBVI	208-260		PHEMA WZUK	507./67	010		PHEMA IAZHZ	306-323		
_	265-280		PHEMA INBAA	110-131	015.007		DUFMA 1A2H3	308-323		
	265-280		PHEMA INSBE	123-138	203:310	1	GUELLA IAZIIK	322.339		
	265-280		PHEMA MABO	116-132	203-30B		THE PARTY	101-118		
	8.04		PHEMA INBEN	123-130	301.316		PHEMA MUMPIN			
	278-203		PHEMA INBFU	108-124	286.301		PREMA MUMPA			
	9000		PHEMA INBOL	110-136	200-311		PHEMA MUMPS	201.101		
			PHEATA INBHK	116-132	203-308		PHEMA NDVA	93-110		
	00/-5		DURWA INRIB	108-124	268.303 .		PHEMA NOVB	93-110		
	901-916		THE PLANT	120-138	200.314		PHEMA NOVD	03-110		
	900-018		PARMA MOIS	123.130	302.317		PHEMA NOVH	93-110		
	420-441		PACENTA MORE	113-120	202.307		PHEMA MDVI	93-110		
	427-442		PARTIE ALBINE	116.139	208.311		PHEMA NOVM	93-110	_	
PVOLY MOPEI	426-440		PHEMA WOME	75.00	288.303		PHEMA NOVO	103-110		
	621-636		PHEMA MORA	120.120	916.106		PREMA NOVTO	03-110		
	380-386		PHEMA INDUM	19.9.90	101.10		PHEMA NOVU	03-110		
PVMBA MPBV9	187-202		THEMA WOOL	10.01	208.113		PHEMA PHODV	36-63		
	378-383		PHEMA INDS	20.00	200. 300		PHEMA PINW	488-503		
PVM8A WHV69	363-386		PHEMA INBUS	1101136	200 300		PUFMA PISE	1111-128		
PVM8A WAN7	383-388		PHEMA INBVI	110-132	200.21		PAFMA PIZHA	111-128		
	363-388		PHENA MBVK	123-139	303.318		1100	865-000		
	383-398		PHEMA INBYB	108-124	286.301		PHEMA PIJHA	1111110		
	334.249		PHEMA MUMPM	133-148			PHEMA PISH	1111111		-
T	97.35		PHEMA MUMPR	133-140			PHEMA PISHU	111-120		-
	3		PHEMA MUMPS	133-148			PHEMA PICHV	111-128		=
	200		PUPLIA PITEM	345-360			PHEMA PISHW	111-120		_
	26-40		TANKE STATE	ARAI		_	PHEMA PISHX	111-120		
	25-40		FREMA FIAN				PHEMA PIANA	80-87		

PVMT2 IALES	126-40	PHEMA PIDE	324-340				LUCIUS BAAL	100		
PVMT2 IALE2	26.40	PHEMA PISHA	324-340				PHEMA BV6	64-101		
PVMT2 IAMAN	28.40	PHEMA PIOHA	324-340				PHEMA SVECM	84-101		
PVMT2 IAPUE	28.40	PHEMA PICHT	324-340				PHEMA BV6CP	84-101		
PVMT2 IABIN	26-40	PHEMA PISHU	324-340				PHEMA BVELN	84-101		
PVMT2 IAUDO	26.40	PHEMA PIONV	324-340				PVF08 VACCC	280-297		
PVMT2 IAWIL	25-40	PHEMA PISHW	324-340				PVPDS VACCP	280-287		
PVMT9 MYXVL	226-241	PHEMA PISHX	324-340				PVF08 VACCV	281-208		
		PHEMA RINDK	368-383				PVF08 VACCC	176-193		
		PHEMA BVB	7.84				PVP09 VACCV	176-103		
		PHEMA BYSCM	7-94				PVG27 H8V8A	200-226		
		PHEMA BV6CP	7.84				PV028 HBVII	173-180		
		PHEMA BV6UN	7.94				PV039 HBVII	646-668		
		PVENV DHVII	42.67				PVQ43 H8VII	109-126	621-638	
		PVENY EAV	26-41				PVG67 HBVII	171-108		
		PVFP2 FOWPV	88-104				PVG72 HBVIS	1262-1269		
		PVFP7 CAPVK	89-104				PVOF1 IBVB	3073-3080		
		PVFUB VACCO	72-87				PVGL2 IBV8	1004-1111		
		PVGO1 H8VEB	169-164				PVGLB H8VE1	736-753		
		PVGO! HBVI!	209-226	317-332			PVOLB HGVE4	675-692		
		PVG08 HSVII	134-140				PVOLB HBVEA	730-753		
		PVQ10 HBV8A	109-124				PVOLB HBVEB	736-753		
		PV0J1 H9VII	103-110				PYOLE HOVEL	730-753		
		PVQL2 H6VII	270-288				PVOLE ILTVO	597-614		
		PVG1 BPV1R	76-02				PYGLB RTV8	607-624		
		PV029 HBVII	20-38				PVGLB RTVT	607-624		
		PVQ86 BPOX2	22-37				PYOLC PRVIF	180-187		
		PVG16 HBV8A	108-123				PVOLE VZVD	469-486		
		PVG37 HBVII	284-299				PVOLF 8V5	401-418		
		PVG41 HBV11	244.260				PVOLH HCMVA	366-382		
		PVG46 HBVII	1244-1260				PVOLH HCMVT	364-381		
		PV056 HBV11	22-37	143.160			PVOLH HBV11	246-202	803-820	
		PVGE6 H6VII	269-283			-	PVOLH HBV1E	246-262	803-820	
		PVQ59 HBVII	101-117				PVOLI HBV11	43-60		
		PVG60 H6V9A	130-146	330-346			PVOLM BUNL?	91.98		
		PVG59 MBVII	207-282				FVOLM BUNBH	91-09		
		PVQØ6 HBV11	362-378	610.533			PVOLM PUUMH	712-720		
		FV071 HBVBA	80-105				PYDLM PUUMB	712-720		
		PVG9 BPPH2	234-240				PVOLM RVFV	344-361		
		PV04 BPPZA	234.248				PYOLM RVFVZ	344-361		
		PVOG SPV1R	67.72				PYOLY LASSO	12-64		
		PVOF1 IBVB	2210-2228				PVOLY LABBJ	12-04		
-		PVOL2 CVBP	123-139	174-100	204-279		PVQLY LYCVA	12-04		
		PVGL2 CVBL9	123-139	174-190	264-279		PVOLY LYCVW	12-04		-
-1		PYOLZ CYBLY	123-139	174-180	264-279		PVOLY MOPEI	12-94		
		PVOL2 CVBM	123-138	174.180	264-279		PVM1 REOVD	250-297		

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148-108	87.10	147-164	147-164	147.184	147-164	147.184	17.184		11.04	186-202	165-202	174-101	11.04	134.101		1	70-	174-101	185-202	186-202	13.04			174-101	174-101	26-42	26-42	26-42	26.42	28-42	28.43		75.07	70.07	20.02	26.42	26-42	26-42			_	-										
PVMAT COVO	PVMAT MEAB!	PVMP CAMVC	PVMP CAMVD	DVILD CAMVE	7 1110 CALINA	TABLE CAMPINE	PVMP CAMVS	LAMY CAMVE	PVM9A HPBV0	PVMBA HPBV2	PVMBA HPBV4	PVMBA HPBVA	DVMAA MPRVD	PARTY COMPA	LAMPA DI DA	PVMSA HPBVL	PVM8A HPBVN	PVM9A HPBVO	PVMBA HPBVP	PVM4A MPBVR	PATER MODINE	LAMON ALBAG	PVMSA HPBVW	PVM8A HPBVY	PVM8A HPBVZ	PVMT2 IAANN	PVMT2 IABAN	PVACTO IAROW	evirto IARDA	MARTS IARDW	A14 PT 9 4 E1	FVM12 IALE	PVMT2 IALEZ	PVMT2 IAMAN	PVMT2 IAPUE	PVMT2 IABIN	PVMT2 IAUDO	PVMT2 IAWIL										-				
					000	17/7/1700																		,																												
264-279					1274-1290	708-814	1050-1086	1050-1066																																												
174-180	1207-1283	1015.1991	10.10	1126-1142	800.810	804-519	676-692	670-692	1277-1203																					205-280	206-280	205.280		205.200	266-280	266.280	265.280							270-282								367.383
1123-130	08-111		30.13	06-111	442-467	440-466	216-233	216-233	803-819	1086-1071	10KK.1070		1000-10/1	1066-1070	1065-1070	701-718	202.218	603.600	046.020	475-470	444-450	427-442	446-401	160-166		160-160	78-84	79-94	204	206-221	206-221	205-221	398-414	205-221	206-221	208-221	208-221	288.302	100 300	200	400-004	270-292	276-292	6-94	273-289	273-289	273-288	27.289	37.280	373,380	4/3/40	200-206
WANT PLOVE	2012	LACE CAME	PVOL2 CVMAS	רטמוש ביומא	PVOL2 CVPFB	באפוז כאנה	PVGL2 CVPRB	PVOL 2 CVPRM	evol 4 Elov	9701 9 10110	TVGLZ IBVO	PVULZ IBVO	PVGL2 IBVD2	PVGL2 IBVK	PVOL2 IBVM	PVOLR MAVBA	100 B 400/16	בייים בייים	MOLE VAND	PVGIC HBVBC	PVOLC HSVE4	PVOLC HOVED	SYOL C BOVIE	0.00	PVOIC VAND	PVOIC VZVB	PVGID HBV11	PVGLD HBV2	PVGLE PRVRI	PVQUE BR3VA	PVOUS BRBVC	PVOLP BRBVR	PVOL COVO	PVOLF HRSV1	DVOLD HRBVA	IVEU PIONE	EVEN BOYE	100 P 100 P	PVGL MEAN	PVGL MEAB!	PVGL MEASY	PVO(P MUMPM	PVOLF MUMPR	PVOUP MUMPS	PVOLP NDVA	PVQUE NDVB	PVOI P NOVM	TYCH 8101	מיטות שוטיש	2000	PVOL NOVO	PAGE PHODY
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743-758
500-625 500-625
366-371
366-371
826-642
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1021-1037
621-630
191-207
135-161
136-161
189-206
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187-202
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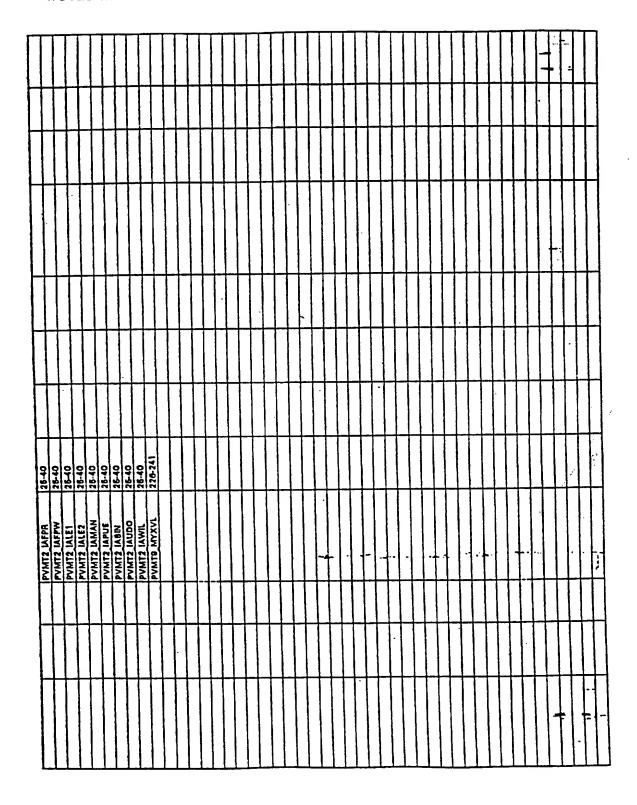


TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP, P5CTLZIP, and P6CTLZIP Motifs

			PACTIZIP			PECTLZIP						
Pacific			I INAARY FILE			LIBRARY FILE			LIBRARY FILE			
LIBRARY FILE	30000		DENVI FREEV	380.399		PENVI FRSFV	380-400		PENV BIVOS	47.69		
PENV BIV27	147-100		BENY AVIEL	08.117		PENV2 FRSFV	380-400		PENV BIV27	47-08	-1	564.575
PENV CAEVC	810-828		DENIV BIVES	147.100		PENV BAEVM	170-180		PENV FENVI	225-240	630-061	
PENV CAEVO	008-820		מבוות הואה	1121.143		PENV FIVPE	781-801		PENV FLVCO	624.645	-	
PENV HV286	760-768		שנאו חושש	0.30		PENV FIVSD	770.700		PENV FLVOL	447.488	605.628 i	
PENV HV2D1	741.758		מברות המשפח	278.707		PENV FIVT2	780-000		PENV FLVLB	467-488	625-646	
PENV HV201	741.769		DENY 19DV	641.600		PENV FLVOL	9-20		PENV FLVSA	444-406	602-623	
PENV HVZNZ	742-780		DENV BOVE	613.662		PENV FOAMV	266-276	924.844	PENV FOAMV	163-174	967-978	
PENV HV2RO	751.750		DIVERS VACOU	173.102		PENV FSVOA	9.20		PENV FSVOA	467.488	026-040	
PENV HV298	743.701		PHEMA VACCE	13.103		PENV HVICE	420.448		PENV FEVOR	447.460	606-626	
PENV HV28T	746.783		PHEMA VACCI	13.103		PENV HV2CA	750-770		PENV FSVSM	450-471	808-628	
PENV JSRV	376-384		PHEMA VACCI	13.00		PENV MIVES	400-420		PENV FBV6T	467.488		
PHEMA PIZH	116-136		PHEMA VACEV	1/3:102		PENV MMTVB	643.683		PENV DALV	62-73	619-640	
PHEMA PIZHT	116-136		PVENV DEV	0.70		PENV MMTVO	643.663		PENV HV28E	760-771	-	
PHEMA BV41	66-73		PVENV MCVI	20.0		PENV OMVVS	76.95		PENV HV201	741.702		
PVENV THOOV	473.401		PVENV MILVE	20.40		PENV RSVP	42.62		PENV HV2NZ	742-763		
PV016 8PP22	83.101		PAYON CHINE	149.188		PENV BFV!	024.044		PENV HV2RO	761-772		
PV024 8PT4	116-133		2001	174 10K		PENY SEVAL	021-041		PENV HV2ST	745-766		
PV036 HEVBA	344-362		PVG01 VACCE	200		PENV SIVMI	766-786		PENV MCFF	600-621		
PVO40 HSVII	14.32		PVG01 VACCV	20.015		PENV RIVME	786.785		PENV MCFF3	601-622		
PVGSO HEVBA	6.94		PVGO1 VARV	20/5		DENIV BIVIN	784.784		PENV MLVAV	630-651		
PVO61 BPT4	63-61		PVG00 BPT4	027-040		DENY BOARA	189.780		PENV MLVCB	625-846		
PVG61 MSVII	84-102		PYGIO HEVII	36.64		PONIO AUX	224.703		DENV MIVES	039.000		
PVG66 H3VII	166-173		PVQ11 H9VII	103-122	160-160	PENV SIVAL	2000	-	PENY MIVE	A19.660		
PVQF1 IBVB	2786-2806	3374-3392	PVG1 BPPH2	31.60		PHEMA COVO	200		DENV MEVED	039.040		
PVOL2 CVH22	1063-1071		PVQ1 BPVIR	020.670		PHEMA CVBLY	381.411		PENY MINE	A3A.A2		
PVOL 2 IBV6	1056-1074		PV020 BPT6	231-260		PHEMA CVBM	100		DENY MENT	167.188		
BVG1 5 IRVR	1066-1073		PYG32 VZVD	00-100		PHEMA CVBO	301-411		PENV MLVAI	90000		
PVGL 4 19VD3	1056-1074		PVG36 BPK3	132-161		PHEMA CVHOC	391.411		PENV MILVMO	050-870		
2001 2001	1055.1073		PV037 BPT2	10.38	620.648	PHEMA CVMAE	402-422		PENV MLVRD	024.040		
PV01.5 10V4	1056-1073		PV037 BPT4	10.38	826.644	PHEMA IACKO	101-161		PENV MICVAL	98.070		
BYOLD USYNI	6.00-6.78	669-707	PV030 HSVII	1038-1057		PHEMA IADMA	101		PENV MOVEB			
	482.710	ł	PVQ41 HSVI1	02-81		PHEMA MUMPM	387.417		PENV RMCPV	20.500		
ANAL AIONG	584.802		PVQ43 BPPF3	360-389		PHEMA MUMPA	307.417		PENV SPVI	0/0./00	3,0	
TAN II TAN	740-758		PVQ46 BPPF1	337.366		PHEMA MUMPS	307.417		FENV BFV3L	0/1./01	9/4.254	
BYOLD II TVB	760-788		PV069 H9VII	142-101		PHEMA PHODV	403-613		PENV BIVAT	43/400		
PVOL B IL TVT	760-768		PVD61 H8VII	117-136	-1	PHEMA PITHW	322-342		PENV BIVAC			
0,0,0,0	431.449		PVO67 HSVII	316-337	1072-1081	PHEMA PIZH	13:33		PENV BIVAL	,		
אמור אלאם	431.440		PVOF1 IBVB	1687-1606	2108-2127	PHEMA PIZHT	13:33		PENV GIVAT	436-456		
PVGIC VAV	70.4		PVOL2 CVBF	991-1010		PHEMA RINDL	407-817		PENV BMSAV	42.03		
PVG(F PI3H4	50.7		PVGL2 CVBLB	991-1010		PHEMA GENDS	322-342		PHEMA CVMAS	402-423		
PVOLH HEVED	314-332		PVOL 2 CVRLY	001-1010		PHEMA BENDE	322-342		PHEMA INDET	200.207		
PVOLH HBVE	614-632		PVOI 3 CVRM	0101.1010		PHEMA BENDH	322.342		PHEMA MUMPM	225246		
PVOLM MEVER	807-828		DAVE STATE	0101-1010		PHEMA BENDJ	322-342		PHEMA MUMPR	225-240	-	
PVOLI HSV11	8.04		2007	0101-1010		PHEMA BENDZ	322-342		PHEMA MUMPS	226-248	-	
VALUE WAR	676-686		1000			DVENV LEIV	97.43	148-168	VOORA AMENA	913.934		

•		3/8:400	379-400	370-400	379-400					_							-			-	-		-																						
1	1		5	370	378	0	-	2	L	_			20	_			11.6		902	08 28	2	8	8	380	926	98	187															_			
		2	2	7.20	7.28	169-180	689-910	314-336	96-89	167-178	288-309	96.109	1165-1178	266-287	30-61	238-269	1666-1877	167-178	1259-1280	1250-1280	1259-1200	1259-1280	1259-1200	1259-1280	1317-1338	1205-1280	1176-1197	83.104	82-103	62-103	83-104	136-160	448-467	336-367	224-246	227-248	224-246	440-467	446-487	446-467	306-326	466-477	460-171	460-471	
PHEMA FIZH	1071	PHEMA BVO	PHEMA EVECM	PHEMA BV6CP	PHEMA SVBLN	PVG01 M3VEB	PVG01 HEVII	PV023 HSVIII	PVG37 BPOX2	PVO43 H9VII	PVOSE HISVIT	PV066 HSVBA	PVQSØ HBVII	PV058 HSV8A	PVOBO HSVII	PVG63 HSVII	PVGF1 IBVB	PVQH3 HCMVA	PVOL2 CVBF	PVOL2 CVBLB	PVOL2 CVBLY	PVOL2 CVBM	PVOL2 CVBO	PVOL2 CVBV	PVOL2 CVM4	PVOL2 CVMAS	PVOL2 CVMJH	PVOLB HBV11	PVQLB HEVIF	PVOLD HBV1K	PVGLB HBV1P	PVOLD MCMVS	PVOLC PRVIF	PVOLF COVO	PVOLF MEARE	PVOLF MEABI	PVOLF MEABY	PVOLF MUMPM	PVOLF MUMPR	PVOLF MUMPS	PVOLF PHODV	PVOLF PINC	PVQUE PI2H	PVOLF PIZHO	
	1	Z.	E .	E E	P.E.	PVQ.	PVG	DAG	970-990 PVG	PVO	DAd	PVQ	074	PVG	PVG	PVG	PVG	PVQ	378-388 PVQ	PVG	PVG	PVOI	PVG	PVO	PVGI	PVQ	PVG	PVQ	M	PVG	ΙDΛα	M	Ž	PVQ	PVG	PVOL	PVOL	PVOL	PVOL	PVOL	PVal	PVOL	PVQL	PVOL	
2007/0	200	/3/.70/	208-318	31.61	31-61	26-46	161-171	300-320	648-668 87	20-40	336-366	117-137	124-144	328-348	327-347	328-348	328-348	327-347	327.347 37	310-330	732-752	760.770	161.771	70.00	20.05	96-96	72-92	279-200	63-03	736-769	283-303	464-474	464-474	464-474	464.474	464.474	010-010	1326-1346	1325-1346	909-1016	0101-000	1000-1020	1001-1001	1001-1001	
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PVENV INCOV		אממו אשרכא	PVG01 VARV	PVG08 VACCC	PVGO6 VARV	PVG00 BPPF1	PVG12 HSVI)	PVG22 H9VII	PVG38 HSVII	PVG61 H9VII	PVG63 HSVII	PVG05 H9VII	PVQ74 HSVSA	PVGL2 18VB	PVOL2 IBVB	PVGL2 IBVD2	PVGLZ IBVD3	PVGL2 IBVK	PVGL2 18VM	PVGL2 IBVU2	PVGLB EBV	PVGLB HCMVA	PVQLB HCMVT	PVGLB HSV23	PVOLB HBV2H	PVOLB H9V28	PVOLB HEVEU	PVOLB HSVB2	PVGLB HBVBA	PVOLB MCMVB	PVOLF PISH4	PVOLO RABVE	PVOLO RABVH	PVOLO RABVP	PVOLO RABVE	PVOLG RABVT	PVOLH MCMV8	PVOLM BUNL7	PVOLM BUNSH	PVOLM BUNYW	PVGLM MANTB	PVOLM HANTH	PVOLM HANTL	PVOLM HANTV	
			1030-1067	1030-1056				771-700	170-789	771.700	170.789	770.780							467.486	467 486								٠																	
949-1016	000./50	866-877	64-83	64.83	814-833	814-833	1041-1060	688.607	697-808	669.607	597-808	687.606	706-726	707-728	117.130	260-276	266-285	266-286	3.04	3.04	475-494	436.466	100.270	44.63	278-207	117-130	162-171	907-1016	166-174	166-174	830-849	830-848	665-674	80.108	1165-1104	621.640	171-190	130-166	174-103	174-103	174.103	171.100			
PVGLZ CVM4	VULZ CVMAD	PVGL2 CVMJH	PVQL2 CVPFB	PVQL2 CVPPU	PVOL2 CVPRB	VOL2 CVPRM	VOL2 FIPV	PVOL2 18V6		PVQL2 IBVD2		PVOL2 IBVM			PVOLB HSV6U	PVOLB RTVO	PVOLB RTVS	PVOLB ILTVT	PVOLC HEVII	PVOLC HSV1K	PVBLC HSVBC	PV010 CHAV	/PLO RABVH	PVŠLI HSVEB	PVOLI VZVD	PVOLM BUNDE	PVOLM PHV	PVOLM PTPV	PVDLM PUUMH	PVOLM PUUMS	PVOLM AVEV	PVOLM RVFVZ	יסנא טטג	PVOLY LYCVW	PVQNB CPMV	PVM3 REOVD	PVME1 CVBM	PVME1 CVH22	MEI CVPFS	PVME1_CVPPU	PVME1 CVPRM	PVME1 CVTKE			
120-144				۵		٩	•	•		۵		۵		•		٩	d	á	٩	<u>ه</u>		هٔ	٩	á	á	Ь	•	d	á	Ь	٤	ď	ď.	٩	(4	٥	١	٤	۵	١	١			
101-101	227.248	227.246	44-02	160-208	100-208	183-201	183-201	103-201	183-201	103.201	103-201	160.186																											-						
PVMO1 VACCV	AT REOVE	PVM1 REOVE	PVMAT HABVA	PVMAT NDVA	PVMAT NDVB	PVMP CAMVC	IP CAMVD	PVMP CAMVE	PVMP CAMVN	PVMP CAMVS	PVMP CAMVW	PVMP FMVD																														-		•	

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463474	220-241	220-241	460-481	460-461	460-481	460-481	460-481	167.171		1	501-712	680-711	304-326	207-318	060-670	2-23	2-23	107-218	180-211	180-211	103-214	237.788	918.960	200.00	97.08	201-302	230-251	٦	-	122-143	64-86	201-222	10-01	244-266	244-265	244-265	233-264	10-01	233-264	233-264	233-264	70-01	233-264	244.206	244.2AR	30.011	345.756	207-707	233-264
PVOLF PISH	PVGLF RINDK	PVOLF RINDL	PVOLF BENDS	PVOLF BENDF	PVOLP SENDH	DVOIE BEND	PVGLF BENDZ			FVGIF BVB	PVOLH HCMVA	PVOLH HCMVT	PVOLH HBVE4	PVOLH HBVEB	PVOLH HBVBA	PVQLI HBV2	PVQLI HSV23	PVOLM BUNDE	PVOLM BUNL7	PVOLM BUNSH	WANTE MINAM	C464 - > 500	2000	PVOLT LABOU	PVGPB EBV	PVM01 VACCC	PVM01 VACCV	PVMAT HRBVA	PVMAT RINDK	PVMAT TRTV	PVME1 CVHOC	PVM8A HPBDB	PVM8A HPBV0	PVM8A HPBV2	PVM0A HPBV4	PVMSA HPBV9	PVMBA HPBVA	PVM8A HPBVD	PVMSA MPBVI	PVM9A HPBVJ	PVMSA HPBVL	PVM9A HPBVN	OVERA MENUS	PVMBA HPBVP	PART NEWS	CAMPA CAMPA	PVMDA KPBVB	PVMBA HPBVW	PVMSA HPBVY
0101-000	926-946	12-32	12:32	12.32	141.161	000 000	308.338	20	300-320	308-328	312-332	312-332	308-328	308-328	74.04	74.04	74.04	74.04	201.221	200.228		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	777.707	212-212	212-232	212-232	212-232	63-63																					
PVOLM SEOUS		Į,			Ī		PVMAI MUMPS				PVMAT PITHA	PVMAT PIAHB							DVIVA UPADA	DANKS AND OF	Part Vema	PVM3A HPBME			PVMBA WHV7	PVM9A WHV8	PVMBA WHVBI	PVM3A WHVW8																					
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233-264	26.46	26-46	26.46	26.40	26.46	26.48	25.48	25.46	26.48	26.40	25.48	26.46				_																			-		-			
PVMSA HPBVZ	PVMT2 IAANN	PVMT2 IABAN	PVMT2 IAPOW	PVMT2 IAFPR	PVMT2 IAFPW	PVM12 IALEI	PVMT2 IALE2	PVMT2 IAMAN	PVMT2 IAPUE	PVMT2 IABIN	PVMT2 IAUDO	PVMT2 IAWIL																												
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TABLE XII

Search Results Summary for P7CTLZIP, P8CTLZIP, and P9CTLZIP Motifs

62cm28		Ī	Pectizip			POCTLZIP			-	
LIBRARY FILE			LIBRARY PRE			LIBRARY FILE				
	202-224	Ī	PENVI FRSEV	360 403		PENV BLVAF	303-327			
	466.620	Ī	PENV2 FREFV	360-403		PENV BLVAU	303-327		-	
	403.616	Ī	PENV BIVOS	176-201		PENV BLVAV	303-327			
	404-510	Ī	PENV BIV27	207.230		PENV BLV82	303-327			
	603-626	Î	PENV FOAMV	604-667		PENV BLVBG	303-327		-	
PENV HVIEL	495-517		PENV HV123	176-109		PENV BLVJ	303-327		-	
	488.820	-	PENV HV2BE	3.20	761-804	PENV FIVPE	781-808			
PENV HV1H3	488.620	Ī	PENV HV2CA	760-773		PENV FIVSO	778-803			
	610-632	-	PENV HV2D1		772 706	PENV FIVT2	780-604		: : : : : : : : : : : : : : : : : : : :	
	480-512	-	PENV HV201	272.705		PHEMA CVBLY	391-415		-	-
	604-620	-	PENV HV2NZ	777-800		PHEMA CVBM	391-415			
	600-622	Ī	PENV JSRV	641-564		PHEMA CVBO	301-416			-
T	496-616		PENV BEVI	004.007		PHEMA CVHOC	301-416			
	489-610	Ī	PENV BFV3L	861-004		PHEMA INCCA	442.468			
Ī	498-520		PENV SIVMI	803-626		PHEMA INCEN	430-464			
	469-511		PENV BIVMK	802-825		PHEMA INCOL	430-464			
	123-146 406-617	Γ	PENV BIVML	601-624		PHEMA INCHY	420-463			
	H	Γ	PENV BIVB4	808-828		PHEMA INC.H	443-467			
	KOK. K27		PENV BIVEP	610-633		PHEMA INCKY	420-463			
Ī	409.620		PHEMA COVO	200-223		PHEMA INCMI	429.463		_	
T	178.100		PURMA PIZM	98.98		PHEMA INCNA	429-463			
	2075		MEMA PISHT	68.68		PHEMA INCPI	430-464		-	_
	20000		DVE11 VACCO	181.184		PHEMA INCP2	430-464			
PENV BHV)	17.80	Ī	PVF16 VACCC	26-48		PHEMA INCP3	430-464			
	17.7		PAPER VACCE	3.20		PHEMA INCTA	430-464			
	17.60		PVG1L AMERY	313-336		PHEMA INCYA	430-484			
T	67.16		PVG28 HSVII	401-514		PHEMA MUMPM	101-126			
T			PVQ43 HBVIS	322-346		PHEMA MUMPR	101-126			
T	21.43		PVG62 HSVII	229-262		PHEMA MUMPS	101-126			
	21.43		PVD67 HBVII	722-746		PHEMA PITHW	20.63			
	21-43		PVOL2 CVBF	10-33		PVENV BEV	02-80			
	21-43		AVOL2 CVBLB	661-674		PVF06 VACCC	280-304			
	37.69		PVOL2 CVBLY	10-33		PVF06 VACCP	260-304			
	28-60		PYOL2 CVM4	1287-1280		PVF06 VACCV	281-306			
	37.69		FVOL2 CVMA6	1216-1238		PVF09 VACCC	170-200			-
PHEMA LAENO 21	21-43		PYOLZ CVMJH	1120-1148		PVF09 VACCV	176-200			-
	37.69	4	PVOL2 CVPFB	1274-1207		PVGOI VZVD	60-62			
	37-68		PYOL2 CYPPU	1272-1285		PVG10 HBVBA	366-370			•••
	37.68	•	PVOL2 CVPR8	1060-1073		PVG12 HBV9A	00.07			
	37.60		PVGL2 CVPRM	1060-1073		PVQ19 HEVII	00-112			
	21-43		PYOL2 FIPV	1277-1300		PVG28 HSVII	173-107		1	1
	37.69		PYOL2 MV6	196-210		FV043 HBVII	100.135			-
	21-43		PVGL2 IBVB	196-218		PVG67 HBVII	108-132	1006-1028	-	
	33-66		FVOL2 IBVD2	100-219		PV072 HBVII	720-744			
	37.60	1	PVOL2 IBVD3	196.219		PVGF1 18VB	3001-3628			
l				 -						

			414.5	229	ロアンドラ ぎっこくの	669.013	_		
39.80		PVGLZ IBVK	907-001	10/10	PVGIR ILTV6	597-621			
37.60	١	PVOLZ IBVM	017-08-1	2	BVT II B IDVO	607.631			
93.40	آھ	PVOL2 IBVVI	178-201		1000	1007.09			
21.43	٤	PVGL2 IBVV2	178-201		1000	417.47			
21-43	۵	PVOL2 IBVUS	176.201	2	PVGIE MSV1				
37.60	1	FVOLS HCMVA	635.660	600	PVOLE VZVO				-
38.60	5	PVOLB HCMVT	636-660	200	PVOLF SV5	401-470	+		
96.63	-	PVOLB HBVBA	483-608	2	PVOLH HCMVA	07500			
	1	PVOLB MCMV8	600-009	2	PVOLH HCMNT	673-697		+	-
1	1	PVOLC HBV11	467.480	DAd	PVOLH H6V11	443-467	003-827	+	+
	16	BVOIC HSVIK	467.400	DVG	PVOLH HSVIE	443-407	603-627		
72.27	1	PAGE MEVS	436-468	PVG	PVOLM BUNL7	31-56			
317.338		יייייייייייייייייייייייייייייייייייייי	410.460	DAd	PVOLM BUNSH	31.66		-	
80-72		PYOLC MOVES	0187.1810	DA	PVOLM HANTH	694-718			
27.5		LAGE M BONE	0303.000	pvq	PVG! M RVFV	344-368			
11.33		PVOLM BUNSH		0/16	BYOLKI BYEN	344.368			
11.33	£	PVOLM UUK	200-000		, Al	SA1. KAK			
98-110	<u>a</u>	PVOLY JUNIN	12:35	2	PVGLM DON :				
134.08		PVOLY LASSO	12.38	2	PVONM CPMV	311-330	1		
	Í	PVOLY LABS.	12.36	PVG	PVGP2 EBV	057.081	1		
į	- 16	PVOI V I VEVA	12.38	DVG	PVQP3 EBV	854-878			
134-166		140.		AVE	PVM1 REOVD	280-304			
71-03		PVOLY LYCVW	95.3	MV	PVM1 REOVE	280-304			
266-288	•	PVOLY MOPE!	12:30		0,030	100			
267-289	•	PVOLY TACV	12.36	2	PVMZ1 AEUVU	200			
43.64		PUDLY TACVE	12.36	A	PVM22 MEDVD				
100	6	PVOLY TACY	12.36	2	PVM2 REOVJ	108-102			1
0000		PVOLY TACVT	12-38	3	PVM2 REOVL	168-182		\dagger	
134/-130	. 18	WOUND COUNTY	741.784	PVR	PVKIAT MEASI	67-111			
29.65		PACE BEOVE		464-477 PVW	PVMAT BEPVB	314-338			
1066-1076		CACOL IMA	T	١.	PVME1 CVBM	197-161			
1068-1077		PVM1 MEDVL		NA O	PUMET CUMOC	137.161			
1066-1078		PVMAT MUMPB	727-ZB0		2000	197.461		-	
\$0KK-1022	۵	PVMSA HP8DB	1200-202	PVME1	CVIKE	20.00			
1008-1033		PVMBA HPBDC	265-201	2	PVME1 18V0	2			
1000		PLONG A HPBDU	231-264	PVR	PVME1 IBVB	74.00		+	
		WARA HPBDW	269-202	PVN	PVME1 IBVB2	74.08			
/40-/0/		MANA NORME	236-269	PVN	PVME1 IBVK	74-00			+
30172				PVR	PVM8A MP8G8	271-206			
308-420	+			PVR	PVMBA WHVI	200.203			
390-421		*		NA NA	PVMEA WHYED	274.290			
266-287	482.604			100	DVIMA WILV?	274.208			
484-508					DATE A WALVE	274.208			
484-806		1			DAUM VE	100			
484-606					PVM3A WHVOI	200			
484.808				Ž	FUMSA WHYND	140.12			
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200									1
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462-4/4							1		
77.00				7					
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1000 CONT. 0000 CONT. 0000								
PVOLI UCANA								
T								
430-462	1640-1668					•		
PVGLY LABBO 420-448								
427-440								
426-447								
657-678								
654-676								
PVMAT PINC 188-217								
Γ								
Γ								
PVMAT BENDH 108-217								
188-217			_					
131.163								
203.318								
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TABLE XIII

SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF

LICENE	PICTIZIP	A 1 V										
LILEMANIE	LROILIN	Tiest and a second a second and	Davis of the state	ARCA !	ABEA	ı	124		1			
PIBILS VACCC	IBETA-IISD	VACCINIA CINIS SERVICE STRAIN SYM)	360-378	00.030	2000	197	3	100	4	AMEAL	V. 1.5.5	
PIBILS VACCV	INETA-IISD	CALCACTURE AND CONTRACTOR OF THE CONTRACTOR OF T	41.56	197.73		7	!		3.140			
PINIS VARY	INICALING TO THE PARTY OF THE P		:5	:::::::::::::::::::::::::::::::::::::::		:						
PATHI FOWPE			*			-						
PATH VACCV		- LOWI FOR VINIS (ISSE) AND IN ANIMARIAN IN)	47.69	-	:	•	:	•			_	
PATH VARV	THE ACT OF THE PROPERTY OF THE PARTY OF THE	VACCINIA VIRUS ISTRAIN WR)	1	<u> </u>	-	-				:		
PATI2 HSVII	N. 11. 11. 11. 11. 11. 11. 11. 11. 11. 1	VANOLAVIRIIS		1								
п.	- 1	FERRES SINCE X LIRUS (TVPT 1. STRAIN 13)			!	1						
		HERPES SIMPLITY VINITY (1) 11 SINAINTI		:		_			:		•	
	=	FOUNDE IN REPORTED AND AND AND AND AND AND AND AND AND AN	Y 12.7		_							
LA III VACCC		VACCINIA VIEW COLONIA	147.222			··					_	
PAILS VZVD	12	CANCEL STRAIG COLUMN STRAIGHT	115.24		_	-			i		_	
PATIS VACEV	- 1	CANCELLA COSTER VIRUS (STRAIN CHINAS)	5:3	10111	: : :	-		1			!	
PATE ISVE		VACCINIA VIRUS (SI IASIN WR)	15			-		i		:	!	
72.74		BOVINE HERPESVINIS TYPE STRAIN		-	·				i		:	
		EQUINE INTERPLEVENCE TANK A SECOND SE	2	277.73			i	:			_	
•		COUNTY CONTRACTOR OF THE PROPERTY OF THE PROPE	2			•						
PATO VZVO		CONTRACTOR OF THE COUNTY AND THE COUNTY OF T	139.140	!		:	. ::	:	:		-	
PATI COWPY		VAUCELLA-ZOSTER VIRING (STRAIN DIRIAS)	100	1	:	-					-	
Van Car		COWPOX VIRIIS			:			i	!!!!!			
	DE LACIE NA	**********		-	_			!	· · ·		:	
2001	TRANSCRIPTIONAL REGULATORY PROTEIN	TERRES SIMPLY CONTROL OF THE STATE OF THE ST	2	_			:		:	•	-	
_	OCAS I PROTEIN PRECURSOR		2.5			:				_	_	
PORLI EDV	TRANSCRIPTION ACTIVATOR BRITE	THE PART OF THE PA	76 133			:						
PCAGE VACCO	CELL SIMILACE BROWN BESTER	EVSTRIN BALL VIRIS (STRAIN NOS 8)	-		:							
PCA1BI VACTO	NI III CAR CAR A STATE OF THE S	VACCINIA VIRUS (STRAIN COPI NITACITN)	-		;		İ			!	; 	
	NI HOLD DENT TO SECURE	VACCINIA VINUS (STRAIN N. R.)		: : :				!	:	!		
	1	VARIOLA VINIT	2			; :	!	i			-:	
MOH MOVE	1		102 101		:	!	-	1 . !	i	-		
MEL HISVII	ı	THE STANDS SAIMING STANDS	1 1 1 1		1	;	!			!	_	
PCELD HISVIR	- [THE SUPPLEX VINUS CITY E 1. STRAIN IN		:::::::::::::::::::::::::::::::::::::::		!		_		-	:	
		HEAPES SWOI EX VIRUS AND 17 CHEANNESS.		-	786 100			!	:		• :	
	CELL TUSION PROTEIN PRECIASOR	IEAPES STOP BY VINITED TO 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	*	213.338				İ	-	<u> </u>	1	
MAN TO	1	INTERPRETATION OF THE PROPERTY IN THE PROPERTY	38 : 38	111.111	181.50	1				Ī		
MAN TED	1	THE PROPERTY OF THE PROPERTY AS	105.233	340.341	İ		1				!	
PCORD HSWSA	-	TANKELLA COSTER VIRUS (STRAIN DURIAS)	346.340		1	1.1				-		
	COAT PROTEST OF	HENCES VIKUS SALMINI (STRAIN III)		`	!	-			_	-	:	
1.	COA HOLEN OF	BUDGENOAR PLEINATING DISEASE VIRIES		7			i		İ	-		
	CONTROLL VI	POLYOMANDUS BK ISTRAIN ASI					İ	İ	ĺ	-	-	
	COAL PROTEIN VP	POLYOMA VIRUS BK	2	2.13	133 331		İ	Ī	İ		į	
	COAT PROTECT VP	BOVINE MY YOMA VIAUS	25:22	17:133	33.73	İ	İ	Ť	İ	-	-	
_	COAT PROTEIN VP	HAMSTER POLYOMA VIBIG	96-120		:	İ		1		-	- !	
_	COAT PROTEDY VPI	POLYDAZAVILIK IC	3			Ì	İ		-	-		
MOA! PONLY	COAT PROTEDY VP	TAMENOTION OF THE PARTY OF THE	7	=	235.743	İ	İ	 		_		
	COAT PROTEIN VP	CONTRACTOR OF THE PARTY OF THE	200		1	İ		-				
		PICOSE FOLIUMA VIRUS (STRAIN KILIJANI)	30.00	231.240								
	COAT PROTEIN THE		17.	1	116.316						Ī	
			101.00			Ì				! 		
MON MONLY		HOVING FOLYOMAVIRUS	77.15						_	<u> </u> 		
MON CAOM		L'TACHUTROPIC POLYOMAVIRUS	1	j						!		
COA! TIVE		MOUSE FOLYOMA VIRUS (STRAIN))						_		<u> </u>		
POLAT ABLANCE		THERMOPROTEUS TENAX VIRUS I (STRAIN KILAI)						<u> </u>		1		
200		ABUTLON MOSAIC VIRUS (ISOLATE WEST INDIA)						-	-	<u> </u>	!	
A NOW	10%	BOOLARIA VIIUS					_	+	-	1	-	
_ i	PROTEIN	PARAMECHAN BILL SABIA CHI CARTI A SISSIE	9					<u> </u>	-	<u> </u>	_	
- 1			14-11	102.409		1	1	-	-	<u> </u>	-	
- 1			165-181			-	-	-	-	_		
5	COATPROTECT	CYMBIDIDA MOSAC CIBIS	63.188	Ī	İ	-	1	-	<u> </u>			
			2.38		-	-	-	_ <u>'</u> 	-		 :	
			7		1	1	i	_ <u>'</u> 			i	
PCOAT CTUSE			119.311	! i		-	<u>-</u>			<u>:</u>		
		THE THE PARTY OF THE PIGE	11.94		-					! -		
PCOAT ICYTE			115.45	13.65	1	1				<u> </u>		
			Τ	100	-	-				! <u> </u>	į	
			7		1	1				<u>:</u> 	<u> </u>	
											•	

PCCENT	PITCTIZIP	All Virgari (No Boccecuphoges)						\Box	_	1	
	LADILER		7	79.50	3.EC-1	AK TAD		ŷVlήγ	A111.4.2	ARIVE	• 1 = 1
4	COATPROTEIN		267.580	099.599	1	-			1	-	:
	COAT PROTEIN UP!	FEI DE PAM EUKOPENIA VIRUS	690.305						-	-	
i	COAT PROTEIN VP	FEI THE PAM EUROPENIA VIRIS (STRAIN 191)	690.105		i						
MOAT IEVS	COAT PROTED	HELF MICHALIAUS S	. 99.6								
Т		KINK ENTERITIS VIRUS (STRAIN ABASHIRI)	685.700								
MONT LONGY		MELON MECHANIC SPOT VIRUS	3.5	i	:				i	:	:
	COAT BEOLEDA	MALLE STRIPE VIRUS	176.193	204.22	:	i		!	:		:
		NABCISSIS MOSAIC SIBIIS	67.16			-	::::::	:		2	
Ŀ		NODAKAHA MANA	110.104		1	1	****	:	:	:	1
≥!	CUAL PROJEIN PRECUASUR	INDUMINATION OF THE PROPERTY O		i	i						
- 1	COAT PROTEIN	ODOMTOGLOSSUM KINGSFOT VIRUS	3								!
	COATPROTEIN	ONOMIS YELLOW AIRSAIC VIRUS	13:42			-					
:	COAT PROJEIN VP3	CAMINE PAR VOVIRIIS (TYPE 2/SIRAIN ATT)	541.562								
ŀ.	COAT PROTEIN VOI	CANDAR PARCOCIRIIS (STRAIN 200929)	865.300					İ		:	; !
-1.			-	İ	:	-	1	:			
_	COAT PROTEIN VP	CAMINE PARVOVIRUS (SIRAIN CTV-1) CORMIT. 120)	3			7	-		ļ	:	:
PCOAT PAVCE	COAT PROTEIN VPI	CANINE PARCOURUS (STRAID IS)	711.726								
•	COAT PROTEIN PRECURSOR	PEPPER MOTILE VIRUS	233.205			-					
_		PARAVA MARAIC POTE VUBITE	19179	İ			1	:	:	:	
	COALTROISIN			12	:	:		1	1	;	
	COATPROTEIN	PISTIN MILLI MILL VIKUS (SI KAIM STAIM)		!	: ::::		i	1 1 1 1 1 1 1		:	!
PCOAT PVSP	COAT PROTEIN	POTATO VIRUS S (SIRAIN FERINCIAN)	139.147			1					
		PICE SIMPE VIRUS	136.152								_
71 1000	COATESOTEN	SATSELLIPE MALLE WHELE LINE MOSAIC VINUS	19:	:		İ					İ
2	COALTROISIN			j	-		1	-		-	
_	COATPROTEIN	SIMMERAT MILU TELLOW PINE ASSOCIATED VINUS		j	1			1			-
PCOAT TAMO	GENOME POLYPROTEIN	TAMARILIO MOSAUC VIRUS	111.137								
•	COAT PROTEIN	TONCATO BUSILY STUNT VIRIS (STRAIN IS.)	139-383		i						
_	200.000	THE MIS CRIME S VISIT	97.5	İ	!	-		!	İ	:	:
				İ							1
COAT TOWY		I DIKATU KALUPIN NOSAK VIRUS									
PCOAT THOM		TOBACCOMILD CREEN MOSAIC VIRUS (TNIV STRAIN UT)	- T								
MONT TAV	COALPROIETH	TOBACCO MOSAIC VIRITS (VUT GARC)	103.136	`			!			i	:
POOR TAVOR		TOBACCO MOSAIC VIBUS (STRAIN 96)	103:131					!		:	
		TOBACTO MOSAIT VIBILS ISTRAIN DAILI BAIFNS	103.131	İ				1	1	:	:
		CONTACTO DATE OF THE AND RES	100							:	:
- 1		THE PARTY OF THE P			-	-			1		:
- 1		TOBALLO MUSALL VIRUS (STRAIN HILLAND) STRAIN			1	į		1	!	1	
		TOBACCO MOSAIC VIRUS (STRAIN U)	2.70		-						:
		TOBACCO MOSARC VIRIIS (STRAIN ON!)	103-128		-			i			į
0		TOBACCO MOSAIC VIRUS (STRAIN TOMATOR.)	107-178		1						
		I DBACCO MECROSIS VIRIIS (SIRAIN A)	119.142								
_		TOBACCO MECROSIS VIRUS (STRAIM D)	101.134								!
7	COLLAGENLIKE PROTEIN	IERPESVINUS SADAIRI (SUNGROUP C./ STRAIN 401)	7.K								 !
1	CORE ANTIGEN	ILEPATITIS & VINUS (SUBTYTE ADWI)	28·180								
1.	COSE ANTICEN	IGPATITIS & VIRUS (STRAIN ALPIA))	3	1	!					İ	İ
	COMPANICEN	INPATITIS DVINUS ISURI YPE ADYWI	39.100								i
N. P. L. P. C.	SECRETARIA BRANCO SECTION	IN BLAN ADENOVIRITY TYPE 9	10.16	!							
1	TANDAL BANDAD BEOTER	COCTON BARB VIBIG COM AND BOLD.	440 411		-						
	TOTAL STATE	THE LANGE OF THE PARTY OF THE P									
∢!	MAUR DRA-BEDGE FRUIE IN	HIGHWAY CT I CHECKLY CVINGS (STEAKIN AD 187)									
Ų	MAJOR DNA BENDEND PROTEIN	HEATES SOUTHER VIAUS (1978) / STANIN 17)	27.476	2			Ì				
	ALAJOR DNA BOIDDIG PROTEIN	DEAPES SOULEX VIRUS (TYPE 17 STRAIN F)	459-436	201 620	:	į	. [
	MAJOR DHA-BONDAND PROTEIN	IEAPES SUPPLEX VIRUS (TYPE, 1/STRAIN KOS)	459.476	597.470							
POWEL LISTE	MAJOR DNA BOOM PROTEIN	BOVINE ICENES VIRUS TYPE 2 ISTRAIN DAIV	451.433	919.95	:						
Т	MARION DINA BRADING PROTEIN	FOUND IN REPESVING TYPE I (STRAIN ABAP)	810 811								
10000	MANOR DAY BROWN PROFESSION	IN BPE CYBELS CALLINE COTBAIN 113	108.137	010.6	100.000	014.1000				Ī	
	TOTAL STREET,	LA BINE CYTOLICA DVIBIL (CTB AND CLASSIS)	413 614	7	7						
	MAJOR DIA BINDING FROID IN	MONING CALLONING AND CONTROL OF THE PARTY OF								-	Ì
_	MAJOR DINA RINDONG PROTEIN	SIMUM CTIONE CALCUMING (STRAIN COLUMN)		2010							
-	DMA LIGASE	VARIOLA VIRUS	26.		1	ļ			!	ļ	i
PDPOL ADE02	DNA POLYNGRASE	INDIAN ADENOVIRUS TYPE 1		938 930							_
Т	DNA POLYNGRASE	INDIAN ADENOVIRUS TYPE 1	П	050 171							İ
ī	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 1	95:161	•	916.761						
T	DNA ME YAFRASE	INTIMAN ADENOVIRUS TYPE 13	263.281	7	176 141						
7			ı	7							

	PINCHLIIP	All Virgat INe Betterlenbesen									
	LROICIN	YIRUS	ARCAI	V V V	- VERV	-			\neg	,	
ADED COLON	NA POLYNERASE	CININISTONE URA BIEMNIS ENTONIOFOXVIRUS	100		1.00	- arre		C. 5545	61.4	ARAL	ABLAL
- 1	IN A POL YMERA SE	CIO ORELLA VIRUS NY 3A	434.402		1	-					
	HA POLYNGASE	PARAMECIUM BURSARIA (10 MAEL) A VIRLIS	1	434.465		+					
- 1	DNA POLYNERASE	PSTUIN BARR VIRIES (STRAIN IN) B	186.334	1	- 635.65					į	
	HA POLYMERASE	10WLM VIRIS	60.77	220.367			1			-	į
DOC IONA	21	MINAM CYTONE GALOVIRUS (STRAIN ADIES)	\$69.517	3	1000						-
DAG. HARDS	HA POLYNERASE	DIRCK IEPATITIS & VARIS (BPOWN SHAMINIAI DIRCK ISOLATE ST)	6,30	13.13		157.73				Ì	
TOTAL INDIC	7	DICK HEPATHIS & VINIS (SIRAIN CHINA)	5	137.134	- 9	***			-		;
DE LONG	MA POLYMERASE	DUCK HEPATHIS & VIRUS									
POPOL HORDW	HA POLYNERASE	DUCK IRPATITIS & VIAUS (WILLE SHANGHAI DUCK ISOLATE SILL	100		17. 61.					j	j
POPOL HERGS	HA POLYMERASE	GROUND SOUTHARE LIEPATITIS VIRIUS							į		
PDPOL IMBIRE D	HA POLYMERASE	HERON HEPATIFIS IN VIRIA			-	-					!
PDPOL IPBV2 DV	NA POLYAFERASE	HEPATITIS B VIRIS (Still 1) PT Allery				:	:			:	:
_	TAN TAN YAS BASE										_
_			=			•					
	TAY BOX WASEA AGE	THE ALTER TO THE STATE OF THE PARTY AND THE PARTY OF THE	20.00	=======================================	76.1 7800	•					
÷	DISA TOLIMENASE	ILETATION VIEUS (STRAIN ALPINAL)	2 0	349-436	434.430	150.760	:	-	·		İ
٦	MA FOLTMERASE	TEPATITIS & VIRIIS (SINDITYPE ADW / SIRAIN INTXONESIAPIDW (20)	10.00	410.013	405.00	141.131					
Ĭ	DAY FOL TAE LASE	ICPATITIS D VIRUS (SUBTYPE AIW / STRAIN JAPANTIDW 11)	26.02	9	445.466	100					
7	DNA POLYMERASE	INPATITIS B VIRUS (STRAIN L'SII/CHIMPANYET ISOLATE	3	18	1				1	-	
POPOL IPRIVA	TANA POLYNGRASE	INCATITUS IN VIRUS AND VER AIR AND AND AND				3					-
ī	NA POL YPERASE	TOPATITION VINITED AND VINITED					:				
POPOL HERVE	VA POLYMERASE	THE WORLD BE VIEW OF THE WIND WATER THE PROPERTY OF THE PROPER	80.08	10.03	145.468	761.17		:	:		!
1	AA BOM VALED ASS	THE VIEW OF THE ADM STRAIN FIRE IPPINOPLOWING	413.439	417.463						Ì	İ
٠.		THE ATTENDED THE ADMINISTRATION OF THE ADMIN	20.00	110.417	761.778				Ì	Ì	
	A FULT MEDIASE	HEPATITIS B VINUS (SUBLYPE ADW)	83.68	105.412	440.456	-				Ì	
	DNA FOLYMEJASE	IEPATITIS & VIRUS (SUBTYPE AYW)	26.02	2	614.417	750.76.7					-
יייייייייייייייייייייייייייייייייייייי	AA POLYMEKASE	HEPATITIS & VIRTIS (SUBTYPE ADYW)	28.02	100.436						į	
	NA POLYMERASE	HENDES SEATLEX VIRUS (TYPE) STRAIN 11	703.613	177.007	1000	1					
٠,	HA POLYKŒRASE	IGAPES SUCHEX VIRUS (TYPE ITSTRAIN ANGELOTTI)	1			7					
_	DNA POLYKERASE	ICENTES SINOLEX VIAUS (TYPE 1/ STRAIN ROS)		-1							
	DNA POLYMERASE	HERVES SIMPLEX VIAUS IT VPE 17 STRAIN (CIA)			060	.					İ
	4A POLYMERASE	HERPES SINITLEX VIRUS HAPE 37 STRAIN 1861									
	IA POLYMERASE	SERVES SIMPLEX VIRGIS PAPER A CTRAMA COLORS		- 1	1078.1075					:	• :
1	IA POLYMERASE	FOURT JORDE CYPET CASE AND AREST	27.0.75		/83-83/					İ	i
1	DHA POLYMERASE		74.74	2	\$ 413	118.00	878.898				
	IA POLYNEZASE		20	=	_				<u> </u>		İ
PDPOL MCMYS DN	IA POLYMERASE	MUTUNE CYTOMEGALOVIRUS ISTRAIN SAUTHI			100	اءِ اءِ	955.973				
	THA POLYRIERASE	Ī			_						
POPOL VARY DA				6,60						İ	
PDPOL VZVD DN											
PDPOL WHY! DHA	POLYMERASE				90.4	713-740	157.781	1006-1324			
POPOL WILVE DHA	POLYMERASE									<u>-</u>	
_	POLYMERASE	WOODCHIEFATITIC VIBILE 9	2/7-100								
			7								
		WOODCHUCK IEPAIITIS VIRIIS 6		25-57						<u>-</u>	
	MENASE	IEPATITIS & VIRUS (SUBTYPE AYW)									
_	DUTPASE	HUMAN CYTONEGALOVIAUS (STRAIN AD169)			100						
Ī	DUTPASE	EQUINE HEAPESVIRUS TYPE 4 (STRAIN 1942)	1	İ							
		EQUINE JEAPES VINUS 1 YTE 1 (STRAIN ANAP)	1								
ī		KTALUND IEAVESVIRUS I								i	
POUT HSVSA DU		PERPESVIAUS SAIMINI (STRAIN 11)		101.0			-				
- 1		HYJUSE ADENOVIALIS IYPE I	10.4			j					
		IN MAKN ADEMOVIRIIS IYPE 7			i		İ				
PEIA ADEM	EARLY EIA 21 KD PROTEIN	IR PLAN ADENOVIRIUS TYPE 4	04.120		-				-		
- 1		HUMAN ADEMOVIAUS TYPE 7	Ē		-			Ī		i	-
7		SPACKY ADENOVIRUS TYPE 7	3118	211.314			Ī	Ť			
FEIML AUETZ	FIB PROTEIN, LANGE T.AMTIGEN	INMAN ADENOVIRUS TYPE 12	191.663							İ	-
						1		1		1	7

FILENAME	PACITION	VIAU3	AREAL	ARCAI	AREAD	ARCAIT	AREAS	AREAG	AREA 3	AREA	ARCAS
PEIBL ADECT	EIB PROTEIN, LARGE T.ANTIGEN	CANTHE ADENOVIRUS 11PE 2	Ī	ī	ì	ī	Ī			•	
PEIBL ADEM	EARLY EIB 44 KD PROTEIN	TUPAIA ADEMOVIALIS	13:101		İ					İ	
PEIBS ADECS	EID PROTEIN, SMALL T.ANTIGEN	CANINE ADENOVIRUS TYPE 1	\$5.77			-					
PEINS ADEMI	EIB PROTEIN, SMALL T.ANTIGEN	MONSE ADEMOVINUS I YPE I	111-131		į						ļ -
PESIO ADEOS		INPICAN ADEMOVIBUS TYPE 1	-7-	3							
		INPIAN ADENOVIRUS TYPE 5	===	\$							
	EARLY ESB 10 4 KG PROTEIN PRECURSOR	INTALAN ADENOVIALIT TYPE ?			1					-	
Z		ILIMAN ADENOVIRUS 177E 2		j					1	į	!
PEJII ADEO		INMAN ADENOVIRUS 1 YFE 3									
PEDIT ADEOS	PROTEIN	HUNAM ADEMOVIALIS TYPE S	9702	İ	-						
VEDI ADER		INMAN ADENDVIRUS TYPE 7	16.62			_					
PEN ADER	EARLY ES 145 KD PROTEIN	INMAN ADENOVIRIIS TYPE S	2		:						
PENS ADEN		INPARA ADENOVIEUS 17PE)	22.23		-						l I
PEJIS ADEN	CURSOR	IRMAN ADENOVIRIIS TYPE ?	11.11								!
PEJIS ADEOL		ILIMAN ADENOVIRUS TYPE)	103-135	İ		!				!	!
		HALAN ADEMOVINIS TYPE 1	166.167		!	-			!		! ;
		HUMAN ADEMOVIRHS TYPE ?	191 91	-							! ::
		CAMINE ADEMOVIRUS TYPE I (STRAIN GLAXU)	135.177	-							
1_		MOUSE ADENOVIRUS TYPE I	105.127		İ	1					
	PROBABLE EARLY E4 11 KD PROTEDY	INDIAN ADENOVITUS 1 YPE 1	36.33	İ		Ī				-	
PEGII ADEBI	PROBABLE EASLY ET 11 KD PROTERY	INMAN ADENOVIRUS TYPE 3	36.33			-		1		i	!
PEAT ADEN	PROBABLE EARLY EASINED PROTEIN	MOUSE ADEMOVIRUS TYPE I	9:19		ĺ	-	-				i
PEAN ADER	EARLY EA 34 KD PROTEIN	INMAN ADEMOVIAUS TYPE 3	80.08	İ		Ī		Ì			!
FEAD ENV	EAKLY ANTIGEN PROTEIN D	EPSTEEN-BARR VIRUS (SIRAIN B93.0)	263.286			-				İ	!
PEAR EBV	EARLY ANTIGEN PROTEIN R	ENSTEEN BARE VIRUS (STRAIN BOS B)	10.104					-	1		-
PERMY ENV	EBNA.1 MUCLEAR PROTEIN	ENSTEEN BARK VIRUS (STRAIN BRY 6)	136.161		Ī	İ		İ			
PEBNI EBV	EBNA. I MICLEAR PROTEIN	EPSTEIN-BARA VIRUS ISTRAIN BOS 61	Ī	19.7	-	F			1		!
PETTI VANV	EARLY TRANSCRIPTION FACTOR TO RD SUBLIMIT	VALUOLA VIRUS	Ť			Ì		-			
PENI IRSPV	ENV POLYPROTEDY PRECURSOR	FATEND SPLEEN FOCUS FORKING VIREIS	30.00			-					!
PENN FREEV	ENV POLYPROTEDI PRECINSOR	FAIENT SPLEEN FOCUS FORMING VIRIES	100.403					İ			:
PENV AVID	ENV POL YPROTEDN	AVIAN RETROVIBUS RPL 10	206-225		İ	-					
PENY AVISU	COAT PROTEDY CP17	AVIAN SARCOMA VIRUS (STRAIN URJ)	Ī	Ī	1	į				İ	-
PERV BAEVIA	ENV POLYTROTEIN	BABOON ENDOCEMOUS VIRUS (STRAIN NIT)	ī	203-234	7	İ					!
PENV BIVE	ENV FOL YPROTEIN PRECIRSOR	BOVINE DIDAMMODE! KIENCY VIRUS (150LATE 104)	Γ		414.450	3 × × ×		İ		1	!
PENV BIVZI	ENV POLYPROTEIN PRECURSOR	BOYING DIGHTHODE FICIENCY VIRUS (ISOLATE 127)	П	:	-	1	316.575			İ	
PENV BLVAS	ENV POLYTROTEIN	BOVON LEUKEMAN VIRUS (AND PUCAN ISOLATE FLK)	301-137								
PDV BLVAU	ENV POLYTROTEEN	BOVINE LEUKEADA VIRUS (AUSTRALIAN ISOLATE)	301.137								
100	EAV TO THE OFFICE	BOVING LEGISLAND VINOS (ANEMORA) SOCIALE VINI)			Ì	İ		Ì			
100	EAC IN VEGETER	MOONE LEGICAL VIEW (SELECTION COLATE LEGIC)						-			
PENY BLVI	ENV POLYPROTEDI	BOVDE LEURENIA VIRUS (IAPANESE ISOLATE BI V. 1)		İ							
May May	DAY FOLYPROTEIN PRECURSOR	EL INE PROGENOUS VIRUS ECE:	Ť	200	10.441	Ī		Ī			-
PEN TIVE	ENV POLYPROTEEN PRECURSOR	PETINE EMDOCEMNIS VIRUS F.CE I	Ī	!	10.00						1
PEN TING	ENV POLYTHOTEEN PRECURSOR	ELINE LEUKENDA PRINTRIS (CLONE CFE 4)	31.55	ī	İ					•	:
PENV FLYGE	ENV POLYPROTEDY PRECURSOR	ELINE LEUKEMIA VIRIS (STRAIN AGLASCOW. 1)	6.19		AJ1 A76	!				:	•
PDV PLVIB	ENV POLYPROTEIN PRECIPISOR	FELINE LEUREMIA VIRIIS (STRATH LANGBOA RI)	Ī			!		-		:	:
PEN PLYSA	ENY POLYPROTEIN PRECURSOR	TELINE LEUKEMIA VIRUS (STRAIN SARXIA)		62.623	:						į
PER FOARY	ENY POLYPROTEIN	RIMAN SPUMARE IROVINUS (FOANIY VIRUS)		35.233	2 8	20.00	10.71	10 19	150 176	811.0110	i
PEN SYGA	ENV POLYPROTEIN PRECURSOR	PELINE SARCOMA VIAIIS (SIRAIN GARDNER.ARNSTEIN)	Ī	13.646						! :	
PEN ISVO	ENV POLYPROTEIN PRECITESOR	EI INE SARCONA VIRIS (SIRAIN GA)		177.00						i	! :
PEW FSVSM	ENV POLYTROIEM PRECINSOR	FEI THE SARCONIA VIRUS (STRAIN SM)	420.031	VOE 629							!
PEN PSVST	ENV POL YPROTEDY PRECITESON	ELINE SARCOMA VIRUS (STRAIN SNITTER THEIR PL)	467.488			!				<u>.</u>	•
PDV GALV	ENV POLYPROTED PRECURSOR	GBBON APE LEUKEMIA VIRUS	219.540								: :
PENV HVIBI	CONTROL MANAGEMENT AND E STATE OF THE STA	25.0	-	- :			i			:	
- 1	CONTROL OF STREET	THE PARTY OF THE PARTY STATE TO THE TOTAL THE PARTY STATE TO THE PARTY STATE TO THE PARTY STATE TO THE TOTAL THE PARTY STATE TO THE PARTY STATE TO THE PARTY STATE TO	500		-	j		1			
PENY HVIEW	COLOR PRECIDENCE	TOWARD WALLENGER CONTRACTOR TOWARD TOWARD SOCIETY	2 3	Ī	-	Ī			Ī		
	With the Chairm	MINISTER INTERPRETATION OF THE STATE OF THE	100 223	1	1			1			

PCGLME	PIICTLIP										
FILLHAME	PROTEIN	Citation Betrieffen (1)									
	CP100 PRI CLESOR		LAHA	12.5	AIR'S J						
PENV IVIEL	GP160 PRECURSOR	THE PART CHAINS IN FIG.	*****		_			-		- 111.	• Y EEY
	CP160 PRECURSOR		(3)-(1)								
	GPI46 PRECIPEOR	CENCY VINES LYPE	691.530			:	: : :	:		:	
	GP160 PRECIETOR	ENCY VIRUS 1YPE 1	478.530	-	:	1					1
1	GP160 PRECIENCE	ENCY VIPLIS TYPE	110.53	-	!						
1	Color Per Cim Con	VINUS TYPE I (INC'SF ISOLATE)	28.5	İ		!			!		
1.	GP 140 PRECURSON	L NCV VIRUS 1VE		100	14.5.74	•	:			- 1	
	Coldobatriment	TIONING THE PROPERTY OF A VINE 15 TAIL	20.23	:							
	GP140 PRECURSOR	HILMAN INDICHOLY VIRUS IYPE I (AIT A ISOLATE)	115-92	İ	!				1	:	!
	CPISOPEFINGE	HUMAN HOUSENCIENCY VIRUS TYPE I INT. W YORK S INDLATE	13.30					1			
	CP 166 PRICINGS	HUMAN HOMINODEFICHENCY VIRUS INPE I (NI)K ISOLATE)	65.50	!			-			- 1	i
1	100 to 10	TIMAN INPHIMATE FICE NO Y VINUS I YEE ! (DYI ISOLATE)	23.180	:	1		İ	İ	:	į	
I.	Calladia	HUMAN INDIGINORIE ICH NCY VIRUS 17PE I (PVZZ 18X A 1E)	1000	:-	:	i	:	!			: :
-1	COLON PARCUASOR	MUMAN INVANIOUS FICH NOT VIELT TYPE - 18 ALL TO LESS T		-	;						
- 1	GP 160 PRECURSOR	CANANA NAME OF PARTY	3			•		!	!		: :
	GP 160 PAE CLASOR	HOBANNIAN AND AND AND AND AND AND AND AND AND A	10.51	338.74	!				i	-	
ŀ	CP160 PRECURSOR	INDIAN INDIAN INCIDENCE IN (NO.) ISOLATE)	38.5			-			-		į
PDV HVIE	Chiebaterin ton	CONTRACTOR OF THE PARTY VIRGIS TYPE I (ZUCDC-ZIA I SOLATE)	13:13	410.427	401.41	1				-	
1	Cold Mit Colon	MANAGE MANAGER TOTENCY VIRUS TYPE I (ZAIRE) ISOLATE)		135.191	1	İ					
ı	Carlo and Carlo	PILMAN INMITMODEFICIENCY VIRUS TYPE I (ZAIME & ISOLATE)	10, 107			-				_	i
١.	CONTRACTOR SOR				-	1				į	:
1	CALLES THE COM SOM	INTRIAN BOADWODE ICIENCY VIRIES TYPE 177 LIBE 112131 1624 5 TES				••				İ	
- (CATEGORISOR	HUMAN INDAUNODEFICIENCY VIBILE TYPE 1 AND ARE BELLE	-		200					İ	
_	GP160 PAJ CITASOR	MUMAN BORNOOFIICIENCY VIBILE TORE 1 1201 125 DECT		730 735	781.804				İ	İ	Ī
	GP100 PRECURSOR	BRAN MARRIED CONTROL VINE CONTROL CONT	2						Ì	Ī	
L	GP 146 PRECURSOR	HEREAL INCHES SECTION OF THE PROPERTY OF THE P	3.16	741.766	73.75	-	İ				
	CP 160 PRECURSOR	INTEREST BANKS CONTROL VINUS 17FE 2 (150LATE D201.7)	9-28			-				į	
ı	CP 100 PA ECURSOR	TOTAL BOLD CHANGE TO THE STREET (ISOLATE GILANA.1)	741-766	777.705				1	Ī		
L	GP 160 PRECURSOR	THE STATE OF THE STATE S	141.767	171.80		1					
PENY HYZS	CP 160 PAECUASOR	INTERIOR DESCRIPTION OF THE STATE STATE ROOT	136.776		Ī	-	Ī	Ì	i	İ	
L	CP140 PAECURSOR	MONTH PROMOMENT (IEM.) VIRUS TYPE 1 (150LATE SBLISY)	343.748	178.804	I	Ī	Ī	-			
PENV ISAV	ENV POLYPROTEDY PRECINGOR	SIEGE STREET	745.730		İ		Ì	İ		<u> </u>	
PEN MOT	ENV POLYPROTEIN PRECINGOS	STEEL FULL FOR AUTHORIA TOSIS VIRUS	_	199.325	176.301	10.00	1	İ	-	-	
PEN MOTE	ENV POLYPROTEIN PRECIMSOR	MAIN CELL FOCUS FORMING MAINING LEUKEMIA VIRUS	_		T	T	Ì	Ì	1		
PEN MENAV	ENV POLYPROTEIN PRECINGO	PERM CELL FUCUS PURMING MURINE LEUKENIA VIRUS (ISOLATE CI				İ	İ	Ì	-		
PENV MEVCB	ENV KOL VYBOTEN PRECIE	AK WORDNE LEUKEMIA VIRUS	630.631		i	İ					
	FAV POLYPROTEIN SECOND CO.	CAS-BR E MUNDE LEUXEMIA VIRIIS	623.646			İ	j	i	-		
PENV ME VIET	ENV POLYPROTEIN PRECISED	MIENO MURINE LEUNEMIA VIRUS (ISOLATE 57)	639.640	İ	-	İ		1			
PENV MA VED	ENV POLYPROTER PRICES	Γ	619 660		Ī	1	Ì		-		
PEN MANO	ENV POLYPROTEIN PRECINSOR		039.019			İ	-	-	i		
PENV ME VICE	ENV POLYPROTEEN		676-647			İ	-	İ	i	<u> </u>	
PENV MENMO	ENV POLYPHOTEIN PRECURSOR	MOLOURY SERVER CENTERS VIRUS	107.111	İ	<u> </u>	İ		1		<u>:</u>	
	ENV POLYPROTEDI PRECURSOR		629-650		İ	İ	İ	İ	İ		ĺ
	ENV POLYTHOTEEN PRECUNSOR		634-645			İ	İ	İ	İ	l	
PENV MATIVE	ENV POLYPROTEIN	KAPLAN	57-645			İ	Ì	T		-	1
╗	ENV POLYPROTEIN	MOUSE MANDARY TURIOR VIRILS (CTR ATA CIR.)	3				-		İ	1	ĺ
7	ENV POLYPROTEIN	SOUGH MASON PFIZER VIRUS	3					-	İ	1	1
╗	ENV POLYPROTE DI	FBI MURDING OSTEOSARCONIA VIRIIS	202					İ	İ	-	
╗	ENV POLYPROTEIN PRECURSOR	OVINE LEWITYIRUS (STRAIN SACOATOVO)	10.01	-			-	 		-	İ
TENV MACV	ENV POLYPROTEIN PRECURSOR			j							<u>.</u>
7	ENV POLYTROTEON		Т					<u> </u>		1	-
ŀ	ENV POLYPROTEIN		į	ī	_	1			-	!	-
١.	ENV POLYPROJEIN			710.737	_	924.951	957.978		<u> </u>	İ	1
- 1	JA 160 PM ECURSON		1		707.724		971.048 05	934.075	<u>:</u> 	<u>:</u>	i
TANK SING	AT IND PRECINISOR	TEMCY VIRUS (AGAI) ISOLATE)		1	İ				<u>-</u>	1	!
	OF IND PRECURSOR	IENCY VIRUS (ISOLATE AGM/CLONE CRI. II		1	-					<u> </u>	1
PENV SIVER	GPIM PRECINCIA	Т	257	İ	1	1					
1	Dried Fatt Un 11/18	II ME VIRIS LISON ARE GALL	100	İ	+	1	1				Ī
		7			1	1	1	1			Γ
]

PCGFNF	PERCEUSIV	All Virgie I've Bacterianhoger!									
H	PROTECH		ARIAI	41.4	V TV	Aller	ARIAS	ANCA	AHIA	AHEA I	A LINE
ı	GP160 PRECURSOR	SIMILAN INDIVIDUE I CIENCY VIRUS (MINISOLATE)	764-793				1		_	_	į
	CP100 PRECURSOR	SIMIAN INDICIONODE FICIENCY VIRUS (KOW ISOLATE)	139-154		\$01 833						
ı	GP:60 PRECURSOR	SIMIAN INDAMODE DICIENCY VIRUS (K 18 ISOLATE)	130-154	164.101	101.01				!	! 	i
t	GP160 PRECLIASOR	SPAIAN INCHANCIPETICIENCY VIRUS (F216/SMITE ISOLATE)	369.789	20.00			- 	!	ļ !	:	<u> </u>
1	CP 160 PRECURSOR .	SIMIAN IMALINODE ICIENCY VIRIS (PRIMCI) ISOLATE)	131:381	10.01	<u>-</u>	!	İ	; !			
PEHV SMSAV	PIST PROTEIN	SINIIAN SARCONA VIRUS	42.63				İ		i 1	-]
100	SAV POLYPROTEIN	SECTION SECTIO	11:11	: :	1	1			İ	-	-
PERRA AVIER	FREA ONCOCOS PROTITO	AVIAN ERYTIFOBLASTOSIS VIRIJS ISTRAIN ESCI	337.346		İ			Ī			İ
PETTI FOWE	FARLY TRANSCRIPTION FACTOR	FOWLPOX VINIS (STRAIN PP.1)	1	29:66		Ī					İ
1 1 1 1 1 1		CHOSE CIBBOALS VIBILS (CORATA NACYA)			-	1	:	-	1		;
1		STORE CHANGE AND		-	1	-		:	:		
-7		VALLINIA VIRUS (SIRAIN CUTLMINALIA)				7		!	1		
		VACCINIA VIRUS (STRAIN WR)	1.4		=						
PETF1 VACCC	EARLY TRANSCRIPTION FACTOR 12 KD SUBUNIT	VACCINIA VIRUS (STRAIN CUPEMIACII N)	50 73	101-113	103.107	_	110-112				
		VACCINIA VIRUS (STRAIN WA)	12.5								
T		VARIOLA VIRIUS	6.5	101.111	103.117	101	(11.11)				
L	AT ICAL DIS STORMICS RASE	ILERPES CIMPLEX VIRUS (TYPE 1 / CIRAIN 12)	997,199		Ī	ī			-	į	i
1	THE STATE OF THE PARTY OF THE P		,			1	-		: :	:	
	ALMALINE CAUMALEASE	ICHO CO SIMPLEA VINCO (1 11 C. 4)		!	!	. !			-		!
PEXON IDVE	ALKALINE EXUMACI EASE	EQUINE IGNIESVIRIS TYPE I (STAAIN ABAP)	1	İ	1	-	į				
PEXON PRIVIL	ALKALINE EXONUCLEASE	PSEUDORABLES VIRIIS (STRAIN MIA. 1)	2			-					
	AI KALINE EXOMUCLEASE	VARICELLA-YOSTER VIREIX CERAIN DERIAL	7	74.74		. ;					
	er experenten	HUDGAN ADEMOVIRUS IYFI. 40	11:13								
PFB3 ADEAI	41 4 KD FIBER MOTEIN	INDAAN ABENOVIRUS 1 YPE 41	=					<u> </u>		İ	
PFIBP ADEO	FIBER PROTEIN	INDIAN ADENOVIRUS 1 YPT. 1			İ						1
PFIRP ADESS	FIBER PROTEIN	INMAN ADENOVIRUS 17PL S	40.00	-		ŀ	-	-	İ		1
	N. 11 C. 64 E. 12	BOVING ADENDVIBUG TYPE 1 ALACTADEMOVIE 10 DOCU		176.00	į			1		İ	
		The state of the s			-	Ī		:	:	:	:
- 1	PIBER PROJEIN	CANINE ADENOVINOS I VIZ. I ISTRAIN IN A 10)				:	:				
- 1	SIBLA PROTEIN	MOUSE ADEMOVIALIS I YEE	3	27.72	=	148.576	19-5-17				
PGAO AVEVI		AVIAN EMDOGENOLIS VIRUS FV.I	53.38	,					!		
		AVIAN ENDOCENDUS ROUS. ASSOCIATED VIRUS 0	1.23					- !	i		
		AVIAN MYELOCYTONIA 10515 VIRUS MC19	5.75		!			-	1		
		AVIAN MYELOCY TOMATOSIS VIRUS IIIII	2.3		!	1			1		
		AVIAN SARCONIA VIRUS (SI RAIN URZ)	27.25		<u> </u> 	i	Ī				
		AVIAN SARCONIA VIRUS (SIRAIN Y7)	27.78		!	Ì					-
		BABOON ENDOCEMOUS VIRUS (STRAIN N.)	107.433	i	-	Ī				Ī	į
	GACIPOLYPROTEIN	BOVINE LEUKEANA VIRUS (AUSTRALIAN ISOLATE)	11.31		-	İ			Ī	Ì	
		BOVINE LEUKENIJA VIRUS (IAPANESE ISOLATE BLV.)	11.316		1	Ī	Ī	Ī	İ		
		CAPRING ARTIGUIS ENCEPHALITIS VIRUS (STRAIN CORK)	103.110	Ì	-	İ				İ	İ
		FUINAMI SARCOMA VIRUS	11.30			1				Ī	
	GAG POLYPROTEIN	IRAIAN I CEIL LEIREMIA VIRIIS TYPE I ISTRAIN ATRI	17.6			İ		Ī		Ì	
	GAG POLYPROTEIN	HINDAN T.CELE LEINEANA VIRIUS TYPE LICARIBREAN ICHI ATEL			İ	İ	Ī	Ī		Ī	
T	CAG POL VPROTEIN	INMAN I CELL LEINENIA VIRIIS TYPE LISTA ATE MT. 31	11.00		İ	Ì		Ī			
Т	GAG POLYPROJEDN	HIDMAN BAGINODE FICTENCY VIBIG TYPE FLARVZYST ISOLATED	10.15			Ì	Ī	Ì			
Т	CAG POLYPROTEIN	INDIANA BOAT MODE FICIENCY VARIES I YPE I (RITIO ISO) A TEL			-	j	Ī			Ī	
1	GACI POC YPROTEIN	HANAN BOATHODESICIEMEY VIRGIT TYPE I CHILL INCH ATEL			1	İ	Ĭ	Ī		-	
MINI DYDA	GAG POL YPROTEDA	HANAN MOGNICIENCY VIRING 1YPE 1 (BELL ISOLATE)		-	i				-		
1	GAG POLYPROTEDN	INDIAN BORNOOFFICENCY VIRGE TYPE LICINIAN ALES		-		!	1	İ		. ::	!
1	CAN BOX YPROTEDA	INDIAN BARGAONE FICTORY VIRGO SAPE LICE FICAL A FILL				:		:		:	i :
1	2000	THE PARTY OF THE P				į				:::::::::::::::::::::::::::::::::::::::	i
T	THE CASE OF THE CA		63.9	Ì	-	j					
ī	CALL TROUBLE	CIERCI VIRUS LYPE			-					Ī	
	OVO TOTAL PROPERTY	CIEMO VINCO				1					į
S 100		THINAS DENIMODER CIEM, Y VIRIS 177E I (MAL ISOLATE)	267-2115	:	:	į		1	!	-	
		PRINTER INCHIBATION IN THE STATE OF THE STAT			: : 1	-	1		::	-	!
	STORY OF THE PROPERTY OF THE P	IN MAN PROPERTY OF THE TARK TOWN TO THE TARK TO THE TA				İ				1	
	12 10 10 10 10 10 10 10 10 10 10 10 10 10	INDIAN PARAMORE CIENCY VISITE TONE LOVE LOVE			-		Ì				
	OAD DO VENDITON	INTERNATIONAL PROPERTY VIEWS 1175 (UTILISALATE)		Ì		Ì				Ì	
CAO IIVIII	TO TO THE PARTY OF	HORACA BOARDON FILERON VIROS 1175 1 (F42130CA1E)		1			Ì			Ì	·
יאוויייי	OAUTHUR.	VINUS LIVE			1	1	1	1	1		7

	PUCTULIF	All Viroses (No Betteriophages)		Γ		-	ſ			Ī	
POAD HIVIUM	GAO POLYPROTEIN	MINAN BACTHONE FICIENCY VIBILE TYPE LICETALLI CALLELLE	TVIEN	AREAL	AREAL O	SEEA	SELAS	48544	4164	ABEAT	ARCAS
POAD IIVIW	DAG FOLYPROTEIN	INDIAN BOOMBOOFFICIENTY VIRIA TYPE I JUNIO 1504 AVE.			İ	1				_	
POAG IIVIZI	GAG POLYPROTEIN	INCARA IMMUNODEFICIEM: V VIRUS TYPE 1727/CDC.714 ICDI ATTI			Ì	1					
POAD IPMA	RETROVIRUS-RELATED GAG FOL YI'ROLEIN	MOUSE INTRACISTERNAL A.PARTICLE	100		1	-			:		
	GAO POLYPROICIN ,	MOUSE MANIMARY TURITH VINUS (STRAIN TRE)			i	: !	;	:		_	
POAD MINTVC	GAUPOLYPROIEIN	MOUSE MARINIARY MINIOR VIRUS (STRAIN COM)	10.7		1	İ				-	-
	GAG POLYPROIEN #	MOUSE MARMARY 1 MIOR VIRIIS (STRAIN GR)			İ						
	GAG FOLYPROTEIN I	ROUS SARCOMA VIRUS (STRAIN PRAGUE C)	15:15	Ī	İ	Ī					1
CAO SCMA	MAKIN COAT PROTEIN	SACCHARDMYCES CEREVISIAE VIRUS I.A	611.645		-	Ī	Ī			-	::
- 1	OAG POLYTHOTEIN	SIMIAN FOAMY VINIS (1 VIII)	16.181	,							
	OAO POLYPROTEIN	SIMIAN BOANT VIRUS (1 VIT. 1/ SIRAIN (K.)	13.101	•		_	:	:			•
_1	GAD POLYPROJERN	SIMIAN INDAMPODEFICIENCY VIRUS (AGAILSS ISCILATE)			-	-					
	DAG POLYPROTEIN	SIMIAN INDAMPOCEFICIENCY VIRUS (AGM) ISOLATE)	117.10		-	1					į
	GAG POLYPROTEIN	SINIIAN IMPRUNOLIEFICIENCY VIRUS (TYO.) ISON ATEL	18.213	ĺ	-	-					
	DAD POLYPROSEIN	CHINDANZEE IMMICHOLFICIENCY VIRIS (SIVICIFAL)	15	•	:	y					
	GAO POLYMOTEIN	SIMIAN INTERIOR INTO VIETE AND COLOR			•	٠.					
ì	GAG FOLYPROJEIN	CIMIAN ININ DIVINE BOTHENEY VIBIGE CLARGES IN SECTION		:		. !					
	GAU POLYPROTEIN	SOURCE MONEY BETTOVIETE CAMEVILL		-	1	·					
PGLRY VACCC	POSSIBLE CALITABEDONIN	THE PROPERTY OF THE PROPERTY O	1		!	-					
PGI RX VARV	POSSUAL E CALLTAREDONIN	VARIOUS VIRIOUS CONTRACTOR OF THE CONTRACTOR OF			: !	Ī					į
PGRAN OVAS	GRANGE IN	ACBOTIC CITY OF ANIMA COLOR CIBERS		:	:	. !	:				!
PORAN OVTN	CHANGE	CHICAGO STATE OF THE PARTY CHICAGO STATE OF THE	97.10								
1.	GROWTHFACTOR	VACCINA VIBILA SETANDA CONCENTRATION OF THE PARTY OF THE		1	1						
٠,	Canada Arthua	CATANIA VINOS (SIRAIR COLL MINOEN)	2		-						-
	Canada	VACCINIA VINUS (STRAIN WA)	2							İ	
PIGE CRV	PROBABIL BIGG ICA III	WAUCH VIRUS	2								
1		CASICIN-BAAR VIACAS (SIRAIR) IVAS B	Ī		431-464	-					
л.	PROPERTY FIRST CASE	HUMAN L'Y IOMEGAL D'Y HUS (S'HAIN ADIGS)	ī	339.360	24 652	-		ĺ		Ī	i
<u></u>	PROBABI S DEL L'ACR	TRACE OF SUPERIOR PROPERTY STRAIN 17)	T	2							İ
1.	PROBABLE FOR PLACE	COUNTY INDICE A VICTOR (177 P. 17 STRAIN HOT)	П	ī							
1	PROBABILE ICACE	STORE MANY SALES THE TOTAL ABOVE	207		396-413					Ī	
1	PROBABLE NOT IN A CO	UABICEL A POSTER UBILG ASTA AN INC. C.	Ī	7	63.63						
1	JEMACOLITICADA META AMBODA CE	CANNELLA-2031ER VIRIS (STRAIN DOMAS)	اء	2	-	981-19				Ī	
PIEMA CVBF	AND CONTRACTOR AND PRESIDENCE		1	2 2							
PIENA CVILY	GEMACIALITIMIN FETTERSE PRECIESCOS				-	·					
PIEMA CYBH	INCHAOCALLI DATA ESTERA SE PRECURSOR	BOVING CORONAVIRUS (STRAIN METRICS)		Ī							
PILEMA CVBQ	TEMACOL UTININ ESTERASE PRECURSOR	T			-	Ī					
PIEMA CYHOC	IEMA OCH LITININ ESTERA SE PRECURSOR	1	107101	Ī	1	Ì					
~	IEMAGOL UTIMIN-ESTERASE PRECURSOR	Ī	401-433	Ī	İ	Ì	Ī	Ī			
	NEMAGOL UTIMIN ESTERASE PRECURSOR	Ī	401-418		İ	İ	Ì		Ì		Ī
_	HEMADOLUTIMIN PRECURSOR		Ī	600	-	Ì			Ī	Ì	1
MEM MEAN	IEMAOGI UTIMIN PRECURSOR	Ī	7	100	-	İ				Ì	
	PEMACOLUL DATA PRECUESOR	INT. UENZA A VIRUS (SIRAIN ABUDGERIGARMOKKAIDOVIAT)	110-111							Ī	Ī
	TEMANCA UI UNIN PRECITASUA			П							
	MANAGE OF THE PRESENT	DISTURBATA A VINCE (STRAIN ACTICK ENGERMANY/NUS)		111.147	16.31						
_	KLACK ITEMS DECIMED	٦	303-319						Ī	Ì	
PENA IACTOR	SELECTION PRECISES	INTEREST A VINCE (STRAIN ACTUCKENTENNEYLVANIALITY)	103.319							Ī	Ī
-	IEMAGOR IT DAN PRECINSOR		\neg							Ī	
+=	GMACK UTININ PRECISE OR		٦	<u> </u>							
PIEMA IADAS	COMACCA LITININ PRECITESOR	THE HENRY A VIBERS OF BATH AND LEAST BEST AND AND LEAST BEST BEST BEST BEST BEST BEST BEST BE	J								
-	BEALAGGE LITINGS PRECURSOR	1000	Ī	200							
-	EMAGGLUT DATA PRECUTSOR	ACCIDENCE CHOSEGARIOS	ī								
MEMA IADIII	EMAGGLUTININ PRECURSOR	ACALICA CINCA INCIDA		8	-						ĺ
	IEMAGGLUT PARTURSON		Ī			j					
₽	MENAGGLUT BYEN PRECURSOR				1						
PHEMA TADM	HEMACCH (17 INTIN PRECINSOR	INTILITIALA VIRIIS (STRAIN AGHICEANNE AINCONN	T								
		In the state of th		3	1	1	1	1	7		

PCGENE	PRICILIF	All Vireau (Ne Betterlenbaget)		П	\Box	П	П	п	П	\Box	
TILKAME	PROTEIN		AN	AKS.	AREAL IS	A8164_1	AREAS	OMEST.	GEV.	AREA!	AMEAS
PIEMA AADIIS	HEMADGLUTININ PRECURSOR	INTLIENZA A VIRUS ISTRAIN ADJUCKAIOKKAIDOGIMI)	11.41	215-233	_						
PIEMA MOIIS	HEMAOGLUTININ PRECIASOR	VIRUS (SIRAN	7	196.33							ĺ
PIEMA LADIT	BELLACOL LIT DATA PRECIDENT	A VIRUS (STRAIN	=	186.333	!!!!						1
PARTY AND	TELLANCE IN SAME PARTIES COM	VINITARIA	5	11:110	<u> </u>]		İ			İ
		5	5		-	İ			Ī	1	
5	TOWARD TO THE TOWARD TOWARD TO THE TOWARD TO THE TOWARD TO THE TOWARD TOWARD TO THE TOWARD TOWARD			-	1						
MENT MOO	TENAUCI INITIAL DESCRI				j	Ì					
PIEMA LAEM	HEMACOL UTININ	VIRUS ISTRAIN	9-	186.33							
	SEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN AENGLAND/11/11)	11.50	111.110							
1	HE MACCLUTION PRECINSOR	VIETS IS THE	210.246	115.33							
4 - 2 - 1	The Land of the Party and the	MAN STREET	111			Ī	Ī	Ī			
1				-	 	+					
PIEMA MOUZ		A VIRUS (SIRAIN			İ						
MEDIA MOUA	HEMAGGLUTIMIN PRECURSOR	A VINUS (STRAIN	318-336								
PIEMA IAHAL	HEMACOL UTINON PLECTASOR	INGLUENZA A VIRUS (STRAIN A/EQUINE/ALGIERS/1)	111111		<u> </u>					-	1
					 	Ī	Ī	1	İ		
3	PERMACULATION PRECURSOR	TIVE COMP			-	-	Ī				1
MENA INIC	IEMAGGLUTINEN PRECURSOR	A VIRUS	230 246	115.332			-				
HENA INHED	HEMAGGLUTININ PRECURSOR	VIRUS (STRAIN	230-346	115.111							!
HEM MOR	ISMAGGLUT DAY PRECURSOR	S GITTIN	230.346	115.331	i 	ŀ					
7	MENTACE INCAM BEECI BODE	PARTITION A VIBIL CONTANT ARCHITERANT AND EATION	114.165		-	1	-			Ì	
	TEMOCROTION FACTORSON	C (+		1		-					
TEM INE	HEMADOLUTINON PRECURSOR	INTLUENZA A VIRUS (STRAIN ACQUINERENTUCKYDAS)	30.00								
PIEMA MART	HEMADGLUTDATA PRECINSOR	INTLUENZA A VIRIIS (STRAIN AEQUINE/RENTUCKY/IAT)	236-252	10:12	İ				İ	ĺ	
PIEMA IAIR E	IN MACCLUTININ PRECUMSOR	INTLUENZA A VIBIUS (STRAIN ACCUMICA EXINGION/1/66)	110.746			-			:		1
C 217 V/12	INTERNACE INTERNACE PROPERTY OF THE PROPERTY O	N	246 016		-			1	-		1
	ILEMA COLUMN FRECUESOR				-	į	1	İ		-	-
PIEMA IMPO	PENADOLUTININ PRECURSOR	A VIRUS	218-22			-					
PIEMA MON	HENADGLUTDAN PRECURSOR	SILA	216-252	36.38		-					
PIERIA IAION	IGMACKELITINEN PRECIESOR	SIRA	115.112	1		İ				i	Ì
		1 2 2 2 2 2 2 2		1		ļ					
THE PARTY	INCAMAGE UTINING FACULTSON				-	-					
MAN WILL	HENACOLULININ PRECUESOR	INTEREST A VIEWS (STRAIN ACCOUNTABLANIANIA)					i	-	1		i
PIEMA MISA	HEMAGGLUTINEN PRECIESOR	INTLUENZA A VIRUS (STRAIN ARQUINE/SANTIAGOLIAS)	236.233	321-336							
PIEMA MISP	IEMAGGI UTININ PRECIMSOR	INFLUENZA A VIRUS (STRAIN AFQUINE/SAO PAULOVIMA)	230.346		_	•					
PIEMA MISW	HEMAGGI UTINDY PRECIMSOR	INTLUENZA A VIRUS (STRAIN AÆQUINE/SWITZERLAND/17/72)	330.346	113.132		~					
PHENA WITE	PEMAGGLUTING PRECURSOR	INTLUENZA A VIRUS (STRAIN ARQUINE/TENNESSEE/516)	36.332	11:11:						İ	İ
PIESTA IAITO	HISTORY PRINCIPLES	INFILITIZE A VIRUS ISTRAIN AFOUNDETOX YOUTH	116.35	11:11:1	<u>:</u>	Ì	I				
	STATE OF THE PARTY IN CO.	PARTICIPATE A COMPLETE AND A COMPLETE CONTRACTOR		1	-			-		1	
	HEALT COLUMN THE CORSON	Sections & Contractions of Contractions				İ			i		
WW WATER	IEMAGGE DI IMIN PAECURSUR	< 1			-	Ì				į	
PIEMA WAA	IEMAGOLUTINO PRECURSOR	A VIRUS ISTRAIN	10.72	19.716	-						
PIEMA LAMAB	IEMAGGLUTININ PRECURSOR	INTLUENZA A VIRIIS ISIRAIN AMALLARIMAS IRAKHAM363A?)	103-226	324.341							
PIEDA INMO	HEMAGGLUTININ PRECURSOR	VIAUS ISTRAIN	13.39	333-339		ĺ					
PIEM WE	HEMACCLUTININ PRECURSOR	VIRUS (SIRAIN	17.50	1	-	Ì					
	HEMAOGLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN AMEAONIIS/102/72)	17.50	31.11		İ					
PHEDAIA TAMBA	SEMANOR UTDAIN PRECURSOR	VINUS (SIRAN	1	100.00		İ					
Т	IGMAGGI UTDON PRECITISOR	DIFLUENZA A VINIIS ISTRAIN ANTINKISWEDENING	15:10	207.107	16.131	ĺ		Ī	İ	Ī	
ī	PEMACCI LITINDA PRECLIRSOR	VIRUS (STALIN	15.	133.310	<u> </u>	İ					
T	ISMANCE ITTONIN PRECIESOR	DOLLIENZA A VIRGIS (STRAIN APROT WILATERINE/170/16)	176.111			Ī					Ì
TO IN THE	HEALACT INTO PRECIENCE	VIEW		100	+	İ					
WIGHT AVENUE	SELLACES ITTO THE PRECISE CON	PART HENCE A VIBIL COM AND THE NATIONAL PROPERTY.			-	İ	Ī	Ī			
200					-	Ì		Ī			
TIENC MAET	ILPHACE UI IMIN PRECUESOR	TIVE CONTRACT	100								
PIEMA IASH	IEMAGGLUTEMEN PRECURSOR		234-150	121.336							
PIEMA INSTA	IEMAGGLUTIMIN PRECIMSOR	DITLUENZA A VIRUS (SIRAIN ASTARLING VICTORIA/SISATS)	330-346	113.332					i		
PIEMA WIKM	HEMAGGLUTININ PRECIMSOR	INTLIENZA A VIRUS (STRAIN A/TIPAEY MAINNESOTAMI) (10)	11.55	130.01		-				: 	! !
PIEMA IATRO	IGAIACCITITION PRECISSOR	INTLIENZA A VIBIIS (SIBAIN ANIBRE YONTANIONTINGA)	33.349	<u> </u>	•		!	i		:	;
PHENA MATER	JEMACCI LITIND PRECIESOR	INTERIOR A VIRIS ISIBAIN ANIMERADE CONTIL	116.744		:	Ì		!	!		:-
PIELLA TATEM	SERVENCE IN THIS PRECIESOR	INTEREST A VIRIS ISTRAIN ACTIONE YANTSCONSINCIAL	100	-	i	Ī		İ		İ	-
CO V	HEMACCI LITININ PRECINSOR	VIRUS (SIRA	25.53	_	100.00	Ì		Ī		1	!
MENA IAVII	HE MACCELLT IN PRECIESOR	VIRUS (STRAIN	19	131.160		Ī		İ		i	į
HELLY LYTHI	STATES OF THE WAY WE FOR MACON	INCHIENZA A VIBING SCHARK K. NII	13.50		-	İ					
	SOLUTION SECTI	INTERNAL A VIBILE SCIENCE AND AND AND AND AND AND AND AND AND AND				Ī		Ī			1
FIRMA IACLU	IL MAINI DI ININ PRINCIPAGE	- 1				1		1			
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PCCENE	PHICHLIST	AB Vir. co. 18. Basis and and an analysis and									
CILLRAME	PROITE	VIRUS									
PHEMA IAZUL	HEMAGGLUTININ PRECUTSOR	INTLUENZA A VIRUS (STRAIN A/SWINEAIONG RONGALDA)	4	7	ACEA.	DEES S	48.54	DAKAL	OREAL	AREA	ABEAS
PIEMA IAZIE	HEMAGGLUIMIN PRECURSOR	VIRUS		3 3	į	1	<u> </u>		j	_	
PIEMA IAZUK	HEMAGGLUTININ PRECURSOR	14			:		1	:			<u>.</u>
SENA PRAY	HENIAGGLITIMIN PRECURSOR	VINIS				-		İ			:
NGMA ZEE	IB MAGGLUTININ PRECIMSON	VIRIS			1						
MENA INBO	HEMAGGI U IMIN PRECIMSOR	VINIS (SI	-								
- 1	HEMAGGI LITININ PRECURSOR	INTI UENZA B VIRIJS (STRAIN BENGI ANDATZITI)	1				İ		-		
MEMA INDE	HEMAGOLUTINIA	LUENZA D VIRUS (ST	100.134		į	:	į	:			
THEMA INDE	HEMAGGLUTININ PRECINSOR	LINENZA B VIRLIS (STAA					-	İ	-	:	:
STATE OF STA	JEMAGG (17 ININ PRECINGOR	LINENZA B VIRUS (SIRA		102	-						
1	HEMACCI, UT BYIN	LIENZA B VIRIUS (SIRA	100.124		:	-	-				
O PARTIE	HEMACOLUTININ PRECINSOR	D VIRUS (S.	120.136	12		1					1
200	HENACH CHININ PRECURSOR	VIRUS	11:11	103.113		-					!
THE WARM	HENAGGLUTININ PRECURSOR	B VIRUS		100							
TICKY MOME		16				1					
THE PART		INTLUENZA B VIRUS (STRAIN BANAGASAKUIA)				-					
PIEMA PAIOR		18		-		-					
PIEMA NOSI		INGLUENZA & VIRUS (STRAIN BUSINGAPORE A) 3 AG				-					
MEMA INDS	HEMADOLUTININ PRECURSOR	DOLUENZA B VIRUS (STRAIN INSTRUCADOR FALL)				4					
MIEMA DABUS	IEMACOLUTININ PRECURSOR	1				j					
MEMA BODY	HEMACOLUTININ PRECURSOR	NAMES OF TAXABLE									
PHEMA DIBVE	HEMAGGLUTINGN PRECURSOR	KSTEA		2							ĺ
FIEWA MBY	HEMACGLUTIN	STRAIN									
MEMA INCCA	HEMAGGLUTININ PRECURSOR	MAN									
PIEMA DICEN	HEMAGGLUTIMM PRECURSOR	INTERNA C VIBIG GODANN FEMAL AND ADDA	997.000			-					
PHEMA INCOL	HEMADOLUTININ PRECURSOR		20.4%			-				Ī	İ
_	HEMAGOL UTININ	MA	200								
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	IEMAGGLUTININ	STRAIN								İ	
PIEMA INCHI	HEMADGLUTININ PRECURSOR									T	Ī
1	MEMAGOLITIPIEN		130							İ	
-	HEMAGGI UTININ PRECURSOR	;;		-					Ī	İ	
-	HEALA GOLL UT BATAN PILE CURSON		10-454			-				İ	
-	IEMACOLUTION PRECUASOR		200							İ	
=	PEMAGGLUTININ PRECURSOR	12									
PIEMA DICYA	HEMAGGLUTENIN PRECURSOR	K	200	Ì		İ					
PIEMA MURO!	IEMAGGLUTININ-NEUNAMINIDASE	MUND'S VIRUS (STRAIN SBL. I)	Ť	ì	7	7				i	
PIEMA MADMI	IEMAGGLUIDAN.NEUTAMINIDASE	ARMOS VIRUS (STRAIN MIYAMARA VACCINE)	Ī	i	7	2.34	11716				
MEMA MARKE	IEMAGGLUTIMM-NEURAMMIDASE	MANOS VIAUS (STRAIN AW)			200	ì	-				ĺ
91	IEMAGGLUT DANI-NELPAARMIDASE	MUNOS VINUS (STRAIN SBL.)	T	7	Ť		7				
TIEMA NOVA	IEMAOGLUI DIIN-NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIAJI)	T		Ī	Ì					
2	ILEMA UGLU I BYDY IVEL TA ANTONIO A SE	MEWCASTLE DISEASE VIRIS (STRAIN BEAUDETTE CAS)	91.6		İ	İ					
	TEMACOLUTINIA PEUTAMINITASE		93.110		İ	İ			Ì	İ	
NO STATE	KANAGA HENNING MANAGANIDASE		93.110	İ	İ	Ì		Ì	İ	j	
1.	EMACALUMIN-NEURAPHINDASE		91:110	Ì	Ī	İ	Ī	Ī	Ì	Ī	
	GENACO ITRON NEIR ALAMINASE		93.110	Ì	İ	Ť		Ī	İ	İ	ĺ
ic	BENACCI ITANA META ALAMIDA CO	(99)	93.110	İ	İ	Ì		Ī	Ì	İ	
-	IEAAACCI ITTIMAN NEIMAANINA CE	ME WCASHLE DISEASE VIRUS (STRAIN TEXAS G B /41)	9)-110		İ	İ	Ī	Ì	İ	İ	
1	IEMAGGLUI DAIN-METRANGUNASE				İ	T	Ī	Ī	Ī	İ	
	CEMACCI (FIGNIN NET) AMENDACE			111.114	116.101			İ	İ	İ	
	IEMAGGI UTININ NEURANINIDASE	INUS (STRAIM WASHINGTON/1957)			1	105.91			İ	<u> </u>	İ
=	EMAGGLUI MIN-NEURANIMDASE	INDIAN PARADE IF NYA I VIETE (19 VOCEMBA)	07.0	_	2	İ		İ	İ	İ	
	EMAGGLUI MIN. NEURANUMDASE	RUS CONTRACTOR OF THE PARTY OF	ī	ī	=					†	
	EMAGGLUTONIN NEURANDMIDASE	BUS (STRAIN MILLANDS)		ī	9						
PIEMA MIRA	EMAGOL UTININ NEURAMINIDASE	HUMAN PARAINTI UENZA J VIRUS (SIRAIN AUSI 2485474)	Т	7	9						
7	I EMACCI. UTININ METAANIMIDASE	RIIS (STRAIN TEXMANDI	T			j	Ì				
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THERANT	PROTEIN SELECTION OF THE ASSESSMENT OF THE PROPERTY OF THE PRO	VIRUS	ABA	AF.	Vulv.	AP. C.S.	AMEAS	AREAS	AREA	ARIA	6 1 (H)
NIE NIE	INCHARCA PRININ NEW ANIMINACE	THE PART OF THE PART OF THE STRAIN THE RAJORAL	=	2	2	7	1				
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PIGMA RINDIE	THE MEANING AND AND AND AND AND AND AND AND AND AND	Physhopped tiplic services and the services of	0.0	İ	j :						
PIGMA ROOM	IBAIACC ITTOWN MET AMINIDA CE	POTENSION CIPE STATE OF COLUMN	1	j	!	-	į	!	;		
PIEMA SENDS	PANAGGI CTIMIL NINE ANIMIDASE	SENDAL VIEWS AS BAIN 2 JUNE AND STAT		;		:				_	
PHICALA SENIX	THE MINISTER OF THE WASHINGTON										
PIEMA SENDI	III NIAGGLUTINIM NEURAAUMIDASI	SCHOOL VEHICLE AND LABOUR		į		•					
PIEMA SENDI	BALAGGE LITENIA WEUR ANGINEDA SE	SENDAL VIEW COMPANY						-		:	•
MEMA SDOZ	GRANGE STRING NEST ALINIST SE	THE PROPERTY OF THE PROPERTY O	737.742		1	1					
MISNA EVE	IS MACCO IN THIS DESIGNATION A CE	17 MINUTED TO THE PROPERTY OF	700								i
MIEMA CVE	RELATED TO THE PARTY OF THE PAR	The Court of the C	2	200	107	•					ļ
	TEMACKE LINE TELECONOMICALE	SIMILAR VIRUS (STRAIN W.)	7.28	101	179 400	,			<u>.</u>		:
1	ILPIACALUIMIN REURANIMIDASE	SINIAN VIRIS S (ISO) ATE CAMPILKT)	7.38	101.4	177 441	:	!	: :			
1	HENIACCE UTIMIN-MEDITAMINIDASE	SIMILAN VIRUS STISOLATE CARINE, CTI-1	7.28	101.10	175 tro	•	!				
PREMA SVS.N	IENIAGGIUTININ NEURAMINIDASE		2	1017	173 410	; :	-	:	:		
PHEMA VACCC	INTRACCIONIN PRECIESCH	VACCINIA VIRUS (SIRAIN COFLINIACION)	137.162	!	:	-	-	į	!	:	:
PIEMA VACCI	IEMAGGLUTIVIN PRECIRSOR	VACCINIA VIRUS (STRAIN 1110-1)	131161	-	!	1	-			!	;
MEMA VACCI	HEMACGLUTININ PRECIASOR	VACCEMA VIRUS ISTRAIN TIAM TAM	173.191	!	:	į.	İ			;	1
VIEW VALLY	PENACCIUM PRECIMSON	VACCINIA VIRUS (STRAIN WR)	173.192			ĺ					!
PIEMA VAIIV	I GENACICATIVIN PRECURSOR	VANOLA VIRUS	2		!				:	1	
MCX ADE	IG KON ASSOCIATED PROTEIN PRECURSOR	INDIAN ADENOVIAIIS TYPE ?	=	100				-	-		!
MEXI ADED	HE XON ASSOCIATED PROTEIN PRECLASOR	INDMAN ADENOVIRUS IYPE I	1			1.				!	
MEXI ADEOS	HE XON ASSOCIATED PROTEIN PRECURSOR	INDIAN ADENOVIRUS TYPE S	1	119.140							1
MEXIS ADEA		HUNKAN ADEMOVIRUS TYPE 41	10.00	128.146	İ	İ					
PIEXI ADEA!		MOUSE ADEMOVIRIJS TYPE I	15.35		1			1		-	!
PIEXO ADEO!	IC XON. ASSOCIATED PROTEIN	HUMAN ADENOVIALIS TYPE 1, AND 1	1111	Ì	I !			!		1	!
NEX ADEC		CAMINE ADEMOVIRUS TYPE 3	11.11								1
MEX ADDA	1		10.09						-		
NGO COM	Ī		117.533	19.35	919.009				-	-	-
_	LATE PROTEIN 1171.		68.83		1			İ			•
┱			169.190						-	i	1
Ī		A BRCAN SWINE (EVER VIRUS (STRAIN BASILY)	60.17		i				1	į	!
-		A HICAN SWINE FEVER VIRIS (STRAIN BATIV)	219.260								
•	Ī	CONTRACTOR COUNTY AND THE CONTRACTOR	2.		:	:					
_		POCIETY DESCRIPTION OF THE PROPERTY OF THE PRO		٠.							:
Ī	PROTEIL	IONIAN CYTOAGGALOVIRUS (STRATM ADIAN)	3		14 21	i					
Г	i	EDES SOOI EX VIRUS (197E 1/STRAIN 17)		1					į		1
П		IERTES SOULEX VIRUS (1 YPE 1 / STRAN ANGTLOTT)		Ī					İ	İ	į
PICIS HSVIF		JEAPES SDOLEK VIRUS (TYPE 1/8TRAIN F)		-	146 741						
_	PROBABLE PROCESSING AND TRANSPORT PROTEIN	BOVING ICAPESVINUS TYPE 2 (STRAIN BAIV)	100	19.00	-	1	Ī			İ	
ī	٥	EQUINE HERPESVIAUS TYPE I	37.56	Τ	13.33			İ		-	
٦	PROBABLE PROCESSORO AND TRANSPORT PROTEIN	HELDES VINUS SAMIND (STRAIN II)	3.40	1	13 63	1			1	Ī	!
	SI.	MUNINE CYTOMEGALOVIRUS (STRAIN SAILTII)	136-144	201.279	1 7 2			ĺ	İ		
T	S	PSEUDORABLES VIRUS (STRAIN INDIANA, FUNKITAUSER / DECKTR)	105.303	12.12		İ	Ī			Ī	
Ī	5		69.88	119:11	13.764			İ			1
Ī	Y PROTEIN		664-684				İ	Ì		i	!
			713.779							-	
	EALT PROTEIN B		13.102								
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T.	SPANCACTON TRANSCRIPTORION PROFESSION	CYCINE IEMPESVINDS 17FE I (STRAIN RENTUCKY A)	1								
Т	Ī	1	Ī	=	101.13						
1	1	THE STREET CHANGES	200			1				Ì	

		All Virues (No Berryleshaers)	-	-							
THERAME	LEGILIN	NING.	AHEAL	- AREAT	- AMEAS	ARCAS	ABILA		11.44.4		!!
	INCREDIATE LARLY PROFEIN IE 130	PSEUDORABIES VIRUS (STRAIN INDIANA JUNKTAUSIR / BLCKER)	111.746					- 27 1 22			
PERSONAL PROPERTY.	MANELOIA IE EAAL V PROJETNIE IN 18.180	FSEUDORABIES VINUS (STRAIN KAPLAN)	110 111		<u> </u> -	1			!	İ	
	TO VICE THE TIME AT THE CASE OF THE PROPERTY O	HILPEAN CYTOME GALOVINUS (STRAIN ADING)	266.304	- 14 - 15 - 15 - 15		-				1	
PIEGO INCOME	TOTAL STATE OF THE PARTY OF THE	THE STATE OF VIRUS (TYPE - / STRAIN 12)	110.104						!	 -	
PIET HOVEN	TOTAL STREET STREET STREET	THE PERSONAL BY VIRGS COVER DASHARD LICENSE	178.194		:	!			İ	<u>-</u>	:
PIEGO MSVSA	S KO MAININATE FARI Y CHARLES	THE STATE OF THE S	2	11.44							
	INDEDIATE EARLY PROTEIN 1568	THE PARTY OF THE P	101-126	!	; _:					•	
PIEGO HISVEA	IMMEDIATE EAST Y PROTEIN 1568	COUNTY OF THE STATE OF THE STAT	100	1	<u>:</u>					-	i i :
PIE68 HSVEB	INDEDIATE EAST Y PROTEIN	FOUNE IN PRESVINIS TYPE I	1	-	!						
ارا	INDIEDIATE EARLY PROTEIN	PSEUDORABILS VIRIS (STRAIN KAPILAN)	101		-	-					
	GENE GIVIO PROTEIN	VANCELLA ZOSTER VIRIJS (STRAIN DUNAS)		1	1	-	1		!	;	
PIRIS HEMVA	IIYPOINEINCAL PROTEIN	HUNGAN CYTCAL CALENDARY ATTENDED		1							!
PKEAB AVER	ENAB TYROSINE KINASE TRANSFORMING PROTEIN	AVIAN ERYTHRONI ACTORIC VIBILE		1	.;	1					:
PRIES 18VCA	TYROSINE PROTEIN KINASE TRANSFORMING PRO-	SEL DE CARCOLA CIPIE AND CARLOL STREET	1	2	!						!
PELES FSVST	TYROSINE PROTEIN KINASE TRANSFORMING PROF	FELDRE SANCORIA VIBITO CONTRA STATE				.					į
PRUCE FSVCE	I YROSINE PROTEIN KINASE TRANSFORMING	PELINE SALCONIA VIBING SCHAZIN CANDARA A SUECON	,,,,,			-					
PKFMS FSVMD	FMS TYROSINE KINASE TRANSFORMING PRO	FELINE SARCOMA VIRUS (STRAIN MICHONOLICIA)			-	·					
PKPPS AVISP	I VROSIME PROTEIN KINASE TRANSFORMING PROT	AVIAN SARCOALA VIRUS (STRAIN PRCII)			0		101	26.2			
PKIPS FUISV	TYROSINE PROTEIN KINASE TRANSFORATING PROT										
PKITH ASIBI	INYMIDINE KINASE		100	5	600 430	100					
PKITH EBV	1	FPSTEIN BAR VIRIA CON AND BOLLEY									
PKITII TLDV		11911 VAPINAT VATIC DICEACE VIBILE	7		-						
TKITH 13VII		STEEDER CHAPTER VIELE AND		25.20							
PKITI ISVIC	THYNODOG KINACE	TENERS STATES AND STAT	2.75								1
PRINT MEVIE		HEAVES SENTIER VIRIOS (177E 1758 ANN CLIO)	23.24			-					
PRING BEVIE	INVANDAL KOLACE	PER SIMPLEA VIAUS (177E 1/5/18/18/18/18	233.249								-
PKITH MSVIS		HERTES SIMPLEX VINIS (1) PL / STRAIN KIS)	133.24			-		<u>:</u>	1	::::	:
PKITH DISV23		TERRET CINETE VINITE TOPE CONTRACTOR	23.74						İ	} :	!
PRITH HIS VIDE		MOVING MEDICALITY TOPE LIGHT AND	224.350	=							
		BOVING ICENS VIEWS TYPE 1/2 PAIN DIES	1	2						!	
<u></u>	TILY MOONE KINASE	BOVING INDRES VIRING TAPE 1/CT ALM ILC III	_			7					
1_	IIIYADDNE KINASE	BOVING HERPENING TYPE 1 1/218 ALL COLORS	_	9	-	-				-	
1	THYMDINE KINASE	FOUNE REAPESVIRIES TYPE 4/518 AIN 1943	770	8		İ				İ	
PKITH HSVED	THYMDONE KINASE	EQUINE IERPESVIRUS INFE I (STRAIN ABAPIAND LISO) ATE HISTORY			-						
PKITH HSVF	HIYMOINE KINASE	FELINE HEAPES VIRIJS (FEI ID HE SVIRUS I)			7.						
TKITI IISVII	THYMODIE KONASE	ICTALURID HERPESVIRUS I		-			Ī				
TRIIN IISVAU	DIYMDINE K DASE		189.715	-	-			İ			
PKTH ATT	THE MINING A LITA SE		108 332								
1			103.303	208.334							
			197.216								
1_			197.216								
Ĺ	III YMDDNE KINASE	VARIET A 2001ER VIBIL SECTION DESCRIPTION	3:5	-							İ
Į		┪	197.216	j	i					İ	
L	KIT TYROSINE KDIASE TRANSFORMING PROTEIN	┰	27.76						1		
		T									
П	GENE 16 PROTEIN KINASE		100		Ī	Ī					
ΙĪ	SERINE/THE CONTINE PROTEIN KINASE	(IVPE I/SIRAIN II)	10.00			1					
ī			2,6,74				İ				
FKE HSVEB	SERINE/THREOMINE PROTEIN KINASE		19.107		!	İ		İ			
ī			101.01				-			:	:
T	PROBABILE SERVENTINE COUNTY PROFILE IN FINANCE		19 197	:	:	i	:	!	i	:	
	يرا پر	ISBNE CHOILE VIRUS (STRAIN 87). 1)	- - -	:::						: ::	
	بيرا		Т								;
Ī	ıT.	PSE(DORABLE VIRIS ATEAN NA. 1)	_[441.462					Ī	İ	1
				107 707							

	Principle	All Vireyer (No Besterlephones)				-					
FILENAME	LACILIN	W.	AKEAL	ABIA J	AHEAU	Z	APLAS	ANIAS	ARIA?	ANCAG	ARIA
•		LIFELLA. 21)STER VIRUS (STRAIN DUNIAS)		_	-	_			1		į
PKR73 IISVII	GENE 73 PROTEIN KINASE	KCTALIMID IN APESVINUS I	141-151								
PKR74 JISVII	CINE MINITURE MANAGE	KTALKINI JOAPESVIRUS I	134.360	\$15.805		-					İ
PKIBI VACCC	TO RD PROTEIN FINASE HUNKINGO	VACCINIA VIRUS (STRAIN COPINIAGIN)	199.214	i i	<u> </u>	-	i	İ	-		<u> </u>
FREE VACCV	TO KID PROTEIN KINASE IKWAN OG	VACCIPILA VIRUS (SIRAIN WR)	18.54			ĺ					į ·
PERRI VARV	TO KIN PROTEIN KINASE IRMON (XC	VARIOLA VIRIS	90.314			Ī				Ī	Ì
PERSONAL SEVERA	POCCINE DE DOUBLE MANAGE CON	SHOPE HIMOMA VIRIS ACTAEN KACZAI	10.	:	İ	Ī		1	İ		-
10000	POCCESS REPORTED AND ACCUSED TO SECURITY OF SECURITY O	VACCINIA VIBILG (CIBAIN COPENDIACEN)	3		-	Ī		Ī	İ		i
	POSSESSION FOR STANKING STANKING			İ	-		Ī			İ	
TAME VACE	PUSSIBLE PROJEIN KINASE PTO	VALLINIA VIKIIS (SIRAIM L.IV.)			-	-				ĺ	
PKR51 VARV	POSSIBLE PROTEIN KINASE FIO	VARIOLA VIRUS	13.100			-					
PKROS AVISU	ROS TYR KINASE TRANSFORMING PROTEIN	AVIAN SARCOMA VIRUS (SIRAIN URZ)	6-39	101-111	284.305						
PRRYK AVID.	TYP PROTEIN KINASE TRANSFURNING PROTEIN	AVIAN BETRUVIRUS RPL 30	134-172	721-241	!	-				İ	
	THE CASE CHIEF CONTRACT OF THE CASE OF THE	AVIAN CENTIFICAL ACTIVITY VIBILS (CTBAIN SIL			İ	ŀ				-	İ
TYPE AVE.	I TRITACIEM KINASE I KANSPOANIMU TACIEM SI	אין		1	1	i		-		:	
PKSRC AVIS)	TYR. PROTEIN KINASE TRAMSFORMING PROTEIN ST	ž	161.177			7					
PKSRC AVISA	TYS PROJECT KINASE TRANSFORMING PROJECT SA	AN SARCOMA VIRU	141.377							:	;
200	NI SICE CANADANA SI SINA MANADA SI	AN SANCORIA VINIT	1			-		i	:	;	į
		200000000000000000000000000000000000000	1	:	_	:.	:	:	:	:	
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PRSAC RSVHI	TVR PROTEIN KINASE TRANSFORMING PROTEIN ST	SARCOMA CIRUS ISTRA	11:11								
PASSE RSV	TYR PROTEIN KINASE TRANSFORMING PROTEIN SE	POUS SARCOMA VIRUS (STRAIN PRACIDE C)	16.31			-		i	i	i	1
PRESC RSVPA	I'VE PROTEIN KINASE TRANSFORKTING PROTEIN SE	IS SARCONIA VIRIUS (SIR	31.31		:			İ	ļ	-	:
100 A 100 A	TO SECURE OF THE	TO CARCOLIA VIBILE ISTO			:	!	-	İ		!	-
			1	i	!		i		-	i	
TK YES AVISY	TERTOLEM KINASE INCANSPONING FROIESP T	AN SAMCIMIA CIRCINISIS			:		1	-			İ
PLISO ADES	LATE 100 KD PROTEIN	INMAN ADEMOVIRIIS 14FE ?	=								
PLIOD ADEOS	LATE 100 KD PROJEDA	INDIAN ADENOVIRUS TYPE S	=	İ	!	!			:	i	!
		INDIAN ADENOMISE TYPE AT	947 937		;	:			i	İ	!
B	ILAIE IOUKUTKUILIN	THE PARTY AND TH		!		::::			:	:	:
PL. 53_ADE03	LATEL! 53 KD PROTEIN	3	20		_	_					
71.53 ADE95	LATE LI 13 KD PROTEIN	INDIAN ADENOVIRUS TYPI, S	111.139		_	-					_
MANUE LUBIN	SEPATIC LECTON MOMOLOG	TOWN POR VIRING (ISOLATE UP 4161A(10)(TILL)	12.		_		!	:	:		
	A 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	TOUR DANS VIEW CORNEY BOX D.	15			:	1	: : :	:	:	:
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	LAILE MEMBRANE PROTEIN	TO THE CONTRACT OF THE PARTY OF		• •	:	-	: : :	1	:	-	:
PLADI EBVA	LATENT MEMBRANE PROTEIN				_	_					
PLACT EBY	CENE TLAMINAL PROTLIN	TEIN BARR VIPIUS (S	\$		267 :01	21.11	146. Jc4	170-410		1	
PAICEL SFYKA	MONA CAPPING ENZYNCE, LARGE SUBLINES	PE FIBROAIA VIALIS	24.260	556.578					i i		
PACEL VACCO	MANA CAPPER ENTYPIE LARGE STRINI	VACCIMA VIRUS (STRAIN COPENIACION)	101:10	365.203	:	101.10	 			1	 - -
AVULA AVULA	MANA CAPPED BYZYNG LARGE SIGNIE	VACCINIA VIRUS (SIRAIN WR)	18:	161.312	ı	1 60			: 	:	į ;
A LANA	LINKS CAPPING BYZYNG LARCE SIMILAL	VARIOUS WRITE	101.10	261.382	,	101	-		1	:	
	STATE OF THE PROPERTY AND THE PROPERTY A	AND AND AND AND AND AND AND AND AND AND				i			:		•
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THE REDVE	FOUND CAT IN IL	ALOVIAUS (1177, 113) RAIN UPANIMI)		1		<u> </u>				-	
PHOVE COMYS	MOVEMENT PROTEIN	CUCUMBER CALEN PIOTILE PHISAIC VIRIS (WATERAILON STRAIN	201		-					-	
PHOVE COLIVIA	MOVEMENT PROTEIN	CUCURCOER GREEN MOTTLE PRISAIC VIAUS (WAIT RAIF LON STRAIN	=								
PLOVE DRSV	MOVELENT PROTEIN	ODONTOCLOSSUM RINGSPOT VIRUS	14.74	138.205	!						
PLOVE PPLVS	MOVEMENT PROTEIN	PEPTER MILD MOTTLE VIRUS (STRAIN SPAIN)	23.50	100 96	:	:	İ		<u> </u>	-	:
PAGVE TACAR	MOVEMENT PROTEIN	TOBACCO MED GREEN MOSAIC VIRUS (TAIV STRAIN UT)	186.201		: :	:		-	i	- : :	:
PADVE TAVCO	MOVELGAT PROTEDI	TOBACCO MOSAIC VIRIIS ISTRAIN COWPEA)	101.10	11991	İ			Ī	-	!	!
PATCI CANNI	MODULICATION METHYLASE CYBI	CHE CHELLA VIAUS NC.1A	39:156		ļ	-		İ	-		
	MODIFICATION NO THYLASE CVIALI	PARAMECIUM BURSAPIA CIO ORFILLA VIRUS I I	19:01		İ	Ī				i	1
Ī.	MODELLA STORY LANGE THAT ARE CURRENT	CLE CARFLA VIBILS MC. LA			İ			Ī		-	
Т					!				-	-	
Ī	PLIS GACHETE-ELS INCOSPONING FROIE IN	AVIAN LEUALMIA VIAUS F.20		-	!					-	
-	MYB TICANSFORMING PROTEIN	AVIAN MTELORI, ASTUSIS VIRUS		9:1:0	į						
PHCAP AIMOV	MICLEOCAPSED PROTEIN	AIMO VIRUS	139.101								
	MICH EUCAPSID PROTEIN	BIMYAMRIIS LA FROSSE	2		. :	:				i	ĺ
PACAP BUNSH	MKLEOCAPSID PROTEIN	AUNYAVIALIS SNOW SHICE LIABE	2		İ			i	- !		-
ONCY ON THE	Mari Bor Apsin Profitin	CANINE DISTEMBER VIRUS (STRAIN ONDER STEPOOR TI	19			Ī			i	!	:
	WILLIAM CONTRACTOR	FELINE WAR CHOICE PLANTONING VIRGIS (CORAIN 30 1146)			:	İ	1	-	:	1	i
	Majord Majord	HANTALA CIBIC CODAIN TALES		:	!	Ì		Ī	_ i	1	:
	The state of the s				-			Ì	-	-	-
THE MALVI	MCLECCA'S WATER	MAZAKA VIRUS (ISOLATE A.210)			-	-	-	-	-	-	į
PHCAP DRV	MIK LEOCAPSID PROTEIN	MICKOSIS VIRTIS (STRAIN ROUND BUT	110-137	210 242		1	1	1	-	1	

MALES CATE DESIGNED MALES CATE OF THE CONTRIBUTION MALES CAT			17.5		-							
MACLECATION PROTEIN	THE HAME	PROTECT	Vinite Constitution of the					Г				
MACHIGOLOGY MACHIGORY MA	PHCS INSV	MUCLE OCAPSID PROTEIN	IMPATIENC MECENTIC CONTINUES	PATA-	OR OF	49.52	AMEAN	ī	0 K 1 H V	1817	ARIAI	7.19.4
MALLOCATION FROM THE PROPERTY OF THE PROPERY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY	PHCAP MEASE	MICLEOCAPSID PROTEIN	NEAST ENGINEERS OF THE PROPERTY OF THE PROPERT	135-179	į		-	ī				1
	PHCA MEASH	MAKE BOCAPCIO PROTEIN	PEASE COUNTY (DRICKS)	40.59						İ	İ	
	PHCAP LATACY		MEASURE VINES (STRAIN HALLE)	60.59		-	!				i	;
	10 10 PM	THE POST OF THE PARTY OF THE PA	MEASILES VIRIIS (STRAIN YAMINGATA. I)	1	1	 -		:	1	:		•
	47.74	MALEUR AND PROJETIN	MUNCS VIRIUS ISTRAIN SILL II	126.12	:	1				: !		:
		POCLE COURT NOTE IN	MOMOS VIRUS ISTRAIN ALIVALIARA VACCINE)	136.178								-
		MOLECASID TO EN	PROSPECT HILL VIRIS	16.51	11.31	146.377	17.					
		MACLE UCASIO PROTEIN	INDIAN PARAINFLIENZA I VIRIIS (STRAIN C)9)	15.0								
MACHICAL-MID FORTH		MUCLE OCAPSID PROTEIN	INDMAN PARAINFLIFENZA I VIRUS (STRAIN WASHINGTON/1953)							İ		
MACLIC CAPID FORTER		MALLEC AND PROTEIN	MOVINE PARAINI 118 WZA 1 VIRUS	167.184	:	!	-		1	i	:	
ACCIT COLUMN ACCID D ACCID		MACLECASIDATOTEIN	PRIMIAN PARAINELLII.NZA) VIRIJS (STRAIN NIII 47815)	161.117	-	!	-			-	j	
ACCITICATION ACCI		MIKELEDICAPSID PROTEIN	PURMALA VIRUS (SIRAIN HALL NAS his				-					
MACLE CA 210 FOOTEN	3		PUTMALA VIRUS (STRAIN SOTRANO)									
MACLE CA 2019 FOOTEN ALABEST VILLEY THE STATE OF TH	PICU PABVA	MICLEOCAPSID PROTEIN	RABIES VIRIS (STRAIN AVOIL	200	716.236	9						
MACH COLNEY FOOLIN MACH CALLED AND MACH CA	PHCA TABVE	MICLEOCAPSID PROTEIN	AABIES VIRUS (CIRAIN PUT	130			7			İ		İ
WELLIGG JISTIN STREAM ST	PHCAP RABVS	MUCLEOCAPSID PROTEIN	BARRY VIDING SCHOOL SCH	120.00						i	!	•
MACI (CG A316) FOOTEN STROAM VIRGS (STATE A) TO TAKE A TO TAKE	PHCAD RVFV2	MUCL FOCAPSID PROTEIN	PITO VALLE CONTRACTOR SAD III P	199-523		,	<u> </u> -		-			!
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WALLEGATIO FIGURE SECON VINUS STATISTS 17-11 11-11 1	PACE SENDE	MCL FOCAPSID PROTEIN	SCALA VINOS (STRAIN ENDERS)	63.38	101-91		j .				1	
WALLEGATION WALLES WALLE	PHCAL SEND?	MX LEOCAPSID PROTEIN	SEADAL VIRUS (STRAIN HARRIN)	43.58	6-102		-				1	
WACHEGO JID ROTTEN STOLE WIND TANKER STO	PHCAP SEDUS	INICI EOCAPCIO PROTETA	SCHOOL VINGS (31 MAIP Z)	19-51	101.98						-	
MCLEGCASID FIGURE	PNCAP LITEV	Mari Encaped Profession	SECOL VIKUS (STRAIN SR. 11)	13:13	117.343		İ			-	-	
MCKLEGGATO FROTEH	77.0	THE PERSON NAMED IN COLUMN	SANDELY LEVER SICILIAN CIRIS	=======================================				İ		-	-	
MCLICOLNID FROITEN VULL HENDORIULGE SPITEMIA VIRIS (ITAN MAKAII) 10-154		PICKLE AND PROTEIN	TACARIBE VIRUS	119.201		::	ļ		1		1	
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		NEURAMINDASE	VIRUS (STRAIN BARAIPHICHMS)	2 2		- <u>i</u>					<u>!</u> !	
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つ !>	NEURANINDASE NEURANINDASE	INTERFACE VIRES (STRAIN BATESRATIONS)	2 2			i					: :
PHS SEEV	PROBABI E MONSTRUCTURAL PROTEIN PRECURSO	DOMBLY DENSOME LOSIS VIRIES	15.50			İ	Ī	i	-		
	PROBABI E STRICTURAL PROTEIN PRECURSOR	_	2	2	3					-	:
A STATE OF THE STA	NOT STATE OF STRUCTURAL PROJECT STATES		2 2		į		İ		!		: !
PNSS TSWAL	NON-STRUCTURAL PROTEIN	TOMATO SPOT TED WILLT VIRUS (STRAIN)	-	10.00	:	-	Ī	-	i	-	1
PHIPI VACCC	MUCI EOSIDE TRIPINOSPILATASE I	VACCIMIA VIRUS (STRAIN COFF MIAGEN)	-	107	:					İ	
PHTPI VACCV	NUCLEOSIDE TRIPINGSPILATASE I	VACCINIA VIRIS (SIRAIN WR)	10.45	107							
LATE VARY	MUCLEOSIDE TROPIOSPITATASE	VARIOLA VIRIIS	8		ļ:	-			i	- ;	
PAPE TOWN	POR VIAN POLI VACE ASSERTED A 108 V SIGNIANT	FOR POR VIRIA	8	20710	<u> </u>			:		!	1
PASS LIVEYA	POLYTAL POLYMERASE REGIL ATORY STRUNIT	MYXOMA VIRUS (ISOLATE AUSTAINTARAATERG BATE)	1		-	1		-	İ	-	-
PAN VACCE	POLY(A) FOLYMERASE REGIL ATORY SINGUNIT	VACCIMIA VIRUS (STRAIN COPT MILAGI N)	1 2	-	!	•				Ī	1
PEAPS VACCV	POLY(A) POLYNGAASE REGILATORY SUBINIT	TRUS (STRAIN	9	: 		•		1			1
PPAPI VAKV	POLY(A) POLYMENASE REGARATORY SUBINIT	VARIOLA VIRUS	9		:	-				İ	
PPCNA MPVAC	PROLUERATING CELL MUCLEAN ANTIGEN	AUTOGRAPITA CALIFORMI'A MIKLI EAR POLYTIC DROSIS VIRUS	9 80	117.144		-				į	1
15E2 NO.	11 1 KD PROTEIN IN PE SPECION	ORCYLA PSEUTXII SUCATA MILL IK APSIU POLYIII DRUSIIS VIALIS	11.110				<u> </u>		İ		
PPEJS MPVAC	25 I KD PROTEIN IN PE. P16 INTERGENIC RFGION	ALTOGRAMIA CALILORNICA NIKI EAR POYVIKINOSIS VIRIIS	=		:	7					
TANK THE STATE OF	PACKET BE CHAIR EARLY FRUITIN	ACTUAL APPLICATION TO THE TANK THE THE TANK THE									
	PENTON PROTEON	IN MANA ARENOVIETIC STORES		j	!			-	İ	-	-
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	MATURATION PROTEDY	HUNIAM ADEMOVIRUS TYPE ?				:-				İ	
		MANISE ADENOVIRUS TYPE I	18	İ		:	!	ì	:		•
PPOLI BATMG		DARIET VELLOW MUSANC VIRUS ILLI MAIAM ININ A 11.3		113.116	1012.1034	140					
PPOLI BATHU	T. I.	BARLEY YELLOW MOSAIC VIAUS (JAPANESE STRAIN II.1)	1 2 2 2	9	003		188.1909	-	:		:
POC. GCMV		HUNGARIAN GRAPEVINE CHRONE NOSAIC VIRIES	661.717	100	1116-1141	<u> </u> -			1		
POLI GILV	THAI POLYPROTEIN	CRAPEVINE FAMLEAF VIRUS	100.1%	. 301		1079.1509	1111.01	341.154	781.1784	1121.1141	2020.2044
POLI TBRVS	RNA! POLYPROTEIN	TOMATO BLACK RING VIRIIS ISTRAIN S)	2						:		1
TOU ARMY		ARABIS WOSAIC VIRUS	2	20.76	3				!	:	
TANK TOWN	CENOME FOR VEROTER'S	SAME EVERTON ACCOUNT VINES AND				İ		!			-
אסרו כנור		CRAPEVINE FANLEAS VIRIS	200				j	Ì		į	1
POLJ TBAVS			25.400	1	156.176	101.101		İ	1		l
1			316.340	137.648	133.133			<u> </u>	Ī	Ì	
	GENOME POLYPROTEIN	BOVINE ENTEROVIRUS (STRAIN VG-5.27)	1113-1189				•	-	÷	_	
POLO BVOVA			617-653	943.963	1	1051-101	161.1307	1860.1897	1460.2487	1608-7678	1017.101
3	Total Control of the		<u> </u>	200	3	1947-1986			-	_	
т	JENNAL COLUMNICIO	SOUTH ALL DIAMMIES VINOS (STANIN SULT)	11.433	9		2	50.1.00	20.20	361-133	778-1807	1170.1191
PPOLO COXAL	GENOME POLYTROTED	AZI ISTRAIN COES	1			8	Ī	Ì	Ì	Ì	
-		AZI (ECHO 9 VIRUS)	26.18		1	Ì	Ī	İ	İ	Ī	İ
		COXSACKIEVIRUS A9 (STRAIN CNCGS)	11111	1601.1626	1		Ì		İ	Ì	
		COXSACRIEVIAUS BI	473.1478	1313-1607	Ī	Ī	1		İ	İ	Ī
_		COXSACRIEVORIIS BI	- FE 18	1415-1501	305.1610		İ	İ	İ		İ
PPOLO COXB4		COXSACK IE VIRIIS BA	31.146	101.10	130	İ	İ	İ		Ī	
PIOCO COMPS		COXSACKIE VIRUS BS	1475-1301	1315-1610						İ	
POCO DENIS		DENGLE VIRUS 117E I (STRAIN SINGAPORE S275/90)	916-743	=======================================	42.15	1743.1760	613-1628	2011 MINI	2341.2165	1401.3476 1	1010 1040
PPOLO DENIW		DENGIE VILLS TYPE I (STRAIN WESTERN PACIFIC)	919-944	113							
Proce Denis	GENOME FOLTFRUIEIN	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA M.)	36.34			_			_		
1			10.00	910 044	113.113	194.1361	101.1101	613 1629	2393-2318	2347.2364	3405.2425
POLO DENT	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 1661) PDK 31)	191-191	919.044	00000	1346.1367	191.1101	176.1194		110.000	177.
_			12	2100-3736			$\overline{}$		_		
FIGURE DENZO	OF NUMBE POLITYRUIEIN	DENGUE VINUS TYPE 2 CATRAIN IN 1949	140.068	919.044							

LCCENE											
LILERABE	PAGIZIN	VIEWS IN DECECTOR DECECTOR DECEL				-					
PULO DENI		DENGIE VINUS TYPE I (STRAIN INCHEA)	3:	75.5	18.02 ×	ONI O	ARTA :	PHENE	ARFA?	AREA!	ARCAS
MEN DO DOGG			2 Trus. 273c.	:						_	1.11. VII.
POLC DENZE	CENCIE POLITICISM	DENGINE VINUS TYPE 2 (STRAIN NI W GITTALA C)	021.001	71.196	20.20	İ			-		
		INFMOLIE VIRUS 1YFE 2 (STRAINFRISES)	919:046	11:41			1174.114	200	i		
POLO DENIT			1667.2333			_					100
POLC DEN	CHANGE NA YPEREN	THE NAME OF THE PARTY OF THE PA	619 664	17.03	1	101.119					1.
	-		.113.113	12to 13:1	12111111	1411111	EH RO	.11 .16.	11.77	1 1 1 1	
POLO DEN	GENOME POLYPROTEIN	DENGLIE VIRIS 1VFF 4	24. W. 17.	11.11							-
POLO ECHO	GENOME POLYPROTEIN	ECHOVIALIS (1) (STRAIN CRECKS)	200.1227	24:124	1611-1627	1170-1146	2347-2350	2400-3470	1045.1064	-	!
POLG EMCV	GENOAGE POLYTROTEIN	ENCENIAL ONIVOCATION CONTRACTOR	064-690	3				Ī			1
PROLID EMCYB	GENOME POLYPROTEIN	ENCENIAL DIVINCA AND THE CHARGE SERVIC	22.50	550.576	12.13	16 (0.1767					i
PPOLO EMCYO	GENOME POLYPROTEIN	INCIPATION OF THE PROPERTY OF	20 ×	<u>=</u>				i	:	:	
PPOLO ENAIGS	GENOME POLYPROTEIN	MANAGEMENT OF COLUMN THE PROPERTY OF THE PROPE	240.580	=======================================	114:1217						
PPOLO ENAIGO	GENOME POLYPROTEDN	MENCO EINCH IN CALLUT ARTHUR VIRIOS (STRAIN 37A)	\$60.580	:	! !	!		:	!	-	:
PPOLO FADVI	GENOME POLYPROTEIN	PIGNO EMERINA UNITO ARTIFIES VIRIES	493.513			-			-	1	i
POLO FEDVS	GENOME POLYPROTED	COLIMINATION IN THE STRAIN AND BE	131-141	914-1003	1016-1017	1106.1811	266.1401	100	Ì		-
PPOLO FABVA	GENOME FOR VPROTEIN	COLLAND MOUTH DISEASE VIRIUS (STRAIN A1)	167:10			<u> </u>					i
POLO INDVO	CENOVAE POR VORGIETA	POULAND MOUTH DISEASE VIRUS (STRAIN ALL)	8	784-100)	1016.1017	194.14	_		::	:	
POLO SLIDVE	CENTRAL POLICE IN	POOLAND MOUTH DISEASE VIRUS (STRAIMS OIL AND OIBES)	=	180	1010	1		2 !	:::		
POLO PURVI	NING POLICE OF THE PROPERTY OF	FOOT-AND MOUTH DISEASE VIRUS (STRAIN CL.SANTA PAU IC. SEL)	100		i	1 2 2	_	9	-	-	i ,
Proto HCVI	MINIOR POLYMENT	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI)	=	979.900		•		Ī			
POLGIEVA	GENORIS DOLVEROLEN	IRPATITIS C VIRUS (ISOCATE 1)	E	100	019.610						
		INDUCTION ERA VIAUS (STIFAIN ALFORT)	103.138	10.116	10.110	100			7442-2457	_	
PPOLO HCVI	CENTRE BOY VARIOUS IN		3077.3093							25.67	167.3782
_	NISIONITA	INDG CHOLERA VIRUS ISTRAIN DRESCIA)	101.131	110.1163	100.000	. 1		-		-	
POLO INCVIK			1177.1169				_			3	767.1782
PROLICY I		HEPATHIS CYRUS (ISOLATE BK)	_	101.160	410 440	1			_		
POLO IICWI	GENOAG POLYPROTEIN	HEFATITIS C VINUS 11504 ATE ECT)	ī	-		1		2	2936-2851	70KE 3007	İ
PPOLO JEVNIA		IEPATITIS CVIRUS (ISOLATE II)		1	A 10. A40			ī			
770L0 SECVITY		IEPATITIS C VIRUS (ISOLATE INCV.476)	ī	- 199		_	ī	99-69	202.202	7837.2859	
POLO ICVI		ILEPATIFIS C VIRUS (ISOLATE IICT27)	Т		ĺ	Ť	j	İ			İ
POLG ICVIK		PREPAILIS CVINIS (ISOI ATE IICT IS)				1	İ	i	j		
PROLO HCVII		TELY TITLS CVIRIS (150) ATE LICV. R.T.	60.21	107.169	!	Ì	İ	İ		į	
POLO ICVI		TEPAILISC VIRIS (ISOLATE IIC 11)	Ī	- 10			Ì				
POLO JICVIE	GENOME POLYPROTEIN	METALLISC VIRUS (ISO) ATE IIC. 13)	113.113	ì	611.646	- 101.68	İ	Ì			
PPOLG HCVII		INTERNATIONAL PROPERTY OF THE			•	667.703	193.66	127.1851	100000	1000	-
POLO HOVIE		PATITIS CYRUS 18501 ATE IN- 161	٦	:	i	1	Ť	_	_	÷	
POLO HCVIA		ISOI ATE TAPANTOTA	ī	3		191 (10	199.69	113:1:11	_		Si Si
TYCE OF THE		ISOLATE RC.113		•	010.010				1117.1347	-	988. 3003
		SOLATE TITI	ī	i	ī		13 63	:	241.34%	3016.3105	!
2000		SONATE TAIWAN)		•	111111111111111111111111111111111111111		-			<u>:</u>	
. i		STRAIN ((IN . I)	ī		<u> </u>	204 644		2011 1111	2441.74%	7816. 281E 7	100
-	GENOME ACI VAROTER		ī		1115.1216		_	_	_		
_			ī		_		-	7/.07			:
PROLO IBANC		STAIN (B)	П	1103-1230	101.100	100 000	2068.3003	Ì	i	-	i
POLO HPANG			Г				+	1	İ	<u> </u>	-
PPOLO HOAVH			776 796		Ì	İ	-	 		-	!
PPOLO IBANL				1195-1210		ig	1069.2001	-	:	-	::
PPOLO IDANI			П		_		100	-		;	
		1111					100.000	-	<u>:</u>	:	:
				2	1101 1101	7013-1004	-	<u>. </u>	<u>.</u> İ	:	:
- 1	GENOME POLYPROTEIN	LIS IA (DIRV IA)						<u> </u>	: !	:	-
		INOVIAUS IB (IIRV IR)	Т	20.20		_	•		_	_	!
S S S S S S S S S S S S S S S S S S S	CENCIME FOLYPROTEEN	INOVIRUS 3 (FIRV 2)	Т	i	_		433-1070	153-1641	-	1861-1761	i
┑.		INOVIBING BUILDY DOL	Ť	1:	50.77	97-97	1610-1634	1000.1615		_	i
			1	┥.	_		S	2. IMI 18	1831.1840	1948-1944	•

Print	918 11-1819	AN VICTOR OF BRIDE AND									
CILL HAMIL	-	YUNUS	AHLA	AiltAi	L VIIIV	-10	A 101 A 4	4 V 101V	1,101.1.3		-
TANO INIV	CHINCHAIL PLANTING	HIMAN PMH MINTHEY TO INDIANA PURCH	,			-	•		•		_
PPULCE IBDVO	STRUCTURAL FOLYPROTEIN	AVIAN INTECTIONS TURS AT INSLAST VINUS (STRAIN INT)	903.033		:	-					
PPOLO JAEVI	GENOAGE POLYPROTEIN	TAPANESE FINE PILAL ITS VIRIS (STRAIN SA. 10)	Ī	106-1125	1647 1656	115.370	136.13				!
TOO MEYS	GENOME POLYPROTEIN	INPANESE EN (PIIAL ITIS VIBLIS (STBAIN SAIV))	2	ŝ	10.00	2165 2370	1376.3331	1467.7461	!		
	CENOME FOLYTROISIN	JAPANT SE ENC (PILALITIS VIRIUS (STRAIN PAC)ARSONIL		200	1612-165E	2245.2270	112: 116:	14.2 Year	•	<u>-</u>	
1000	CLACKER FOR VPRINCIN	TATABLE TO COLOR OF THE COLOR OF THE WAR AT ARIAS									
.)		Positive of the present of the prese	1	3	201	164).1644	2	22.22	3441 24th	1	241.2618
PANA I O IONY	CEMOARE POLYPROTEIN	THE PROPERTY OF THE PROPERTY O		-	إ						
			1	::	٠,	113-115	2	2	1909	?!	22000
PPOLO LANYY	GENOME FOLYPROTEIN	LANGAT VIBUS ASTRACTOR VIII ANIMEN			<u>.</u>		-	:::::::::::::::::::::::::::::::::::::::	:	;	:
PICE LIV	GENOME POLYPROTEIN	LOUPING SEL VIRUS (LI)					:				
PPOLO LIVES	GENOME FOL YPROTEIN	I DIPRACIFIC VIETS COLORAN CHICAN	Ī	1	!		İ		1	İ	
PPOLO MOA	CENCRE FOLYPROTEIN	AND COLOR OF STREET, AND	Ī			.					;
Aven o local	CENTRAL BOY VORDIERA	TOTAL STATE OF THE PROPERTY OF	Ţ		70.	1		2011	312	1 4 1 : 1	-
Value of the Value	CONTRACT FOR VERD TERM	MARKET OF MUSICAL PINOS	Т		1	·				ļ	
V-00 0 044	Charle for velocities	CONTROL OF THE CONTRO		╗	1	303.03	2	<u>§</u>	3	İ	
PACE OF PACE	CELOVAE BOLIVE VIEW	Property Principal Control		ī		20.00					
	CHANGE TO THE OWNER.	PLATER MOI ILE VIRUS (LALITURAIA ISULAIL)	2 1 . DA	176-1146	8		1455-1482	1484-1500	1676-1697	1921-1945	1002-1001
	CENTRE POLYTRUIEIA	POLIDVIAUS TYPE : (STACIN NAMONEY)	69-1432								
1000	COMPRESSED TO STATE OF THE PARTY OF THE PART	MI DVIKUS ITTE I (SIKAIN SABIN)	10			••					
	DEMONS FOR THE OFFICE AND ADDRESS OF THE OFF	PALIDVINUS 1 TP. 1 (STRAIN LANSING)	8		j						
	CONCRETE TO THE PARTY OF THE PA	POLIOVIRUS TYPE I (STRAIN W.1)	_!						j		
	GENOME FOL YMOTEIN	POLIOVIRUS TYPE 3 (STRAIN 23127)		1407-1410						-	
ᆡ	GENOVA POLYPLOTERN	POLIOVIAUS TYPE 3 (STRAINS PULE (IN/)? AND PJ. EON 124(1)0)		0							i
	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN D)			12.72	30.00	1491 1491	(407.151)	3676.3634	1064-1136	-
MOLO PYEA	GENOME POLYPROTEIN	PI.UM POX POTYVIRIS (STRAIN EL AMAR)		-	Г					:	-
	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (ISOLATE NAT)	Г		200	1901.18	1086-1517	3603.2629	1068 3090		
_,	GENONE POLYPROTEIN	PLUM POR POLYVIRUS (STRAIN RANKOVIC)	ī	`	_	1467.1494	1496 1512	3605.2621	1081.1105		i
_	GENOME POLYPROTEIN	PAPAYA RINGSPOT VIRUS (SIRAIN PIMUTANT HA)	372.390	:	-	!	1	1	:	:	
	GENOME POLYPROTEIN	PAPAYA AMGSPOT VIRUS (STRAIN PANUTANT HA S.1)	161:111	<u>.</u>	:				!!!	į	i :
PICIO PISM	GENORE POLYPROTEIN	PAPAYA KINGSPOT VIRUS (STRAIN W)	i		i	-					į
Proto Pany	GENOME POLYPROTEIN	PEA SEED BORNE MOSAIC VIRIIS (STRAIN ()PD)	ī	231-348 T	18.19		1001-186	14:1:1438	1861.193	3701.3736	
PPOLO PYYC	GEMOME POLYPROTERY	POTATO VIRUS Y (STRAIN (.)	Ļ	ī		Ţ					1
אייים	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN INDICARIAN)	155.776	216.196	1010 1010	100.1135	456-148)	105 717	1671.1671	375.19.6	7418 7600
			9201-9001					i		_	
POLO PYTH	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN N)	ī	20.13	1010-1016	100-1135	436-1413	1485.156	1677.1691	1977.1946	360.366
٦	GENOME POLYPROTEIN	POTATO VIRUS Y (STRAIN O)	378-884	•		İ					
-7	GENOME POLYPROTEIN	PARSHIP YELLOW PLECK VIRUS (ISOLATE P.171)	<u> </u>	134.1141	1636-1651	1901.1924	1621.7642	2701.178	1766-2783		
_	GENOME FOLTPROTEDY	ST LOUIS ENCEPHALITIS VIRUS (STRAIN MIST. 1)	1301-1334								Ī
POLO SURVS	GENOME FOLYPROTEIN	SUGARCANE MOSAIC VIRUS (STRAIN SC)	⊢								İ
POLO EVDVA	GENOME POLYPROTEIN	SWINE VESICULAR DISEASE VIRIUS (STRAIN IVI 16)	103-1301	1819.1610				-			
Prote svove	CEMONG FOL YPROTEIN	SWINE VESICULAR DISFASE VIRIIS (STRAIN (RG/27/72)	ŝ			_				İ	
	CEMONE FOLITAGE IN	TICK BORNE ENCEPTIALITIS VIRIIS (STRAIN SCHIEN)		-	=		1630-1653	1340-1761	_		2765.2781
A STATE OF THE PARTY OF THE PAR	CENONE FOLTFROIER	HICK BOINE ENCEPHALITIS VIRUS (W. STERN SCRIVE)		137.551			_	1330-2337			i
Prode ity	GENORG POLYPROTEIN	JOBACCO ETCH VIRUS (TEV	127.653		016.1042	0(1	107.1336	130 1306			
_	CENCHE FOLYTROTER	THE LEA'S MANUE ENCEPHAL CHIYELITIS VIRUS (STRAIN BEAN 6166)	924.941	_		\$20.1546		-			-
200	GENOME POLYPROTEIN	MEGLER'S MURINE ENCEPHAI ONIYEL HIS VIRUS (STRAIN DA)	1033-1093	<u> </u>	# 1 2 E	1616-1675	Ī				
POLO TAEVO	GENOME POLYPROTEIN	THE LEAS MUNINE ENCEPHALONIYELINS VIRUS (STRAIN COVII)	£5.670	1	1074.1005	2	530-1546	658-1677	Ī		
700	GENOME POLYPROTEIN	TURNE MOSAIC VIRUS	91:18	ī	36-1156	131.18			Ī		İ
POLO TWO	GENORG POLYPROTEIN		1	401.511		10.06	967.992	137.1374	337.2562		İ
~	GENORG POLYPROTEIN	를! 날!					-	-	İ	İ	
	GENOME POR TYROTEIN	WEST MILE VIRIES		950-160		639-1655			437.3455	_	1101.101
יישנים יישנים	GENOME FOLYTROIEIN	YELLOW FEVER VIRUS (STRAIN 171)			2	363.1405		1623 1641	1761.1778	1179-2154	-
	CENTRAL FOR STRUCTURE	TELLOW PEVER VIRILS (STRAIN PASTEUR 17) 201)		1157.1179			100		12.13	77.24	İ
_	GENOME POLITICOLE IN	VELLOW FEVT R VIRUS (STRAIN 1894/81)	74.95	<u> </u>					i	:- :	1
POCH FOLIM	CENOME POLYTROIEIN	POLIDVIRUS TYPE I (STRAIP MARIONEY)	3			_	_		Ì	Ī	í
╗.	NONSTRIKETURAL POLVEROTETN	VENEZIELAN FOUDIF FREE FIELS VIBILE STRAIN TRINIDAD HOW	П	21.11	411416	1001.101	1111.1111	1911.1910	117 114	1811	
					1						

INCOME.	11/41 916										
1	PROTEIN	Capital Control of the Control of th								$\overline{}$	
	YON-STRUCTURAL POLYPROTEIN	BELINE CALICIVISITS STRAIN CLIMA FIVE	7	3	3	7	AREAL	ANTA S	ARTA!	ARTO !	AMEAS
POLK TOYS - N	VON-STRUCTURAL POLYPROTERN	PELINE CALICIVISIS COMAIN TARANCE IN		8	12.10			1		:	
	HON-STRUCTURAL POLYPROTFIN	HELINE CALICIVINES (STRAIN 19)			1					;	į
PROCH REVISOR	HON STRUCTURAL POL VPROTEIN	INFRATILISE VIRGIS (STRAIN PRINCE)					17.6		. 1	-	
POLN IEVAE	ON STRUCTURAL POLYPROTEIN	INFATITISE VIBIUS (STRAIN MEXICO)			!			!		.]	
١.	ION STRUCTURAL POLYPROIRIN	LIEPATITIS E VIETS (STRAIN ANY ANA ARIA			! !!	-					!
	ION-STAUCTURAL POLYPROTEIN	TIEPATITIS E VIRUS (STRAIN PARISTAN)			1			:		i !	
Ī.	HONSTRUCTURAL FOLYFROTEIN	÷			Just 2 25						
Ь	HONSTRUCTURAL POLYPROTEIN	ONYONG NYONG VIRUS (STRAIN GULL)					İ			1	-
POLK RIBOV	NON-STRIKETURAL POLYPROTEIN	PANNIT IEMORNIACIC NICE ACE VINITE									!
L	NON-STRUCTURAL POLYPROTTIN	PADDIT IGACHANIACIC DISEASE VIBILE SCHARE VILLE				!				:	:
T	DASIRICTICAL POLYPROTEIN	BOCCEIVE VIEW CONTRACTOR AND			-	-				İ	į
ī	MONTE STEET AT POLYBECT	The state of the s	8	10 11	2				!		i
1	CANCELLA LE BOL COMO COLO	ACCORDED A VINE OF THE PARTY AND THE PARTY A	2	24.834	-						_
7	MUNICIPAL POLITICAL	RUBELLA VIRUS (STRAIN 1916 RIEN)	14.33			649.019	91.410	114.11	2015.205	!	
	ONSIRIAL FOLYPROIEIN	SEMUNI POREST VIRIJS	100	617.643	2062-2017	3114.3114		!			
_	OWSTRUCTURAL POLYPROTEIN	SIMDBIS VINITS (SURTIVE) (A KIT NO / VIRAIN I DAINE NEW HE) ()	230 64		I Protesti		22 22 40				
_	ONSTRUCTURAL POLYPROTEIN	SINDBIS VIAUS (STRAIN LINST)	620.646	121.1150	1744.870		1146 7161	2216 2216	<u>!</u> !	i	-
	RMA REPLICASE POLYPROTEIN	ECGPLANT MOSAIC VIRUS	100.03	!		İ					1
POLA OYMV A	NA AEPLICASE POLYPROTEIN	ONONIS YELLOW MOSAIC VIRILS	101 311		!	;	:	:			•
	BNA BEDLICASE POL VPROTEDI	TIBELIA VELLOS AN CIGIN			1	1	-		1		
_	NA REPLICASE POL YPROTEIN	TIERRIP VELL DIE MACCAST CHILD CALCAST AND TANK THE PARTY OF THE PARTY			-	1		:			
PACIFIC TANAN	DEAD PROPERTY AND ADDRESS.	TOWN TELEVOLUTION OF THE STANDING THE STANDI			=	•	:				
-	THE PARTY OF THE P	TORNIT TELLOW MOSAIL, VIRUS (ISOLATE, TYNIT)	66.2	3	12						
Ī,	SI AUCTURAL PUR TYRUIRIN	EASTEAN EQUINE ENCEPTIALITIS VIRUS	15.30	23.23	* 1.30						
٦	TRUCTURAL POLYPROTEIN	EASTERM EQUINE ENCEPHALITIS VIRIIS	35.30	314.330	493.500			İ		!	:
	STRUCTURAL POLYPROJEIN	VENEZUELAN EQUINE ENCEPTIALITIS VIRUS (STRAIN TC-83)		239.341	100.00	+			-		
	I AUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIAUS ISTRAIN TRINIDAD DON		336,346	13	İ					
Т	TRUCTURAL POLYPROTEIN	AVIAN INFECTIONS RIPSAL INCRASE VIBIGACINALIN SYNAM		-	:		:				
PPOLS LIBOVA	STRUCTURAL POLYPROFEIN	AVIAN INGECTIONS BUILDIAN DISCRASS VIBIOS SCHIMAL AND TANK		İ	-	-	ļ				
ī	INICHIMAL POLYPROTEIN	AVAN BESTERN BIR (A) DICEASE VIBILE SCHOOL STATES							ļ		
	TRUCTURAL POLYPROTEIN	AVIAN INSECTIONS BIREAL DISTANCE CONTRACT AND MACHINE			1		:	- :			
PPOCS ISBUY	BUCHANT POLYPROISIN	AVIAN METTING BILLERY WAS VIBER STREET				1					
	BITCH TAIL FOR VORDICEIN	ONCOMO MODEL CERTIFICATION CONTRACTOR CONTRA		1		1					
PPOL C BRVF	BITCHIRAL POLYBONEIN	POSSESSION OF COMPANY COLOR									
TOTAL STREET	CIBILITIES NO VOICE	Property Assessment of the second second	200		.						
700	THE PART AND	AUSTIN THUS IN ALLINE SIK AIN HEVY I	20.	-						ĺ	- -
	STRUCTURAL POLITICAL	RUBELLA VIRUS (STRAIN MIJ)	280.301		: !				[:	
	INDCIDITAL FOLTER	RUBELLA VIRUS (VACCINE STRAIN RATT.)	381.303				!			-	Τ
Т	STACE DATE TOLITICISM	KUBELLA VIKUS (STRAIN THERIEN	261-302	1041-1040	_						
Т	MUCH DESCRIPTION OF THE PROPERTY OF THE PROPER	SEMLIST DREST VINUS	2.2	=	780 101					İ	
Т		THE WAS STORED THE WAS LINE TO STANK LONG TO	20.00								
200	STRUCTURAL FOLITROISIN	SINUMS VIKUS (SIKAINS TIKSP AND HIKLP)	2								
7	INC. INC. TOURNESS	WESTERN EQUINE ENCEPTIALITY VIAUS	16.51	308-911						:	i
Ì,	TO TO THE STATE OF	A VICA RELICULUE NUMBELINS SIKUS	9.30							 	
ī	POR PROPERTY	POUNT EMOUNT OF THE STRAIN MAY	200	2	866·1018	1070-1091					
T	A POS VARIO 1774	BOUNE BARNOW TOWNER WAS ASSESSED.		3	9						
T	Carlotte Management	BOUNE INTERNATIONAL VINCENTIAL INTO	-	2	8v1 110						
	OLIVE TROICE	BOVINE LEUKEMA VIKUS (AUSTRALIAN ISOLATE)	187.504								
ī	اپ	BOVINE LEUXEAUA VIRUS (IAPANESE ISOLATE BLV-1)	117.504							İ	
Ī		CAPRIME ANTHRITIS ENCEPITALITIS VIRUS (STRAIN CORK)	111-111	636-671							
- (CAULIFLOWER MOSAIC VIRUS (STRAIN CM. 1841)	184.204	110-407	471.494					Ì	1
ı		CAIL BLOWER MOSAIC VIRUS (STRAIN DAI)	35.18	115-402	466.419		Ī	Ī	Ī	Ī	Ī
- 1	ENZYMATIC POLYPROJETN	CALL DI OWER MOSAIC VIRUS (STRAIN BBC)	2	100.407	207		Ī	Ī	Ī	Ī	Ī
		CAULIFI. DWER MOSAIC VIRIIS (STRAIN MYBISS)	10.91	200	181.406	477-495		Ī	Ī	Ī	
S CANAS		CAULD LOWER MOSAIC VIRUS (SIRAIN STRASHOLING)	10.20	100-001			ĺ				
7	ENCINAL FULLIFIER	CANATION ETCHED MING VIRITS	161-116	4) Z J B							İ
	I ALIVE FOLTEROISIN	COMMELINA YELLOW MOTTLE VINUS	126-343	116.1311	1606-1632	- FEE					
TANK THE PARTY OF	POLYTICAL PROTEIN	EQUINC BY ELITARS ANENIA VIRUS (CLONE 1969)	37.5								
7	A. CALLINGTON	I GUINE INFE HEAV AND AND VINUS (C.COME, C.L.73)	93.436								Ī
											1

47.4004										Ì	
PILE WANT	PROTITION	VARIS	ARFAI	ABFA	T V J V V	77.10	7867	7 7 7 7			1
1	POL POLYPROTECH	EQUINT INFECTIOUS ANEMIA VIRUS (150) ATE WYCHING)	Se :	•		i	ī		ī	i	1
	POL POLYPROTEIN	FELINE EMINICENDUS VIAUS LCI.I	100	18.0%	!	:		: !	i	:	•
PPOL FIVE	POI. POLYPROTEIN	FELINE INTRINDIN FICH NCY VINIS (ISO) ATE PETALUNIA)	407.476	755.775				:	:		
. 1	POL POL YPROIEIN	JEI INE INDILINODE I ICII NEY VIRIIS (ISOLATE SAN DILGO)	407.436	35.115					i	1.	_
- 1	POL POLYFROIEIN	I EL IME INDICHOUGH ICHENCY VIAITS (ISOLATE TAIL)	8	665.470	22.22	98					:
- 1	POLINALIL POLITICAL	STORTIST MUSEUM VIRGINIA STORTIST									İ
יוסר סער	POL POLYPROTEIN F	GIBBON APE L FUKENIA VIRUS	9.0	8	1048.107						
	POL POLYPROTEIN	HUMAN T CELL LEIMENIA VIRUS TYPE I (STRAIN ATK)	20.00		İ	1.		İ		i	
	POL POLYPROTEIN	HUMAN T-CELL I FINE MIN VINIS TYPE I [CANHILLEAN ISOLATE)	330.346					İ	:		:
1	POL POLYPROTEIN	HIGHAN T CEI L'LEUNENIIA VIRUS TYPE II	609-617			+					-
PPOL 11V1A3	POL POLYPROTEIN	INMAN BORNODE PICIENCY VIRUS TYPE I (ARVISTS ISOLATE)	180 881		! :	1					
	POL POL YPROJEIN	INDIAN BOUNODEFICIENCY VIPILS TYPE I (BITIOTSOLATE)	93.660	872.899						Ī	
PPOL HVIBS	POL POLYPROTEIN	INTIMAN INDITINOPELICIENCY VIRUS TYPE I (BIIS ISOLATE)	81.09								1
	POL POLYPROTEIN	HUMAN INMINMODE FICIENCY VIRUS TYPE I (IIRU ISOLATI.)	100			i				i	!
	FOL POLYPROTEIN	HUMAN DIMINODELICIENCY VIRUS TYPE I (E) I ISOLA 11)	13.643	10 116		-	1	!	i i	:	
	POL POLYPROJESN	HUMAN MANIMODES ICIENCY VIRUS TYPE I (IINBZ ISOLATE)	100	<u>:</u>	-	-			İ	<u>;</u>	1
t	POL POLYPROTEIN	INMAN BARRIODE FICIENCY VIRUS 1YPE I (IRCSF ISOLATE)	151		1						
	POL POLYPROTEIN	HUNIAN BOMMODEFICIENCY VIRUS 1 YPE I (NIAL ISOLATE)	150 050		-						
- 1	POL POLYPROTEIN	MONINODEFICIENCY VIAUS TYPE I	861.890			-					
POL HVINS	POL POLYPROTEIN	ICIENCY VIRUS TYPE	14 C	110.01							
POL IVIND	POLYPROTEIN	ICIENCY VIRUS TYPE I	1	33.00							
	POLYPROIEIN	ENCY VIRUS TYPE I	100.000		į	:			İ		
10 1V	POL POLYPROTEIN	ICIENCY VIRUS TYPE I	613.640	833 838							-
- 1	POL POLYPROTEIN	CIENCY VINUS	_								!
POL IVIUS	POL POLYPROJETN	ICIENCY VIRUS 1 YPE I									-
- 1	POLYPROTEIN		2.5	910 618		-					
•	POL POLYPROIETY	≥!	2								
FOL. INTRE	POL POLYMOIEM	MANAM DEMINIONE RICENCY VIRIUS TYPE 7 (150) A 1E BEN)	3	8	i						
- 1	POL POL VACUEIN	THE MAN WASHINGDER RULE MOT VIRTUE 1 VINCE A 11501 A 18 CANTE	106.91)		1	-				;	
1	Mail Odd And Pod	INCLAN MACHINEST CIENTY CIRCLE TOPE 5 CICAL ATE STOCK			İ	1					į
1	POL POL VPROTEON	INDIAN DARBOOK HICKORY VIRIA 1975 3 HOU ATE CHANA.				Ī	İ			1	
	POL POLYPROTEIN	THAN BARNON FICTENCY VIBIG TYPE 7 150 A 15 MILL 7	-					Ī			i
PPOL HVJRO	POL POLYPROTEDI	III MAN BOADHORFICIENCY VIRIS TYPE 1 (150) A 1E BODI			-	1				İ	1
	POL POLYPROTEIN	INMAN DORAMODES ICIENCY VIRUS TYPE 3 (1501 ATE 56) 15Y)	159.386	106.711	-	ĺ				1	
1	POL POLYTRO1ETH	HUMAN DOMINONEFICIENCY VIRUS TYPE 2 (ISON ATE ST)	979.406	ī			Ī	Ī		İ	
	PUTATIVE FOL POLYPROTEIN	HANISTER INTRACISTERNAL A PARTICLE	25. 26. 28.	$\overline{}$	1 1						
1	PULATIVE POL POL IPROTEIN	MOUSE INTRACTS TENAL A-PARTICLE	0.0	٦	1	3	69.78				
- 1	PROBABLE FOL FOLTFROISIN	MOUSE IN MACIS LEWAL A FARINCE		i	2	÷					
	POL POL VPB 11 EDA	MANY CELL FOCUS FORMING AND AND ENTER VEHICLE MENT FELL	100	20.00	29 00		Ì				
1	POL POLYPROTEDY	AKR MARNE I EURENIA VIRIJS	_	271 100	İ		Ì				:
	PUL POLYPROTEIN	AKV MIRINE LEUKEMA VIRIIS		978.908	1004.1074	1001	İ	-	-	:	;
	POL POLYPROTEDY	CAS BR E MUNDIF LEINENIA VIRIS	1 3	8-15	_	į	-			i	:
1 1	POL POLYPROTEIN	FARNO WIRING LEUKENIA VIRUS (ISOLATE 57)	340.339	981-(00)	ie.	7011-900	Ì		Ī	Ì	-
700 KEVE	POL POLYPROTEDY	FREIND MURINE LEUR EMIA VIRUS (ISOLATE FB19)	140-159	100	ě	1048-1102				İ	
	POL POLYMOIE IN	FILEND MUTURE LEUKFINIA VIRUS (ISOLATE PVC.211)	146.359	993	6201 600	1011-910					1
TOTAL PROPERTY.	FOL POLYFOLDIN	ARK UNET AIUTURE I FURE MIA VIRUS	ž	2	_						!
	TO TO VEID IE STATE OF THE STAT	PADIATION MILITIAL ELIVERIA VIRUS	200		- 2: 8:	100	į				
1	POL POLYPRUIEIN	AFOUSE MANDIARY TIRIOR VIRIS (STRAIN BEE)	1			İ			İ		
1	POL POLYPROTEIN	SPAAN MASON-PILLER VIRUS	1		i	Ī	İ	Ī	!		
1	POL POLYPROTEIN	OVINE LEMITVIAUS ISTRAIN SA ORIVV)	201.00	EE 690	1981	1901.190	İ	Ī	-	-	!
1	POL POLYPROTEIN	ROUS SARCONG VIRUS (STRAIN PRAGUE C)	Γ		.		İ	Ī		İ	
PPOL RTBV	POLYMOTED	RICE TUNGRO BACILLIFORM VIALIS (RTBV)	19:915	1031-1013	İ			İ		İ	
PPOL RENT	POLYFROTEIN	RICE TIDNIRO BACII I ITORNÍ VIRLIS (ISOLATE PIIL IPPINES)	814-141	1016.1011			Ì				Ì
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		A 1 VI (1)									
FILT NAME	PROTEIN	VIIII		L	L						
100 SI V.	POL POLYPROTEIN	SOUTH FORMY STEELS AND THE STATE IS	185	VEC.	AREA 3	Г	ARFA 9	1000			
PPOL SFVJL	POL POLYPROJEIN	SOUTH FOARS COME STATE OF THE S	_	33.34	2	100 20		3	d d d	AREAL	3852
PPOL SIVAL	POL POL YPROJETN	SHAND THE STATE OF THE PARTY OF THE STRAIN LK IN		200	161.00	1					
PPOL SIVAO	POL POL VPENTERN	CHANGE THE THE PICTURE (ACMISSISOLATE)	۳			Т	1				
POL SVAI	POL POL VPROTEIN	SIGNATOR INTERPODER IN TENCY VIRIIS (AGAI) ISOLATE)	311.31	26.95		1					į
PROL SIVAT	POLICE CONTRACTOR OF THE POLICE CONTRACTOR OF	SIMILAN INTRIUMODE! ICIENCY VIRIIS (ISOLATE AGM/CLONE GRI. I)	ī			-				•	
1000	TOTAL TOTAL	SIMILAN INDALINOIS IT IEINCY VIRIS IT YO. I ISIN ATES	7			-					
	TOU TOUTHOUGH &	CHAPANZEE INDITIONS FICIENTY VINITE	Ť		-						•
3	POLYPROTISM I	SINIAN INTRIUNODE LICIENCY CORDS AND AND AND	7	_							İ
TO SWE	POL POLYPROTEIN	SIMILAN INCHES	620.65	86.9 B'16			-	:	1 -1	-	:
Prof. SIVAK	POR POR VPROVEIN	THE WALLE OF THE TOTAL OF THE PARTY (NINE A) THE PA	110.60	10.	:	:					
	TOTAL PROJECTION	STATION INCHINODEFICIENCY VIRUS (KOW ISON ATEN	107.51								
	TOUR POLYTROIEIN	SINITAN DORDWOOF IC IF NOT VIRING ASSAULT SELECTION			200					!	İ
Proc. SIVSP	POL POLYPROTER	CHAINE TO THE CONTRACT OF THE	363.330	17:19					İ	1	
POL SAGA	POR POR VERONIEM	PARTY INTO THE ICH. NCY VIRITS (FRUITCE) ISOLATE)	146.33	15	<u> </u>						!
	TOL TAKE FIN	SQUAREL MONKEY AFTROVINIS			:						
FFUL SMSAV	POL POLYMOTERN	2175	10.								:
PPOL SOCHV	ILAZ YMATIC POLVPROTEIN		- 0.20 - 0.20	12.		!	;				
11111	THE PROPERTY OF THE PARTY OF TH	SOTUEAN CHLOROLIC ACULUL VININ				_	_				
A 4		SIMOAN RETROVILLIE									
70.7			3.5			-		-		-	
PPOL VII VI		VISING CALLAND (STRAIN ISLA)	503	24.6	100	-			•		
200	- 1	VISNA LENTIVIRUS (STRAIN 1510) CLONE LVI-1KSII	15								
		VISNA LENTIVIALIS (STRAIN 1917/FI DUE 1917/FI				-					
LLL INCHAN	200	HANAN CYTORICAL DURING ASSESSMENT OF THE PROPERTY OF THE PROPE	10.50	999 159	166-116					-	
PP28 SCMVA		CHARLE COLOREST CONTROL ACTION OF THE PARTY AC	22	10.210	:	!	İ	İ	1	- !	!
PPP41 HSV60		TIOTING CT TOWER ALLONINGS (STRAIN AD169)	1		1	-					
AND INTERNA		HEAVES SUPLEX MRUS (TYPE 6 / STRAIN GS)	1	-	-						
	EN LOWER MATRIX PHOSPHOPROTEIN	IRMIAN CYTONEGAL OVINUS ISTRAIN ATTIKEN									
	H KD LOWER HATRIX PHOSPHOPROJEIN	MACAN CYTOREGAL OVINITE SEES SEES SEES SEES SEES SEES SEES S									
TY ION	THE UPPER MATERY PRINCESSORES	TOTAL OF THE CALL OF THE PARTY	101.133			1		:			
PPRO LOCITY	PROTE DE PROPE	HUMLAN CYTOMEGALOVIRUS (STRAIN AD169)	79.102		!	-					
	TAULUS PRO	MOUSE MANMARY TIMION VIRUS (STRAIN BRA)			-				İ		!
DATE OF THE PARTY	PROTEIN PRIN	MOUSE MANAGEN TIMENDE VIETTE SETTE ZE								i	-
PPRIL MOST VO	PROTECUPAN	MAN ME SAME STATE OF THE SAME OF THE SAME STATE	-			-			Ī		
PPRTA MONTYO	PROTECUPATS	TOTAL MANAGEMENT THE STRAIN GE	59.00		!						
PATH MSWIA	TEANCEDEVENCE PROPERTY AND AND AND	PLOSE PLANELLY TIMOR VIRIS (STRAIN CR)	9.0		1	-		İ			
PRACE OF ACC	S AND FINE	HARVEY MOUNE SARCONIA VIRUS	1	1							
		RASILEED RAT SARCOMA VIRUS			!						
1		CAMPOLETIS SOMORE NEIS VIBILE	2			-			İ	-	į
PRESE VACCV			÷.		-			Ī			
PREFA VARV	RIFALDICIN RECICE ALICE PROFESSION	STRAIN WED, AND ISTRAIN COFFINIAGEN	270.294	114.114			j	Ì			
PREV CIVAR			334.900							i	
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PRI EBV	RIBONUCL EOTIDE REDUCTASE	POLICIA BARB CIBIC COST	30.00	012.60	99.410		İ	Ì	i		
PRICH HONVA		BALL CHOICE (SIRVIN IIV).	393-113			Ì	Ì		İ		
PRIN IISVII			192.212	119.099	İ		1		j		
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Philes Elle		4 DUMAS)		27. 166							
		EPSTEIN-BAUR VIRUS (STRAIN BOS. IN	T		012.367					Ī	
FRIRZ HSVII					!		İ			i	İ
PACE INSVIK				235.292					-	<u> </u>	i
PRIDE HEVE			59:00	165.761	374.301	İ	İ	İ		-	į
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İ.		VACCINIA VIAUS (SIRAIN L'OPENIAGEN)	107.70		İ	1	Ì	1	1	1	
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INFLUENZA A VIRUS (STRAIN AMIAL LARIMEW YORK 673070)	14-262					 	<u> </u>	
INITUENZA A VIAUS (STRAIN AAGLACTIIS/10/10)	1979			<u> </u> -		<u> </u>	-	
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CASE HENDA A VIBIG OCTE AIN ANCINCIANT ABSOLUTE.	1 125	<u> </u>	<u> </u>	1		i	<u>.</u>	1
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INFLUENZA A VIRUS (STRAIM ASWINIVIENNESSEE/26/77)	16.762							
INGLUENZA B VIRIJS (STRAIN BJANN ARBONJING (COLD-ADAPTED))	03-222		_					
INFLIENZA B VIRUS (STRAIN BIANN AFRORITAS (WILD: TYPE)	1	!				i	i	İ
T CIBITO A DE DE CELLOS						-		1
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C VIRUS (STRAIN C/II/30)	ī	-	-			:	-	
A VIBITS (STRAIN ANN ARBONVECO)	14.537	_						
A A VIRUS (STRAIN ANUCKANOKRANIX) AND A VIRUS (STRAIN ANUCKANOKRANIX)	16.537			:	:		_	
A A VIRIIS (STRAIN AGOWL PLAGUE VIRUS/ROSTOCK/14)	15.55	:	:	 		:		i
A CONTRACTOR ACTOR ALABAT AND TOTAL		-	!			!	<u>:</u> :	-
		 		!		i	-	
A A VIRUS ISTRAIN AN QUIMEA UNUX INVATIGATI)	1	<u> </u> 					_	
A A VIRUS (STRAIN ALENINGRADVITUS)	14-557							
LA A VIRUS (STRAIN AS FNINGRAD/1184/17/57)	14.157						-	
DIAM DIRECTED BIAM POLYMERASE 131 ED POLYDONA DIRECTED BIAM POLYMERASE 131 ED					PADOVINUS STANDAR			The control of the

PCCLME	P11/71 919	ľ									
FILERAME	PROTEIN	Т				-					
	RNA DIRECTED RNA POLYMERASE STREET, PS	PAGE 15 COLUMN	14.1.6.J	ONLA?	ART.	12	ARIA	AHIAG	AUTAT		
PAUL IAPITE	NA DISCORDANCE OF ANY O	STATE OF THE PARTY	134-557		!	_	_	-			7
1	STATE STREET FOR THE RASE STREET PA	INTLIENZA A VIRUS ISTAAIN		İ	!	-				:	
1000	THE CHARLIED AND POLYMERASE SUBINITION	INFLIENZA A VIRIJS		-	:				į	!	1
500	MAY DAKE TED KNA POLYNIERASE SCIEDLING P.	NIVELS SUBIA Y YZUE IN	-	;	-	-					
A TATE	ANA DIRECTED ANA POLITICERASE SITTINITY	THE LIFTLE A VIETE								į.	İ
PRRP IAWE	PNA-DURECTED RNA POLYNERASE SIBINITES	TALLEY A AVELLEY	125.							-	
PIUM IAZIU	RNA DIRECTED BNA POLYNISHAGE COMPANIE 65		91.19	330.513		<u> </u>		-	-	1	-
PRES AZED	BYA DISCORD LANGE CONTRACTOR OF STREET	SULL OF WAY	\$14.557		!	-		1	!		!
	MINISTER STATEMANT STREET STREET FOR	INTUENZA A VIRIIS	135.53	1		!		1			
	MANA-DIRECTED RIVA POLYNIERASE SUBIRNIT PZ	INFLUENZA A VIRUS		-	:	-	1 :: 1				
TALES INCH	ANA-DIRECTED RNA POLYNERASE STRUMIT PT	DOGLIFT A VINITE							!		:
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PRRP2 DOBAD	BNA NORPHEN BUY BY WATER STATE OF THE STATE	Ť	23.54		ĺ		i	i		1	-
	MAN TO THE PART OF	INFLITENZA D VIAUS (SI	135	-		1					
X I	KINA-DIRECTED RNA POLYNŒRASE SUBUNIT PZ	PAFLUENZA B VIALIS AS									
PREPARED	RNA-DERECTED RNA POLYAGRACE CONTINIT BY	The state of the s	12.34								
PRUP I AANON	BNA. DARFOTEN BNA BOX VALES AND BUTTER	Ŧ	406-425			İ	!	:	:	!	
Parent Ivair	NA NECTED BY THE PASS SUBURILLY	INTLUENZA A VIRUS (STRAIN A/ANN ARBORVASO)	36.51	\$43.460		1			Ī		
	THE WAS TO THE MASE STREINING P.)				-	1	İ				
	MMA.DIRECTED RIVA POL YMERASE SUBUNIT PI	_				_:					:
TAUS LANGE	AMA-DIRECTED RMA POLYMERASE SUBLINIT PI	INFLIFTA A VIBIL OF THE	Ī	241.360		•					
PRES LAST	RNA-DIRECTED BNA POR VASTA OF TIME TALL BY	THE PERSON AND ADDRESS OF THE PERSON AND ADD		242 567							
PRUITAGE	ANA PARKTER BAY SOLVE THE SAFETY OF THE SAFE	INTEREST A VIAUS (STRAIN	219-234	342.560	İ					İ	
	AND DIRECTION AND THE RANGE SUBURILLY	INTLUENZA A VIRUS (STRAIN	Τ	101.160		1		1	-		
	MAN-DIMECTED KINA POLYNCHASE SUBLINIT P)	INFLUENZA A VIRUS (SIRAIN A/GULLASTRAKITAN/2)7/44	ī			•					
WILLIAM WAS	MAA DIRECTED RNA POLYACIACIE SUBLINIT PJ	PALLENZA A VIBILGIGIA A A COMPANIA COLOR	7	2007-700							
	ANA DIRECTED RNA POLYNGRAGE LIMIDAIT PI	DELIENS A MALIE STATE OF THE PARTY OF THE PA	10.4	947-360						-	!
PART MOR	BAA DISECTED BUY BOX IN SECTIO	THE TOTAL OF THE STRAIN AR QUINE, ONDOWISING	219-234	\$42.560					i	1	
	MILETON ANA POLITICIANE SUBLIMITY	INTLUENZA A VIRUS (STRAIN ACQUITE/FRACTIT/1/36)		5							
	MA DIRECTED ANA POLTAGRASE SUBUNIT P.	INFLUENZA A VIRUS (STRAIN AKIEV/1979)				-					
TAK'S MAKON	ANA-DIRECTED RNA POL YMERASE SUBLIMIT PJ	POLUENZA A VIBING COM AN AN AND EAGAING	٦			-					
	ANA DIRECTED ANA POR YAGRAGE COMPANY ST	PAGE INCOME A STATE OF THE PAGE AND A CONTROL OF THE PAGE AS A STATE OF THE PAGE AND A CONTROL O	Ī	943.560			Ì		İ		
	RNA DIRECTED BUY POR VACE ALE STATES	MY LUCKEN A VIRUS (STRAIN AR ENINGRADY)	Г	13:38	Ī	1		İ	Ī	i	
	BMA DIRECTED BMA BOX SOLES STREET	IN LUENZA A VIRUS (STRAIN AL ENINGRATYI) 4/17/57)	ī	\$47.560							
13	AND DESCRIPTION OF THE PASS SUBDING PO	INTLUENZA A VIRUS (STRAIN ALENINGRADY) 34/47/57)	Τ	- 57	Ì	1	İ				
	ANA-WARE LIED WAS TOLYNG RASE SIZE IN IN P.	INTUENZA A VIRUS (STRAIN AAIA) LARIMEN VORKATIANI	T				j				
	RMA-DIRECTED RMA POLYMERASE SUBIRNII PI		Т		1					Ī	
	ANA-DIRECTED ANA POLYMERASE SUBUMIT PI	INTLUENZA A VIBILICACIDADA ANTIMANAS	Ī	785.20		~				İ	-
PRINT IAPUE	ANA DIRECTED RNA POLYNERASE SIMINIT PI			200		İ		İ	Ī		i
0	ANA DIRECTED ANA POLYNGRASE SIBILINII PI	Maria Maria Anna Maria M		169.415	347.560	İ		İ		j	İ
	ANA DURECTED THA POR PAREA CE CITATION DE	-	Г	1360	1	ĺ		Ì	1	i	!
PRINT LASE	RNA. DIRECTED BNA BOX VAGE AND COMPANY		319.234	24.560	İ		İ			İ	
-	NA DIRECTED BAY BY STORAGE STREET	INTEREST A VIRIS (STRAIN ASINGAPORE/1/57)	219.214	\$47.560		Ì	İ	İ			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NAME OF THE PARTY	-	Ī	143.66	Ī	1	j				
	MAN DIRECTED RIVA POLYNE RASE SUBINITY PI		T							<u> </u>	
	WAS DIRECTED AND POLITICE RASE SUBINITY P.	Т	ī								
	WA DUCK IED RINA FOLTIGRASE SUBLINIT PI	ī	Ī					•			
W	THA DIRECTED RINA POLYNGRASE SUBUNIT PI	Ť	1	2						Ī	
PREVIOUS INTEREST	RNA-DIRECTED RNA POLYMERASE SITBLINIT PI	Ī.	-1	2.360						İ	Ī
OVER CANA	UNA-DIRECTED AWA POLYMERASE SUBLIMIT PI	_[Ī	33.361				İ	<u> </u>	! !	!
MAN DACE	ANA DIRECTED ANA POLYMERASE SIMUMIT PI	POLUENZA C VIRIUS ISTRAIN CAPRI INCIDEN	1	2			-	İ	İ	İ	ĺ
	INA DIRECTED ANA POLYNERASE SUBLIMIT PS	7		332-571		İ		İ	İ	İ	
ī	ANA DOMECTED RNA POL SUBLIMIT P.		72.96	192.571		İ		İ	İ	1	-
_	ANA DIRECTED RNA POR YNG DAGE		19:101	_		İ			Ì	1	
7	NA. DIRECTED BNA POR VARBAGE		20.50	410-436	10.83			-	÷	_	
PRAPA CVATIL	BAA DIRECTED BUT BOX WATER SE	MUNINE HEPATITIS VIRUS (STRADA DEFECTIVE JIM)	L	T	ī				\$ 12.5	1974-1992	1517-1550
+	CALCULATION TO THE KASE		Ť		-		7	-	_	_	
734 8488			Ī,	_			-1	=	763-1306 2	2165-2192	2117-2156
1		-	7		100	- :	405-3425	1433.3954		<u> </u>	
THE CAMAS			ī		=	11.1154					
TAMES CANDI		•		107.70	2:	_			<u>:</u>	<u>:</u> 	1
PRUP CVPFS		PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIBLIS STRAIL	ī		_	- I	696-2721	<u> </u> 	İ	÷ İ	!
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FILE MAME	-	Vinnie			-						
PRUL BUNYW	⇌	BINAAMUEE	C. LO.	7	V V V V	APLAX	AMIA			4 80 1	0 7 127
PRUPL EBOY	÷	I'MOLA VIBILE	8	2	50.46.5	100		141.16	1119.11	104.9.1936	7 and 100.7
15	BWA POLYNGRAGE		-		-		_				!
	THE PARTY OF THE P	INVESTMENT OF THE PROPERTY OF	151-160	11.19	110.467	1361.1313	2011-1005		i i		!
PRES IGNOVA	BNA POLYNCHACE BETA SIGNIAL	HIMMAN RESTRAIGHT STINCTIME VIRUS	•				_				<i> </i>
	PAR DIRECTED BAY POLYTICE AND THE PARTY OF T	HUMAN RESTINATORY STACTIAL VIRUS (STRAIN A2)	=	100	1675.1647	1633.1633	1910-1016	10. B.O.			1
		WARBORG VIRUS IS I WAIR MIUSOR []	2	\$			100	106.569	911.00	1043-1083	1410-1416
PRUM MABUP	ANA DIRECTED LINA FOLVAIR RASE	MANAGEMENT OF THE PROPERTY OF		200	20.00						
		The state of the s	2	_	_	-	\$46.169	¥.	1M2.10.7		16.71.16.26
PREM LEASE	BMA PON VACE ACE BETA CONTINUE		Ē		1040-3013	2011-1074	3333.3346	!	: !	:	:
PREM MANON	INA POLYMERACE DETA CIPEINA	MCASCES VIACIO (SI KAIN EIINI) (N.)	22.5	617.632	_	160-1715	_	1920-1940	1038-1061		
	NAME OF TAXABLE PARTY AND THE PARTY OF TAXABLE PARTY OF T	MUMPS VINUS (STRAIN MIYALIARA VACCINE)	*	10.115	-	82.94	-	1112.1153	-	136.314	
	MAN POLITICAL DE LA SUBORIL	MEWCASTLE DISEASE VIRUS (STRAIN BEALIDETTE CAS)	704.724	1571-1592	96 7. 1974	1040, 7063	-		_		i
TARK NOT	MAN POLYMERASE BETA SIMUNIT	HUMAN PARAING LIENZA I VIRUS (STRAIN TOSHIDA)	20.00	741.70	Ť	9					
	RMA POLYMERASE BETA SUBUNIT	HOMAN PARAING LLIENZA I VIRUS (STRAIN NISI 43885)		13	1				_		
_	RNA-DIRECTED RNA POLYNIERASE	PUDMALA VIRUS (STRAIN LIAI LINS III)					191	1001	2		
	ANA POLYNERASE BETA SUBUNIT	RABIES WRITE COR AND PUT				_	2016-2110				
PRINT RABVS	ANA POLYMERASE BETA SIRINIT		2 2 2	200		1446.1461	1403-1517				İ
PRINT RDV	KNA DIRECTED RNA POR YAJFRA (6	The Parket View of the Parket Vi	200.2	35.75		1466-1461	1441.1311	194-1761			
PREP. BVEVE	BNA DIRECTED BUA POLYMERANE		10.27	111.560	400 40						
No. of Lines	BLA BOX SOCIAL BOOK STREET	ALL VALLET PEVER VIRIS (STRAIN ZILSOLAIIZ)	383.609	2009-2015	_						
1	SAN DO SAN	SEMBAL VILUS (STRAIN Z / HOST MUTANTS)	3	104-120	196.218	199.00	900.691	1405.1430	1144.1864	2017.001	
1	MAN FOLLT MEANS BEIN BUBURIL	SEMDAL VIRUS (STRAIN ENIVERS)	=	189 799	105 220	1725-1340	1664-1614	1927.1948			
יייייייייייייייייייייייייייייייייייייי	ICHA FOLTRIERASE BETA SUBUNIT	SENDAJ VIRUS (STRAIN Z)	199	104 130		144.141	114. and	15			
/ KAY	KNA-DIRECTED RNA POLYNGRASE	SEOUL VIRUS (STRAIN 60.10)	3:18	77.15	194.410	106.4	100		-		
WALL SYSWA	ANA POLYNERASE BETA SUBUMIT	SINGAN VIRUS 5 (SI RAIN 21004 WR)	17	10.10	900.194						
PRR. STAV	AWA POLYNGERASE BETA SUBUNIT	SONCHUS YELLOW MET VIRUS				-::	2	338-1380	2117-2113		
PARM, TSWVB	AWA DERECTED RWA POLYNGRASE	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CENSITIONAL)		417			107	100	484-1510	1776-1792	
ŀ	RNA POLYNERASE	UDKUMEM VIRLIS				2	70.7.8.407				
ī	RNA POLYMERASE BETA SUBINIS	VESCHI AB 410MA 11714 VIBILIA 1888 OF US ASSESSED.		76.00		2.0.2	7060-2081				
PRINT VIVIO	ANA POLYNERASE BETA SUBUNIT	VESICIA AR GIONATINE CIRINA SERBOTANA MANUELLA SERVICIA S	*			1936-1917	2080-2063			İ	
Γ	ANA POLYMERASE BETA SUBLINIT	VESKUR AR GEOLASTER VISITE ASTRACTOR AND STATE OF THE VIEW OF THE VIEW AND STATE OF THE			1956-1912	2080-2101					
7	RMA-DIRECTED RMA POLYMERASE	APPLE CHE CHOTHER FARE CONTINUES AND LUCKY									
PRING BWYVE	PUTATIVE RNA-DORECTED RNA POR	BERT WESTERN VET DAWN WINDS STORY	20.27	1036-1054	1132 1155	1718-1101					
_	PUTATIVE BNA DOJECTED BNA POL	MARIEY VEHICLE DEVANE CONTROL CONTROL	24.3%			-					
PAUS BYDY	PUTATIVE RNA DEFECTED ENA POL	MARI BY VELLOW DAYAR CARIES (COLATE PLAY 1)	159.366	=	503-513						
-	PITATIVE BNA. DIRECTED BNA POP	TOTAL STATE	20.5	716	505.512						
1	PROBABLE BNA DORECTED RNA PON	CARLATION MATERIAL VINOS (ISOLATE P.PAV)	136-186	91.416	503.512						
7	PITATIVE BMA DIRECTED BMA BOX		4.30	93-103		1					
Т	PROBABILITY THE PROPERTY OF THE PARK POR	CICLOMBER WEER MULITLE MIDSAIC VIRUS (WATERVIELON STRAIN	44).466	174.501		120.151				Ī	
Ī	PROBABLE BNA DORFOTFD BNA POL	Ī	277-300	3.	470.494						İ
Ļ	MITATIVE BMA. NIBECTED BUA BOX		=	345.371	470.494						
1	BLA BOX VACE ACE		221.218		ī		ĺ	Ī			1
Ť.	PLA POR VASEA CE	LIMOTOCITIC CHURIOMENINGITIS VIRUS (STRAIN ARXISTRONG)	15-53	101.611	639.682	100	34-138	130.1365	1077.3000	Ī	
Т	PACIFIC IN THE PACIFIC	LI POTICE LIKINGOMENINGILIS VIRUS (STAATN WE)	33.52				÷				Ī
L	DAA DARCHED BAA BOLVACEARE	MAGGE CALCHOLIC MOTILE VIRUS	79	101.127	173.590	Ī	İ	Ī		Ì	
T	MICATIVE BUT DOSCIED BUT BUT		144-161	16.36	431.456	338-334	İ			İ	
ī.	MATANTA BUT DESCRIPTION AND BUT	PUINTULEA/ROLL VIRUS (STRAIN 1)	331-158	276 600				1			
Т	MAINTE MAY DIRECTED MAY FOL	POINTO LEAROLL VIRUS (STRAIN WAGENINGLN)	381-186	276.600				Ì	Ī		-
Т.	MINITER MANDELLIED MAN POL		375.395	101.126	1069.1096	691.160	Ī	İ	Ī	Ì	
7	TOTALIVE MAY DUCK LED MAY FOL		178.300				Ī			Ì	
÷	ANA-DIRECTED RINA POLYNERASE	AEOVIAUS (TYPE 1/STRAIN DIVIONES)	101-176			Ī		į			1
⇁	MAN DIRECTED KINA POLTABLASE	MEOVILUS (TYPE 1/STRAIN LANG)	2			İ	-	-			
	ANA-DIRECTED RAY POL SUBURIL VII		95	107.760	198	906.021	- No. 150	101	-	-	-
	MA-DORECTED MA FOL SUBLIMITY		33:136	307.769	T	ī	ï			İ	
_	NA PRECIED FOR FOL SUBURIL VP	PORCINE ROTAVIRUS (GROUP CASTRAIN COWDEN)	ī	1	111 111	ī	1	- 600.11	Ī	İ	
Т	MA. DIRECTED BAY DO: SUBJECT UP:			:	i	ī	ī		947.96.7	400 400	-
ī	PROBABILITY OF THE PARTY OF THE	411)		:	198 351	174.00	190 176	1017.1046	1	!	;
PLENO TACY	RWA POLYMERASE	TACABIDE CIPIES		13.141		100.101	П		23.046	1	1
1			9	=	1311.1301	676.1402 3	3014-2046		-	İ	
											1

PCCCME	PROTEIN	AR Vienes (N. B									
THEMAK	PROTEIN	VIRUS				+					ſ
VENT OF	MITATIVE RNA-DIRECTED RNA POL	TOMATO BUSHY STUNT VIRUS (STRAIN CHERRY)	200	3		77	A STATE	1225	ANIA	10110	AREAS
	_	IURMIP CRIMILE VIRUS	31.58	14:10		-					
A PROPERTY OF THE PARTY OF THE		TOBACCO MILD GREEN MOSAIC VIRUS (TNIV STRAIN UZ)	20.00	8		1					
PRATO TAVE	PUTATIVE AND DIRECTED AND POL	FOBACCO MOSAIC VIRUS (VALGARE)	186 724	1000	1387-1610	-					
PARTO TANTO		I UBACCO MOSAIC VIRUS (STRAIN KONEAN)	700.714	1090-1105		Ī				Ī	
PRILITO THVA	-	TOBACCO MOSAIL VIEUS (STILAIN TONIATOL)	700-724	1070-1105	131.113	1317.1610			1	Ī	1
PRING TAVE		TINDACCO MECADISIS VINIS SERVINES						-			
PRUT CHAV	RNA POLYMERASE ALPINA SUBUNIT	CHANDIMEN VIETE CENTER LANGER	45								
PREST MARTI	ANA POLYMERASE ALPHA SUBUNIT	MIROS VIBIR (CIBARA CALL)							!	-	
PARP MAPE	ANA FOLYMERASE ALPIGA SUBLINIT	MIRAS VIRIL SCIENCE STATES	11:338							Ì	
ΙΣ.	ANA POLYNGAASE ALPHA SUBUNIT	MARCE VIEWS VIEWS	212.239			L				Ī	
•	ANA POLYMERASE ALPHA SIMINIT	MEMORANDE DISEASE CIRIL STRAIN VALLINE	112-239							Ì	
PLUT NOVE	INA POLYMERASE AL PILA CIPILINIT	MEMORALE MISSAGE VIRIS (STRAIN AUSTRALIA. VICTORIA/1)	194-176								
THE PARTY	RNA POLYNOBASE AI PAIA CIMINALE	TEMPORALE INSCAND. VIRUS (STRAIN HEALIN), I II. ('NA')	156-176		!	-	: :	•	:		
ł	ANA POLYNOBASE AL PILA SI MIDALI	INCREMENTATION OF THE PARTY OF	216-343			1.			Ī	Ī	
PARTY PINHA	ANA POLYMERASE AL MIA SIMINIT	HADING TOWN TO THE TOWN TO SHIRT I DO SHIP I D	216-343			-				Ì	İ
PROPERTY.	RHA POLYMERASE ALPHA SUBURIT	HUMAN PARAINT I FINZA AR VIRUS (STRAIN TOXILLA)	230.247							I	
PRILITY PIRKY	ANA POLYNERASE ALPIIA SUBUNIS	PAR VALIK	e e							İ	
PARP BABYA	ANA POLYNERASE ALPHA SUBLINIT	PARIS VIRILIA IN A VOIL	134-161			-				İ	
PRICE EXEVE	ANA POLYMERASE ALPHA SUBURGE	GABIE VILLA CERAN COC.	7			·				İ	Ī
PARP EASVE	RICH POLYMERASE ALPHA SUBUNIT	MABIES VIBILS (STRAIN FRA) AND 16 PAIN BALL	2							İ	Ī
THE IMA	AMA FOLTMERASE ALPHA SUBLIMIT	AABIES VIAUS (SIRAIN PV)				-					
TWY WAY	RMA POLYMERASE ALPHA SUBUMIT	PABLES WINUS (STRAIN SAD BIT)	Ī								
S AME	ANA POLYMERASE ALPHA SUBINIS	SUMIAN VIRUS S (STRAIN W.)				-					
200	RNA POLYNGRASE ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS ISERDITPE NEW JERSEY / STRAIN OF			Ī	1					
TANK AND	STOR MOTEIN	AFRICAM SWINE FEVER VIRUS (STRAIN BATIV)			1	1					
	SUPEROXIDE DISMUTASE LIKE PROTEIN	VACCINGA VIRUS (STRAIN COPENTAGEN)	19.40		Ī	1					
MOS VAN	CONTROVER DESMONDER LIKE THOUGH	VACCIPILA VIRUS (STRAIN WA)	19-40		Ì		T			1	
	SHE BOOM	VAUOLA VIRUS	9.40		İ	1				Ì	
VAID DIV	CHIE ACCION PRECINCAL	AMSACIA MUDICE ENTORIO POXVIRUS	Γ	637.646		-	T		Ī	1	
PSPII MYXVI	SELVONI	CHOMS TOWEURA BIENNIS ENTOMOPOXVIRUS	197.701		Ī					1	
	SWIEA PROTEIN	MI AUMA VIRUS (STRAIN LAUSARINE)	08-19	100				T			
т	CARGE I AMTIGEN	BIDGESIGAL FEDGING NICE AND TH	(1.6)			Ī			Ī	İ	
П	LAIGE TANTIGEN		٦							İ	
-	LANCE I ANTIGEN		707-776								
	LANGE T AMTIGEN	BOVINE POLYDMAVIRUS	Τ								
	ANGE I ANIMEN	HAMSTER POLYONIA VIRUS	T	3.5	Ì	1	Ì				
Τ	LANCE I ANI ICEN		Ī	100	Ì	1					
TALA POWE	Alog Tannon	LTMORITOTIC POLYGMAVIRUS	Г	16.30	İ	T	T		Ì		
1	LANGE T ANTIGEN		165-965				Ī	T	1	T	1
PTALA POWIC	LAKGE TANTIGEN	MOUSE POLYDMA VIRUS (STRAIN CRAWLORD STATES	374.389						İ	İ	
¥	LAIGE I ANTIGEN		Т	1					İ		
_	LANGE 1 AMIGEN	T	111.000		2	Ì					
-	MIDOLE I ANTIGEN	HAMSTER POLYOMAVIRUS	Τ		İ	1	1				
TASH POWE	SWALL I ANTIGEN			İ	Ì	1	1	1			
	SHALL TANTIGEN			İ	Ì	1	1	Ī			
THE PROPERTY OF	77.	Γ	T		1		1	1			
	TRANS-ACTIVATING TRANS REG PROTEIN	PROSIS VIRUS	Ē		\dagger	T	†	Ť	1	1	
Т	TRANCACTIVATING THANK SECTION		411-436			T	1	Ī			
Т	INANE ACTIVATION TRANS REGINDER	BOWNE DOWNOR FULL NOT THE STATE OF THE DATE OF THE DATE OF THE DATE OF THE STATE OF	119-414			T	Ť	T	T	†	
FTAT MY2?	TRAMS-ACTIVATING TRAMS REG PROTEIN		44.39				T	T	T	\dagger	
П	TRANS-ACTIVATING TRANS REG PROTEIN	Т	64.59	1				Ī	T	t	Ī
П	TRANS-ACTIVATING TRANS REG PROTEIN	HUMAN T-CELL LEUKENTA VIRUS TYPE I CARINEAN ICH AFEN		1	1				T	\dagger	Ť
		1	717.74	1	1						Ī

FILE RAME PLAT MYLUS FIEGE HEVED	KITIOV2	SHEIA									
PIECE HISTORY		MINISTER BANDONS STREET, VIOLET VOE 1/810 A IN THE AND		ABEA!	48141	ARTAK	AMEA 3	ANTAS	ARKAI	49FA	9K146
PTECP MAYE	TALL PROPERTY DETA CHAN PARTIES	THE THE PART CHAIR	2			1					
201911	+	FORMS TO REP SYREIS TYPE I STRAIN ARAP.	101.111			1					
5	TICHEM PROTEIN	ECHINE LEGALE SYRUS TYPE I (STRAIN KENTICKY A)	101.116							-	
PTECU EBY	•	EPSTEIN-BARR VIRUS (STRAIN BOS.D)	3	11:52	14:135	1052-1075	1194-1220	1469-1494	1866.1193	1001	1162.1134
PTEGU HOAVA	I PROBABLE LARGE TECHNENT PROTEIN	INDIAN CYTOMEGAL DVIRUS (STRAIN AD169)	101.151	64.48	1061-1077	307.132	1331.1345	4.0.1444	200	10(7,10)4	
PREGU HISVII	LANCE TECHNEYI PROTEIN	HEAPES SOMEEX VIQUS (TYPE 1/STRAIN 17)	13:27	53.64	1711.1119					-	
PTEOU HSV60	LANCE TECHNOSTY PROTEIN	HERPES SWALEX VIÂUS (TYPE 6/STRAIN GS)	131-153	305.365	35.5	1037-1043	1308-1338	1563-1579			
PTECU HISNED	LARCE TECHNENT PROTEIN	EQUINE HERPESVIAUS TYPE I (STRAIN ARAP)	937-10	31.32	1077-1099	1107-1111		1961-1961	226)-1265		
PTEGU HSVSA	PROBABLE LARGE TECUMENT PROTEIN	HERPESVIRUS SAIMIN (STRAIN II)	(67.48)	114.137	1001-686	HIII-HIM	1135-1174	1177.1193	1501-133	1607-1622	1896.1915
			1411-1439			-					
MEGU VAVO	LANGE TEGUNENT PROTEIN	VANCELLA-20STER VIRUS (STRAIN DUMAS)	133.456	494.511	-	101-123	195-920	1013-1034	1360-1376	1632-1637	1380.180
	7		1004-1674	200	3684-3711						
VIEW ADESS	╗	INDIANA ADEMOVIAUS TYPE 1	43.80	391-616							
PTERM ADEDS	DNA TERMONAL PROTEIN	INDIAN ADENOVIAUS TYPE 5	6)-80	393-616							
TERM ADES!	DNA TERMONAL PROTEIN	HUMAN ADEMOVIRUS TYPE !	63.60	\$40.000		-					
MENA ADELS	DHA TERMONAL PROTEIN	HUBAAN ADEMOVIRUS TYPE 12	£43	334-350	546-569						
PTOP3 ASTEP	DHA TOPOISOACEKASE II	AF FUCAN SWINE FEVER VIRUS (STRAIN BATIV)	119-146	100-919		-					
PTOP2 AUTO	Ħ	AIRICAN SWINE FEVER VIRUS (ISOLATE MALAWILIL TOVI)	119.146	105.706		-					
PTRIN HONYA		HUPLAN CYTOMEGALOVIAUS (STRAM AD169)	139-165			-					
PTRIL AVOLE		AVIAM RETICULOEMDOTICIOSIS VIRUS	56.74								
TYSY VZVD		VANCELLA-20STER VIRUS (STRAIN DUMAS)	11.29								
PUISK MSVeU		HEAPES SOULEX VIRUS (TYPE 6 / STRAIN UGANDA-1101)	400-415								
PUZL HSV6U	Т	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UCANDA-1182)	ŝ								
PUDPE NEVAC	ľ	AUTOCAAPILA CALIFORNICA MUCLEAR POLYIII DROSIS VIRUS	452.433								
PULBS HOMYA		INDIAN CYTOMEGALOVIRUS (STRAIN ADIAS)	2.5						!	:	!
PLEES HOWA		HUMAN CYTOMEGALOVIRUS (STRAIN ADTES)	1:1			-			!	;	-
PULOS EBV	VINOW PROTEIN BBIFF!	EPSTEIN-BAUR VIRUS (STRAIN B15-6)	153.244								
PULBE HCD/VA	HYPOTHETICAL PROTEIN UL6	HUMAN CYTOMEGALONTRUS (STRAM AD169)	101.704								
PLEAS HIS VII	VINION PROTEIN ULA	HERPES SMOLEX VIAUS (TYPE 1 / STRAIN 17)	404.479								
PLOS MSVEB	7	EQUING HELPESVIRUS TYPE I (STRAIN ABAP)	437-461								
PUL OF HIS VSA	VINON GENE AL PROTEIN	HENESVAUS SAMIRU (STRAIN !!)	9								
	7	ESTERNE AND THAIN BY THE	27-10		Ĩ						
1000	PROTEIN ALTON	THE PACE CHAPTER VINITE ACTOR 1 (CORP.)	100	10.70							
THE PARTY OF THE PARTY.	CALE (1 SOCHED)	COMME DESCRIPTION 1995 1 COMME TO 1995	200								
100.00	CALLE AS DECISION	LACAR MACHINES AND THE CONTRACTOR OF THE CONTRAC									
	Carle of Partition	1377437									
PAT OF LITTLE	PHOTEINIBE			77.72							
MEN WWS	CELO US PROTEIN										
HAR SEAL	CANCIN OF REM ICATION BOODING PROTEIN			20.747							
PLEAS MAYES	ORIGINAL DEPLICATION BRODING PROTEDI		Τ	11.74.17							
PULM VZVD	7		Т	41.100	414.40						
FULL HOWA	Т	HUGGAN CYTOMEDALOVIRUS (STRAIN AD169)	111.301								
PULIT HOWA	HYPOTHETICAL PROTEIN UL 13	HENGALM CYTOMEGALOVIRUS (STRAIN AD109)	19 65				T				
PULIA HONYA	_		200.799								
PULIS MEVII	HYPOTHETICAL ULIA PROTEIN		9178								
PULL HISVED	INTOTACTICAL GENE 48 PROTEIN		100								
ratio HSVII	PROTEIN UE 16		17.71								
PULIS HISVES	GENE AI PROTEDY	ATN AB4P)	26-43	911.10	174.330					Ī	
PULIS HSVSA	GENE 33 PROTEIN		19-13	274-265							
PULIS YZYD	GENE 44 PROTEIN	VAUCELLA-ZOSTER VIRUS (STRAIN DUNIAS)	65-10	117.333							
1	(New York of the Control of the Cont	CENTRIN-BACK VIXUS (STRAIN 895-0)	11.3								
THE LIEVIL	INCOME TO THE PROPERTY OF IT		2								
PUL IS ISVEA	CONE DI PROTEIN		36.18	011			T				
AVACUATION A	7	DV ADIME									
	7						1]		

	7										
THE PARTY OF	CAOTZIN	VIRILA VIRILA		L							
10.16	Т	PSEUDORABES VIBILS (STRAINS)	ABEAI	AREA	ARTAS	1	Т	П	П		Γ
The second second	Т	VAUCEL A. ZOSTER VIBILIZATE EL CALICA	24.76	L			7	ARIAA	AREA! AR	AREA! A!	AREAS
	7	JROKAN CYTOKE GALOGARIE 44	101-134							,	Ī
	7	INTEREST OF THE CALL OF INCH A DIGE.	91:16	L		-					Ī
HIAN HEAD		THE PARTY OF THE PARTY IN	1						-	-	
TOTAL HINES		THE PERMITTINGEN						-		ł	1
אנא ורחו	Г	EQUINE HEAVES VINUS TIPE I (STRAIN ABAP)		90.16					1	1	
PULLY HOWA	INPOTATION PROFESSIONS	VANCELLA ZOSTE A VIRUS (STRAIN DURAS)			179.403	413.437		\mid		1	·
7U.24 EDV	7	MIMAN CYTONEGAL OVIRUS (STRAIN ADISS)	1	<u>8</u>				1	1	-	1
PULZ4 HOLVA	۲	EPSTEIN-BARK VIRUS (STRAIN BOS.A)						1			
PUR 24 HEVEL	T	PICECH CYTOMEGA! OVIETIE COM	134-155					1			Ī
7 H 1/4 H	TAU EM ULJA	HEAPES SINCE BY VIBILE PUBL.	204-222			1				<u> </u>	Ī
	7	INTEGRAL OF THE PROPERTY IN								1	
AND SERVE	7	THE STATE OF THE OFFICE STATES (STATES THORNE VIEW	Ī	-		-		-		I	1
TULIS HIS VII	_	INDIANA CYTOMEGALOVIAUS (STRATH AD169)	1				İ		1	1	-
PULJS HSVED	г	HERPES STAPLEX VIAUS (TYPE I / STRAIN II)	B			1	Ì	1		1	
Man of Merce	Carlotte and Carlotte	COCKE STATES OF THE PARTY OF TH	€.00	İ							
ACACH IN BUILD	VINCH GENE 19 PROTEIN	TERPECKING CALANTER AND AND THE PERSON AND THE PERS	- TO	110.143		~	-	_	<u>:</u>	:	
1	7	Marchine Scientific [1]	Ī					_	_		-
MAN HOWA	_	THE CHOOS LAN THEOTRACTETTIS VIAUS (STRAIN THORNE VIETA	T						1	1	
PLR 29 HCL/VA	-	FRIMAN CYTOMEGALOVINUS (STRAIN ADIAN)	Т	316-336		-			+		-
PLE 20 HOLVA	-	HUMAN CYTOMEGALOVIRUS ISTRAIN ARIAN	77.77	486.307				+	1		
	т	MANAN CYTOMEGAL OVIRIJE STRAIN A DIEGO	239-366			<u> </u>	1				
TOTAL STATE	_	EPSTEIN BARR VIRIX 4518 A 10 12 12	£.33		Ì	†				L	_
1	-	MINISTER CYTOSCOCIO	20.50		-	-					1
TACK TO		LESSES STEERING (STICKIN AD169)	1000						!	<u> </u> -	1
	OEME 29 PROTEIN	TEST CO SHOULEN VIRUS (TYPE I / STRAIN IT)		700-701		-		I	T	1	1
PULJI HSVSA	GENE 49 PROPEU	EXCIPIT HERES VIXUS TYPE I (STRAIN ABIP)	7			-		1	1		1
PULJI VZVD	GENE 19 MOTEN	HERPES WAUS SADARU (STRAIN III)	7	288.309	-	-	\mid	1			
PUL 33 PRVII	PROBABLE	VAUCELLA-TOSTEA VIRUS (STRAIN FIRES		163.130			1				Ī
PLE 13 HOUSE	THE PROPERTY OF THE PARTY OF TH	MEAPES SPAPIER VIBILS TIVE 1.75	117:138	385.316		1	1			L	Ī
	POWER ENVELOPE OF YCOPROTEIN 300	FOUNDS HER BESTURE CONT. TO STRAIN 17)	9:6	166.500	\dagger	1			L		Ī
	PRUBABLE MAJOR ENV GLYCOPROTEIN 26	VARIOUS A Proper Craise 12 E. H. Allah Allah)	8		1	1				1	Ī
VALUE OF THE PARTY	WATCHEST COUPLED REC HOMOLOGICALIS	MALAN CATOLOGY (SIRAIN DURAS)	33.55					L			T
V.	HYPOTHETICAL PROTEIN ULIA	IN THE STATE OF THE STRAIN AD LESS	15.18	1	1		L			1	1
	VIBLON PROTEIN U.S.4	LEASE OF THE CALONICOS (STRADIA AD 169)	T.						1	1	7
	KOTEN	THE SECULE YAUS (TYPE I / STEATH IS)	T				-	I	1		7
		EQUINE MERLES VIRUS TYPE I (STAKIN ABAP)				-		1	1		_
		HEAVES VALUE (STRAIN (1)		`		-	-	1			ī
-	27.0	VAUCELLA LOSTER VIRUS (STRAIN DAINAGE	107:107		-		1	1			
PULJE HONVA		HUPLAN CYTOMEGALOVINUS ISTRAIN ANIAM	204.766				1				1
-		HUMAN CYTOMEGAL OVIRUS (STRAIN ADJAC)		316-326	100		1			L	Ī
		EPSTEIN-BARR VIRING 1512 A IN BOLD AL	145-161	107-410		1					
T		PEAPES SURTEX VIRILS (TYPE 1/518: 11:	Т	Т	201.710	1000	1			-	T
T		EOUDIE MENDESVINITE TOPE	239-352	Т	T	Т				I	T
T	CONTRACTOR IN	(FAPESVIR) A CAMPAGE (STANLING ABAP)	414.400	T	7	7	7	915-9-1	8701		1
		VARICELLA ZUSTER UNITE SET	Τ	T	ī	8 103.07	916-106		L	1	T
		S S I WAY S (3 I MAIN DURINS)	Ī	1:		ī				1	ī
7		GALLY COOK RET	١	7	٦	161:191	196-212 279.	279.244 248.360	100		1.
Y WOM		BASE COLONIALOS (STRAIN ADIAS)	2	1	1			Т	Τ	†	1
3	3	BALAN CONCOLUNIAUS (STRAIN AD 169)		1					<u> </u>		1
٦		TOWERS OF TOWERS (STRAIN AD169)	T			L	L	I			1
		CENTES SOULEX VIRUS (TYPE 1/ STRAIN 17)	1	7				+	1	4	
MACO VZVD G		EQUINE RELUES VIRUS TYPE I (STRAIN ABAP)	7		343.365 104.	16421	1	+		1	
		VAUCELLA-20STER VIRUS (STRAIN DURIAN)	1	16-107		-		1			_
î		GAVES SINDLEX VINUS (TYPE I / STRAIN)	11.114	27.146	56.110	201 100					ı
۳		EAPES SOUPLEX VIRUS (TYPE 17 CTRAIN # 25	37.46	<u>!</u>	Т	Ť	8				<u> </u>
Т		USAPES SOCREEX VINUS (TYPE I / STRANS AND	3.46		<u> </u>	+	1			_	
Т			2.44	1	$\frac{1}{1}$						ī
T			195.181	111.44		7			<u> </u>	1	<u> </u>
Т	Ī		Т	7	200	741.764	3		<u> </u>	1	_
S S S S S S S S S S S S S S S S S S S	10 7 KD ALPHA TRANS-DAUCING PROTEIN		101431	1	1			L	<u> </u>	1	
٦		FOR THE STATE OF THE CONTRACT POLICY	18.19	1						1	7
			1979	+						1	7
				$\frac{1}{1}$		-	H	-	+	4	
				٠					$\frac{1}{1}$		_

PCGEME	NICTURE.	All Viruats (No Bacterisphages)			-					ſ
ZIL LANK	PROTEIN	VIRUS	AREAI	TVILY TVIIV	A. AREAS	AREAL	BREAS	ABEA	AREAL	AREAL
Т	ALPHA TRANS INDUCING FACTOR 91 8 KD PROTEIN	VARKELLA-ZOSTEA VIRUS (SIRAIN DIMAS)	18:00	608.627	<u> </u>					
PULM ESV	HYPOTHETICAL BIRET PROTEIN		100		<u> </u>					ĺ
	HYPOTHETICAL PROTEIN I.E. 49	HUMAN CYTOMEGAL OVIRUS (STRAIN AD169)	20.00	105.88	<u> </u>				1.	
П	ECUMENT PROTEIN ULA	IERPES SIMPLEX VIAUS (TYPE 1/STRAIN 17)	216-252						Ī	
Т	HYPOTHETICAL GENE 66 FRUTEIN	IEAPESVIRUS SAIMUL (STRAIN !!)	13:35)							
J	TOTEIN ULSO	HUMAN CYTOMEGAL DVIRUS (STRAIN AD169)	-		<u> </u> 					
٦	MOTEUR ULS	HEAVES SWOLLER VIRUS (TYPE 1/STRATA 11)	9	:						
1	GENE B PROTEIN		171.170		_					
CALST ICANSI	(A-NG) B FLC J F.CN	FIGHTON THE RESERVE OF THE PRINT AND THE PRINT OF THE PRI	2	::	1					į
٦	LENE / FAUIETA	VAUCELLA-ZOSTER VIRUS (STRAIN DURIAS)	30.49							
THE STATE OF	PROBABLE DRA REPLICATION PROTEIN BSLF!	EPSTEIN-BAKK VIKUS (STRAIN BOLD)	5.							
П	NA REPLICATION PROTEIN ULS	MENUES SIMPLEX VIAUS (TYPE 1/STRAIN 17)	17.33	16:61						
3	DNA REPLICATION PROTEIN U.S.	EQUINE HEAVES VIRUS TYPE 4 (STRAIN 1942)	6-27	i						
MALSI HSVE	DNA NEPLICATION PROTEIN ULS	ECUINE HEAPESVIRIES TYPE (STRAIN ALLE)	1.33	115.19 116.117				į	_	
4		UCATION AND SAIMING (STANIN IT)	5	See boy	-	-				
Ī.	STATES OF SEPTIMENT OF SEPTIMENT	WALELLA-LOSTER VIROS (STRAIN DUMAS)		679						
	IN CONTRACTOR DOWNER OF	HOPEN CALL OF COME CALL OF THE ACTION AND INVITATION OF THE ACTION AND INVITATION			<u>†</u>					
T	SOUTH TIEST PROTECT AND	MANUEL SEPTICES VINCS (TITE 6/3) AND CORRUPTION								
7	INTO THE PROTECT BY	HALAN CHONGAL COMER AND	1	100	1					
7	HYPOTHETICAL PROTEIN IT AL	HENAN CYTOMECA! DVIBIR (STRAIN ADIAN)	17.103	200						
Т	ROBABLE DNA REPLICATION PROTEIN UL 10	HUMAN CYTOMEGAL OVIRUS (STRADY AD169)	275.363	409.410 409.414	474.44	130,001			Ī	
Т	PROTECTAL PROTEIN ULTI	HENCH CYTOMEGAL OVIRUS (STRAD) AD169)	14.3%	Ť	T					
Т	HYPOTHETICAL BLAS I PROTEIN	EPSTEDLEARK VRUS (STRAIN ROS.B)	10.69		<u> </u>					
	HYPOTHETICAL GENE SI PROTEIN	HERPESVIRUS SAIMIRI (STRAM II)	81:33		1					
۳	HYPOTIETICAL PROTEIN U.N	INDIAN CYTOREGALOVINUS (STRAIN ADISS)	11:11		<u> </u>				Ī	Ī
	VINION PROTEIN ULT	IRIDIAN CYTOMEGALOVIRUS (STRAIN ADIES)	368-291	607-628	<u> </u>				I	
PULTS HON'A H	YPOTHETICAL MOTEIN UL 18	INDIVAN CYTONEGALOVIRUS (STRAIN AD169)	71.60	190.203	-					
	HYPOTHETICAL PROTEIN UL79	INMAN CYTOMEOALOVIRUS ISTRAIN ADIG9)	8 5 2							
WITH HOLY	OS KO EALLY MONSTRUCTURAL PROTEIN	HEMAIN CYTOME DALOVIRUS (STRAIN ADISS)	90-110							
┱	SAU EXALT POPOLACE UNAL PROJECT	RUMAN LTICHEUALOVIRUS (STICIN TOWNE)	98		•					
L	APPOINT TRAIL PROTEIN (4.8)	IN BLANC VICTORIO (STRAIN BEST)	204-222	330-337		191				
Т	MYOTHETICAL PROTEIN SA	HEAPES SOCKER VIRUS (TYPE 6/8TRAIN UCANDA-1101)	701.323	Т	Т				Ī	
	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIDUS SAINOU (STRAIN !!)	165.367	402-412 579-595	36				Ī	
	TONETICAL PROTEIN U. II	INDIAN CYTOMEGALOYIRUS (STIAIN ADIES)	133-191	152-279						
PLEAS HEWEL	HYPOTHETICAL PROTEIN OR	HEAPES SUPPLEX VIRUS (TYPE 6/STRAIN UGANDA-1102)	<u> </u>							
T	INTO THE INC. THOUGH OF W	THE PER COME OF WALLE PARE A PROPERTY AND	25.50		1					
T	AMPOING TICAL PROTEIN III 65	HERLAN CYTOALTON OVER CITE AND ABILEN								
7	HOPOTHE TICAL PROTEIN PR	HEAPES SAPLEX VIRUS (TYPE 67 STRAIN LIGANDA-1101)	15.51	111	1					
Τ.	MOTERNULM	HEMANN CYTONEGALOVIRUS (STRAIN ADIAS)	6.70			-			İ	
_	HYPOTHETICAL PROTEIN BOLFT	EPSTEDY-BARR VIDIUS (STRAIN B95-8)	201-323						Ì	
PULSS HON'N H	HYPOTHETICAL PROTEIN ULFS	HOMAN CYTOMEGALOVIAUS (STRAIN ADIA)	506-526							
-	HYPOTHETICAL PROTEDN 13R	HERPES SEAPLEX VIXUS (TYPE 6 / STILAIN UGANDA-1102)	9-30	328-346		Ŀ			Ī	
_	HYPOTHETICAL GENE 34 PROTEIN	HEAPESYRUS SAMURI (STRAIN 11)	187-309							
MEN HOWA	CANCILLOVIA REMASE	FUNDAM CTIONE DALOVINUS (STRAIN AD169)	22.20	541.567						
_	MITOINE IN TACIEM OLIVE	HUMAN CTIONEGAL UVINUS (STRAIN ADION)	3							
	Walcal Beoffice In the	HUMAN CTIME CALUVING (STRAIN ADIM)	2		-					
_	WOOD PROJECT BEATER OF THE	RUMAN CT TOMES ALL VINUS (STRAIN AD10)	5	53-450						
_	HYPOTHE TICAL PROTEDY (A. III	INDIAN CYTOAGGALOVIETE (CTEAN ADIAN						Ì	1	
-	HYPOTHETICAL PROTEIN ULII)	INDIAM CYTOMEGALOVIRUS (STRAIN AD169)	38.110	1					1	
PLEED HONNA H	HYPOTHETICAL PROTEDY UL 117	HIPALM CYTOMEGALOVIRUS (STRAIN ADISS)	178.105							1
		HUMAN CYTOMEGALOVIRUS (STRADI ADIM)	2.0						1	
PULCI HONYA H		HUMAN CYTOMEGALOVIRUS (STRAIN ADIM)	13.5	-	-	I	I		†	Ť
				-					1	7

150	MICHIGA	All Viruse and Bacterias Lagarit									
NA PLANT	CACILLIA STATES	XIANS	AREAT	ABTA	7.4.4	7 7 4 11 7				П	
Man Found		PICHANA CYTOME GALOVIRUS (STRAIN AD169)	1		1	100	3	1	2882	PEAL	4 KZ 4 2
MINO HEAT	-	FOWLPOX VIRUS (STRAIN FP.1)	100								
MAC VACCA	INVESTMENT OF THE STATES	EQUINE HEXPESVIRUS TYPE I (STRAIN ABAP)	224.336			-					
A PACE	UNIVERSITY OF STREET	VACCINIA VIRUS (STRAIN COPENIAGEM)	197.183			1					
PING VARV	IN ACTUAL CONTRACTOR	VACCINIA VIRUS (STRAIN WR)	1913								
ABO CON	THE PERSON OF THE PERSON	VAROLA VIRUS	9								-
PINES LIVES	CONT. LA DECITE OF TANK	VANCELLA-ZOSTERPIRUS (STRAIN DUMAS)	17.25								
PINOS INVER	IKI POTEN	EQUINE HEILPESVIRUS TYPE I (STRAIN ABAP)	3								
PINO PENNI	PROTEIN IN THE ACT OF	EQUINE HERPESVIRUS TYPE I (STRAIN KENTICKY A)	(9-9)			ŀ			-	:	
STATE OF THE PARTY	TAULEIN UST HUMOLOG	PSEUDORADIES VIAUS (STRAIN NIA.1)	100	İ							
1000	MACH PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	16.10								İ
1000	_	HEADES SUMPLEX VIRUS (TYPE 1/ STAAIN 17)				-					
TARK CACA		HERPES SIMPLEX VINUS (TYPE 2)	2								
LOS HOW	HYPOTHETICAL PROTEIN HALF)	HUMAN CYTOMEGAL OVIRUS (STRAM ADIAS)	2			-					
LOS HOW	HYPOTHETICAL PROTEIN HALF!	HIMAN CYTOMEGAL OVIRUS ISTRAIN APIGO	8	Ī		1					
TUSES HOWY	HYPOTHETICAL PROTEIN INLIG	HUMAN CYTOMEGAL DVIBITE ISTRATIVA PRILAD									
PUSES HONA	HYPOTIETICAL PROTEIN HYLFS	HUMAAN CYTONEGAL DVIRUS (STRAIN ADIAS)	2.50		32.22	-					
PUSIN HOUNA	7	HUMAN CYTOMEGALOVIRUS ISTRAIN ADIASI		2		·					
MSIS HOWA	_	INDIAN CYTOMEGALOVIRUS ISTRAIN ARISES	200			-					
PUSIS HOMA	_	INMAN CYTOMEGALOVIRUS ISTRAIN ADIAS	17.00	9	1	-				İ	
MEIN HOWA	HYPOTHETICAL PROTEIN HVLF!	IRMAN CYTONEGALOVIRUS (STRAIN ADIAS)	2	2		•			:	!	-
AND HOW	MEMBILANE PROTEIN INVLF4	PROMAN CYTOMEGALOVIRUS AFTRAIN ARIASI		ī							
PUSTS HOWA	HYPOTHETICAL PROTEIN HYLES	HUMAN CYTOMEGAL OVINCES ISTRACES ADIAM			<u> </u>						
PUSIZ HOWA	EAST Y MUCLEAR PROTEIN I'MLE!	INDIAN CYTONEGALOVIELIS SETBANA ANIAN	-	23-62							
PUSID HCAPA	HYPOTHETICAL PROTEIN IGE FT	MALAN CYT DIVEGAL OVIRITY STRAIN AD1461	270-203			-					Ī
PUSTS HOWA	HYPOTHETICAL PROTEIN HELF	HAMAN CYTOMEGALOVINUS (STRAIN ADIAN)	**************************************		1	-				İ	Ī
П	OPROTEIN COUPLED REC HONOLOG US31	HUMAN CYTONEGAL OVIAUS (STRAIN ADISS)	T			1					
_	O-KOTEM COUPLED REC HOMOLOG US28	HAMAN CYTOMOGOAL OVIRUS (STRAIN TOWNE)	T	2		1					
TUST HOW	HYPOTHETICAL PROTEIN INDUS	HILDLAN CYTOMEGALOVIAUS (STRAIN ADJON)	Ţ,	3		Ī					
A POST OF THE PARTY OF THE PART	HYPOTHETICAL PROTEIN 15005	HUMAN CYTOMEDALOVIRUS (STRADI AD169)	101.171	11.00	1						
Т	TEN PROTECT PROTECTION FOR FU	HUMAN CYTOME GALOVIAUS (STRAIN AD169)	85:10		T	+					
1	THE PROPERTY	LELY SYNOTOMEESS VIRUS	17.45	1	Ī	1	1				
PANTE PARE	TAN	POTATO VINUS & (STACIN PERUVIAN)	1	Ì	Ì	Ť	1	1			
l	THE PROPERTY OF THE PROPERTY O	POTATO VIRUS X (PVX)	7	Ì	Ť	Ť					
Ī	PACIFICATION OF THE PROPERTY O	POTATO VINUS X (STRAIN XJ)	27	İ	Ì	1		1	1		
T	I I I I I I DECIMENT	POTATO VIRUS X (STRAIN XC) (STRAIN CP)	77	İ		T		1			
Т	THE PROPERTY OF THE PROPERTY O	AFRICAM SWINE FEVER VIRUS (STRAIN LISST)	Z C	İ	T	Ì	T	1			
1	13 KD PROTEIN	POSATO WILLIAM STATEMENT AND A SOCIATE LEIDEN	19.79		T		T	Ì		1	
1	16 KD PROFEDI	TOTAL OF THE STREET RUSSIAN	79.96						İ	Ì	
I.	FLICASE	ATTOCA AND THE VICTOR (STRAIN PLB)	14.51			Ī		T	İ	Ì	
_	14 KD PROTEIN	BART BY STRIPE MASSIC WILLIAM FOR THEOROSIS VIRUS		5	013-1037	T	T	T		1	
	IS KD PROTEIN	ABEL TON INTERPRETATION VALUE		0.13 0.13					T	\dagger	
2	PROTEIN B19	VACCIMIA VINUS (STRAIN WR.)								T	T
J	IA PROTEDI	BROAD BEAN MOTTLE VIRUS	T		1	1					
T	IA PROTEIN	BRONE MOSAIC VIRUS	Ť		1						
T	IA PROTEIN	COWPEA CHLOROTIC MOTTLE VIAUS	144.363	\dagger	1	1					
Ţ	A PROTEIN	CUCLEMBER MOSAIC VIXUS (STRAIN FAY)	916.800	1	1						<u> </u>
ON TO THE	IA PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	23.600	1	1	1					
T	A PROTEIN	CUCLAMBER MOSAIC VIRUS (STRAIN Q)	174.799	1	Ť	1					
12	I CENTRAL	PEAMUT STUNT VOIUS (STRAIN I)	T	803.808		T	Ì		-		
Ť	H P D D O D D D D D D D D D D D D D D D D	TURKEY IEAPESVIRUS (STRAIN HD)	Ť		\dagger	Ť	1	1			
Ī,	M KO MOTEU	POTATO LEAFROLL VILUS (STRAIN I) (Т	107.761		1		1	1		
	NED PROTEIN	POTATO LEAF HOLL VILUS (STRAIN WAGENINGEN)	Τ	101.101		1	1	1	1		
VY39K PEBV	29 A K D PROTEIN	BEET WESTERN YELLOWS VIRUS (ISOLATE FL.1)	Ī	134-157	\dagger	Ť		†	1	1	
	14 MOTEN	PEA EALLY BROWNING VIRUS	П			T	\dagger	\dagger	Ť	†	T
		PANE MUSAL TINUS	285-363 7	759.777	r	T	T	T	1	\dagger	7
								1	1	1	٦

	Piscrizir	All Virace (No Bactertophoges)		-	-	-	-			ľ	
THENAME	PROTEIN	YIRUS		AREAL ABI	ABEAL AR	AREAM AS	AREAS A	ARCAL	ARCA!	AREAL	ARCAS
PVIA COR	1A PROTEIN	COWPEA CHLOROTTE VINUS			<u>!</u> !	1	-	-			
A LANGE	A TRUISIN	TOWARD BATTLE UNITE ASSESSMENT TOWARD		<u>:</u> !	:	+	!	-	:	-	!
VIII TORSY	11 7 KD PROTEIN	TOBACCO STREAK VIRUS (STRAIN WC)	9	1	1	1	T	Ť	Ì	Ť.	
PVI63 ASFBI	K'141 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATTV)	3.5		<u> </u> 		Ì		Ī	Ť	
PV775 ASPL3	LIS 315 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LISSY)	£ 1								
PVIES ASPLIS	LIS JOS PROTEIN	AFRICAN SWITE FELT A VIRUS (STRAIN LISST)	2		<u>!</u> 	1	;	:		-	
NAME OF THE PERSON OF THE PERS	TA PROTESS	COCIDANTE MOSAIC VIBILS (CIBAIN FNY)		-	1	+	i	Ī		İ	1
VYA OVY	1A PROTEIN	CUCUMORA MOSAIC VIRUS (STRAIN M)		<u> </u> 	$\frac{\perp}{1}$	+	T	Ì	Ī	İ	Ī
PVIA GAVO	IA PROTERY	CICCIMBER MOSAIC VIRUS (STRAIN D)		-	<u> </u> 	<u> </u> -	1	Ì		İ	Ī
PVIA CAVO	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Q)	18:31		1	╁	\dagger	İ		T	
PV3A CMVY	CUCUMBER MOSAIC VIRUS (STRAIN Y)		214.235		<u> </u>	-		İ		T	Ī
PV3A IBVB	1A PROTEIN	AVIAN DIFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	3.20		<u> </u>			İ		İ	
MA BAN	IA PROTEIN	AVIAN BG ECTIOUS BROWCHITIS VIRUS (STAKIN MAI)	2			<u> </u>					
PVJA (BVP.)	NA PROTEIN	AVIAN BG ECTIOUS BRONCIBIIS VIRUS (STRAIN PORTUGAL) 12/12/13	3.28			-					
PVIA BVUS	JA PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN UTCHEING)	2.5		1	-					
PVJA TAV	NA PROTEIN	TOMATO ASPERMY VIRUS	3		<u> </u>	<u>-</u>					
PVIR BOV	SI KD PROTEIN	BALLEY STUPE MOSAIC VIRUS	90.00		-	+		Ī			
	THURSDAY OF THE PROPERTY OF TH	THE AND VELL OF LOS LESS (STACING LAND)		1	1	- -	1	Ì			
NAME AND B	•	ALEAN MANAGE WHILE COM AN ANGLISM AND		1	1	$\frac{1}{1}$	1	1		Ì	
PVADA VACOL	-	VACCINA VIBIS (STRAIN COPENDIAGEN)		1	<u> </u>	+	1	İ	Ì	İ	
YVADA VACEV	-	VACCINIA VIRUS (STRAIN WR)	77.74	1	+	-	İ	Ť	Ī	1	
PVADA VARV	-	VARIOLA VIRUS	303.214	1	1	<u> </u>		Ì	Ī	Ì	
PVASS VACCC	_	VACCINIA VIRUS (STRAIN COPENHAGEN)	3	1	1	1	†	Ť		İ	Ī
PVAM VARV	_	VALIDLA VIRUS	35		+	<u> </u>	İ	Ì	Ī	İ	
PVAIL VACCC	PROTECUALI	VACCINIA VIRUS (STRAIN COPTINIAGEN)	2		113	-					
PVAII VARV	PROTECNALI	VAUGLA VIAUS	3.46	41.160 300.	900.318	. •					
PVA14 VACCC	PROTEIN AIR	VACCIMIA VIRUS (STRAIN COPENITAGEN)	3		_	+		ĺ			
TALE VALUE	INTERIOR AND THE PROPERTY OF T	VACCEDIA VIRIA			1	- -	+	1		1	
AUTO VIEN	PROTECTALA	VARIA A VINIA			<u> </u>	1	1	İ	Ì	1	
PVAIL VACCE	N KD ABORTIVE LATE PROTEDN	VACCIMA VIRUS ISTRAIN COPENIIAGENI	29.44		+	+	Ì	İ	Ī	İ	Ī
PVAIS VACCV	14 KD ABOATIVE LATE MOJEN	VACCIMIA VIRUS (STRAIN WR)	(39-40)		<u> </u>	1	$\frac{1}{1}$	Ì	Ī	Ť	
PVAIL VARV	54 KD ABORTIVE LATE MOTEIN	VARIOLA VIAUS	Τ		L		T	l			Ī
PVAJO VACCC	PROTEIN AJO	VACCINIA VIRUS (STRAIN COPENTAGEN)		193-309		-				Ì	Ī
PVANO VARV	PROTEIN AND	VALIDIA VINUS		193.200							
22.0	SECULIA ASE	VACCING SOURCE S			1			j			
PVASI VARV	PROTEIN A34	VARIOLA VIRIS		1	1	\dagger	\dagger	1		1	
PVAJI VACCV	PROTEIN AJI	VACCIMIA VIDUS (STRAIN WR), AND ISTRAIN COMEMIAGEN)	205.2	1	<u> </u>	\dagger	l			İ	Ī
PVAJS VARV	PROTEIN AJS	VARIOUA VIRUS	2		+			Ì	Ť	\dagger	
PVAJJ VACCC	PROTEDIALIS PRECURSOR	VACCONA VOLUS (STRAIN COPENIAGEN)	\$	_	<u> </u>	-		İ		İ	Ī
PVAJS VACEV	PROTEIN A35 PRECURSOR	VACCIMIA VIRIUS (STRAIN WIL)	11-49	41.164	_	-			İ	İ	
PVAJ) VACCC	PROTEINAUT	VACCINEA VINUS (STRAIN COPENIAGEN)	8								
WAS WACC	PROTEST AJ	VACCORIA VIRUS (STRAIN WR)	2			1					
VALLE VALLE	PROTEIN ALL PRECINCOL	VACCINIA VIBINI (TIBANI COFINIACEN)	?		<u> </u>	+		j	Ì		
PVA41 VACCV	PAOI EN A41 PRECURSOR				$\frac{1}{1}$	\dagger	\dagger	\dagger	1		Ī
PVA41 VAXV	PROTEEN A41 PRECURSOR		10.00	T	ł	+	\dagger	\dagger		\dagger	
VACCC	PROFESSI A49	S (STRAIN COPEMIAGEN)		201-126	<u> </u>	-	l	T	T	Ì	Ī
Ы	PROTEBN A47	VACCINIA VIRUS (STRAIN WR)		31:10	-	-	\mid		T		
- 1	PROTEIN A11		П	201.726							
- 1	PROTEIN ASS	EMIAGEN	П	384.464							
אינו איננא	MOTEOR ASS	VACCIMIA VIRUS (STIAIN WR)	3	24.404	-						
	ALL TROICES				$\frac{1}{2}$	1	1			1	

		A 1 Version (12)									
THERAME	PROTEIN	VIRIS									
יאבו מאצ	ALI PROTEIN	CASSAVA LAYENT VIBILE VERNING TO THE PERSON OF THE PERSON	Į	AREA?	AREA 3	ARCA	ARFAS	ABFA			
PVALI CLYM	ALIPROTEIN	CARACTA CARACTA CARACTA WEST KENYAN GAG	Г		7		1	9	i	ABILA J.	ARTA?
VALJ BCTV	ALIPROTEIN	CASSATA LA ILA VIACIS (A RAIN NEL BIAN)	2 2		:	-					
VAL 3 CLVX	A SPOREN	DEET CURLY TOP VINUS	180.2	:	:	. <u>-</u>	:				
NA D LIVA	AL PROPER	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 144)				-					
VAL TAN	+	CASSAVA LA JENT VIRUS (STRAIN MIGERIAN)									
	Т	TOMATO YELL OW LEAF CUTL VIRUS ISTRAIN MALMANDED									
A 100 A 100	_	TOMATO YELLOW LEAP CURL VIRUS									1
	_	CAULIFLOWER MOSAIC VIRUS (STRAIN CH. 1811)			i						
CVINA	-	CAULTOWER MOSAIC VIBITE ACTORING DAIL	2					! !	;		:
AT CUMPE		CAIR DI OWER ADOLE THE PERSON OF THE PERSON	134-137								
AT CAMPR	_	CALE HI DESENSON CONTROL STRAIN BBC)	134-157			1					
AT CAMP	_	CALE WI OWER MOJAK, VIRIS (STRAIN NYBIS)	18:18			-					
VAT CLICY	7-	CALLET UMEN MOSAIC VIRUS (STRAIN PVIAT)	100			1					
AT CALOW	APMIN YEAVELMEET MEDICELLI	CAULILOWER MOSAIC VIRUS (STRAIN STRASBOURG)	136.181				Ī				
VAT CERV	AHIR TO AND ALTON THE PARTY OF	CAULIFLOWER MOSANC VIRUS (STRAIN W260)	3			-					
VAT BASE	ANIMA I MANSHITTANIA PROTEIN	CANNATION ETCHED KING VIRUS				-					
Approx Control	A TAIL I PARTSHUM PROTEIN	FIGWORT MOSALC VIRUS (STRAIN DAS)				-					
2000	TROIEUNES	VACCIDITA VIDUS (STRAIN COPENIAGEN)				-				İ	
AND ANCE	PROTEIN B2	VACCORIA VINUS (STRADH WILL)	2			:					Ī
AACCC	PROTECN B4	VACCINIA VINUS (STRAIN COPENNACEIN	21:42								Ī
VBO VACCV	PROTEIN B4	VACCONTA VIBILIS (STRAIN) WES									Ī
PVBON VARV	PROTEDNIM	VARIOLA VIBILE	409-311			-				1	
BOS VACCO	PLAQUE-SIZE / HOST RANGE PROTEIN PRECLIRSOR	4-	416-311						1	Ť	
BOS VACCC		-	111.111		İ					1	
VBOS VACCE	PLACUE SIZE/ HOST BANGO PROTEIN SECTIONS		111:11	İ		I					
VESS VACEV		TACCINIA VICIO (STIAIN LISTER)	147.182		T	ŀ	1				
1	THE THE PARTY OF T	-	16:15		İ	+					
	PROTEIN BILL	VACCORA VIRUS (STRAIN WR), AND (STRAIN COFEMIAGEN)	25.52	İ		1					
	PROTEIN BILL	VACCINGA VIRUS (STRAIN COPENHAGEN)	21:12	Ì	1	1	1				
PVB15 VARV	PROTEIN	VACCINIA VINUS (STRAIM WA)	127-127	İ	1	1					
VBIT VACCE	MOIENE	VAUGA VAUS	131.10	İ	1	ŀ		1			
VAIL VACEV	PROTEGNET	VACCIMIA VICUS (STIMATIN COPEMIAGEN)	# 14 H	İ	Ť	T	1				
VALI CLVK	BLI PROTEIN	CASSAGE AND STRUCK WR.)			T	F	1				
VIII. CLVV	BLI PROTEIN	CASSAVA LA LENT VIRUS (STRAIN WEST KENY AN 144)	1	İ	1	+	1				
ADT 17	BLI MOTEN	CASSAVA LATERT VIRUS (STRADA MICERIAN)	1	 		Ī					
RI ABANY	BAI PAOTER	AVAIN LEAV LOIL VICTOR	345.364			Ť	1				
AL BONV	BRIPAGIEN	AND ILLUM PROMICE VIRUS (ISOLATE WEST INDIA)	161-39	İ	T	Ť	1	1	j		
Al Prievo	BAI PROTEIN	POTATO VELLORIA MUSARC VIRUS	161-93	T		İ	1	Ť			
PVBAI SLCV	BRI PROTEIN	COLLA SUL EAL CITY MUSARC VIRUS (ISOLATE VENEZUELA)	- 1 ±	T		T	1				
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VOUL VACEV	MOTEDICI	VALCENTA VIBILITIES AND CONTRACTOR	20-90					1	1		
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	G-PROTEIN COUPLED RECEPTOR HOMOLOGICS	CHOOL PEROMA VIRILATE EN LESSA	1.31		l			1	1		
Т	PROTEIN CA	VACCIDITA VIRGO (31 MAIN MASCA)		139.163	-			1			
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	HYPOTHETICAL PROTEIN CA	SUCRE SINGLE SIN	102-(11	-				1	1		
VCOL SFVKA	HYPOTHETICAL PROTEIN CE	CHAPTE FEMANT VINUS (STRAIN RASZA)	Ę		\dagger	T	1	1	1		
Ι.		MATERIAL VINUS (SIRAIN KASZA)	6.30		-	†	1	1			
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NCA HSVI	MAKOR CAPSID PROTEIN	HEINES SIMPLEX VIRUS (TYPE I / STRAIN 17)	163.301	П	131.131	ĺ					
PVCA HSVEB	MAJOR CAPSID PROTEIN	EQUINE HERPCSVIRUS TYPE I (STRAIN ANALY)	37.35	7		1	Ī	T			
PVCAP HSVSA	MAJOR CAPSID PROTEIN	ICENESVIRUS SAIMINI (STRAIN II)	=======================================	1	11.11	100.2.1019	Ī			Ţ	
	MAJOR CAPSID PROTEIN	PSEUDORADIES VIRUS (STRAIN INDIANAS)	13:362		İ	Ī		Ī		-	
200	_	VARCELLA-ZUSTER VIRUS (STRAIN DURIAS)	181.40)	010-10	136-1176			Ī			
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	ALL DE MANAGEMENT	VAUCILA VIRUS	13.39		-					i	
	VI WOULDING	TOWNED ON VINUS (STRAIN IP. 1)	246-365	115.337		L					
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A A A C C A	PROTEIN DS	VACCINIA VIRUS (STRAIN VR)	120-140	T	716.316	Ī					
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A MEDITAL FROTEN PAECUASON VACCEDA VEUS (STANT COFENIAGEN) NECHOLANE PROTEN PAECUASON VACCEDA VEUS (STANT LIVY) A MEDITAL FROTEN PAECUASON VACCEDA VEUS (STANT LIVY) A MEDITAL FROTEN PAECUASON VACCEDA VEUS (STANT MAN) VACCEDA VEUS (STANT WA) VACCEDA VEUS (STANT WA) VALUCA VEUS (STANT COFENIAGEN) VALUCA VEUS (STANT COFENIAGEN) VALUCA VEUS (STANT COFENIAGEN) VALUCA VEUS (STANT COFENIAGEN)	A MEDITAL PROTEIN PRECUSSOR VACCHA VIDUS (STAIN COPENHAGEN) NACCHA VIDUS (STAIN L. 177) A MEDITAL PROTEIN PRECUSSOR VACCHA VIBIUS (STAIN W.) A MEDITAL PROTEIN PRECUSSOR VALUS VACCHA VIBIS (STAIN COPENHAGEN), AND (STAIN L. 177) VACCHA VIBIS (STAIN COPENHAGEN) VACCHA VIBUS (STAIN COPENHAGEN) VACCHA VIBUS (STAIN COPENHAGEN) VACCHA VIBUS (STAIN COPENHAGEN)		Ī	Т	Τ							
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A PERBLANE PROTEIN PRECURSOR VACCINA VIRUS (\$ 15 AN WR) A PERBLANE PROTEIN PRECURSOR VALUE A VACCINA VIRUS VACCINA VIRUS (\$ 15 AN WR) VALUE A VALUE A VIRUS (\$ 15 AN WR)	A MEMBIANE PROTEIN PRECURSOR VACCINA VIRUS (\$ TAXIN WR) A MEMBIANE PROTEIN PRECURSOR VACCINAL VIRUS (\$ TRAIN COPENITAGEN), AND (\$ TRAIN L.IVP) VALVOLA VIRUS VALVOLA VIRUS VALCOLA VIRUS VALCOLA VIRUS VACCINAL VIRUS VALORIAL VIRUS	ANDRI MEMBRANE PROTEIN PRECINSOR		î î			-				1	Ī
A PENGEN PRECURSOR VALUED AND STRAIN WED. VACCINIA VIRUS STRAIN COPENIAGEN, AND ISTRAIN LAVO, VACCINA VIRUS VACCINA VIRUS VACCINA VIRUS VALUCIA VIRUS VALUCIA VIRUS VALUCIA VIRUS VALUCIA VIRUS STRAIN COPENIAGEN VALUCIA VIRUS VACCINA VIRUS STRAIN COPENIAGEN	A PERMINE PROTEIN PRECURSOR VALUED STAND WAY VACCINIA VIRUS (STAND COFFINIAGEN), AND (STRAIN L.IVP.) VACCINIA VIRUS (STAND WA.) VALUA VIRUS (STAND COFFINIAGEN) VALUA VIRUS (STAND COFFINIAGEN) VALUA VIRUS (STAND COFFINIAGEN)	AUCH MEMBERANE PROTEIN PREMINE CON		20.303			l		1	1		
VACCENA VIRUS (STRAIN COFENITAGEN), AND (STRAIN L.IVP) VACCENA VIRUS (STRAIN WA) VALUCA VIRUS	VACCHA VRUS VACCHA VRUS (STRAIN COPENIAGEN), AND (STRAIN LIVE) VACCHA VRUS (STRAIN WA) VACCHA VRUS VACCHA VRUS VACCHA VRUS VACCHA VRUS	A LOS LAS LAND A LAST DE PORTE DE L'ANDIEN		101	İ		İ					
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VARIOLA VRUS VACCINA VRUS VALCIA VRUS VALCIA VIRUS ISTRAIN COFEMILAGEN VALCIA VIRUS ISTRAIN COFEMILAGEN	VALGOLA VIRUS VACCINIA VIRUS VALCENTA VIRUS VACCINTA VIRUS ISTAIN COFEMILAGEN			200				İ	1	-	!	
VACCINA VILUS (STAJIN COPENTIAGEN) VALUCIA VILUS (STAJIN COPENTIAGEN) VACCINA VILUS (STAJIN COPENTIAGEN)	VÁCCINA VIRUS VÁDOLA VIRUS VADOLA VIRUS VACCINA VIRUS IS I BAIN COFEMIAGEN)	100		8.5		+	1	1				_
VACCINA VRUS SETAIN COFEMIAGEN VACCINA VRUS SETAIN COFEMIAGEN	VACCINA VRUS ISTRAIN COFEMIAGEN) VALIOLA VIRUS VACCINA VIRUS ISTRAIN COFEMIAGEN			26 300	İ	1						ĺ
VADICIA VIRUS VACCINIA VIRUS 13 TAJIN COFENIAGEN	VADOLA VIÈLIS VACCINIA VIÈLIS IS I RAIN COFENIAGEN			3							l	Ī
VACCINIA VIRUS (STRAIN COFFINIAGE IN	VACCINA VIRUS (STAAIN COFFINIAGEN)			1	-	_		Ì		1	1	
VACCINIA VIRUS (STRAIN COFEMIAGEN)	I VACCIMIA VIRUS (STRAIN COFFINIAGEN)			61:184			1					
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Ļ	PROTEIN	And the second s	ABFAT	4864.9	ABEAT ABEAT		V 1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2 1 2 1	17.	
5	PROJECTIVE	VACCINIA VIAUS (STRAIN L.IVP)	Ī	ī	à.	To the second	- N. W.	700		
1	PROTEINFIS	VARIOLA VINUS	15.	<u>.</u> :	:					
VANOT INVA	PROTEIN PPI	FOWLYOX VIAUS	101.00				İ	1	-	:
PVFF1 TOWEV	PROTEIN FP	FOWLPOX VIRUS	10.00						 	1
WIN COM	PROTEIN F7	CAPADOXVIAUS (STRAIN KS-1)	111-69					-	<u> </u>	1
PUTET FOWTY	PROTEDVEPT	FOWLPOX VIRUS	65.90					 :		
PWM CAN	CHA MOTEIN .	CAPRIPOXYIRUS (STĮAIN KS-I)	51.76					_		
PYTUS DRINZ	I SKD FUSION PROTIZIN	ONE VIRUS (STRAIN M.2)	20.41					••	-	
	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN WR 65-16)	73.54							
	INTOTHETICAL GENE ! PROTEIN	EQUING HELLIESVIRUS TYPE I (STRAIN ABIP)							<u> </u> - 	
	INVOINE TICAL CEME I PROTEIN	ICTALURID IERPESVIRUS I		911-110	319-616					
	PROFEING	VACCOMIA VIRUS (STRAIN COPEMIAGEM)	346.316	336-365						
PVOS: VACEV	PROTEING	VACCINIA VIRUS (STRAIN WR)	Г	315.130	 -				-	
PVCBI VARV	PROFEDUCI	VARIOLA VIRUS	11.36	136-395				<u> </u>	-	:
Г	INVOINE SICAL CENT I PROTEIN	VALICELLA-ZOSTER VIRUS (STRAIM DUMAS)	ī		<u> </u>		i	:	!	!
PVORY VACOC	PROTEDICAL	VACCINIA VIRUS (STRAIN COPENHAGEN)	200		<u> </u> 			1	+	Ī
Т	PROTECHO	VARIOLA VIRUS	110			\[\]	İ	+	T	Ī
L	PROTEING	VACCOMA VIALIS (STRADI COPENSIAGEN)							 	Ī
Т	MOTERIO	VARIOLA VINUS	1						-	Ī
PWOS VACCE	PAGIEDICA	VACCINIA VIAUS (STRAIN COPENNAGEN)	===						T	
Т	PROTEIN 04	VARIOLA VIRUS	15:16							Ī
Г	HYPOTHETICAL GENE I MEMBRANE PROTEIN	ICTALUNID HEAPES VIAINS 1	12.14	139.103					1	
PWGIO HSWII	HYPOTHETICAL GENT 10 MEMBRANE PROTEIN	KTALUND HERPESYRUS I	32:55	-						
		HEAVES VIRUS SALMEN (STRAIN 11)	199-134	155.170						
_	SIYPOTHETICAL GENETII EDICADING PROTEDI	KTALUAD HEAPES VIAUS I	103-133	20.00						I
PVGIS HEWI	HYPOTHETICAL DESIGN 13 ZINC-BOOTHO PROTEIN	KCTALURID HERVESVIRUS (181.178	270-284				-		
J	HYPOTHETICAL CENE (1 PROTEIN	HEAPESYTRUS SABABILI (STRAIN 11)	48.93							ĺ
	HYPOTHETICAL GENE 19 MEMBRANE PROTEIN	KTALURED HERMESVIRUS I	11:113							
<u>.</u>	OIL PROTEDI	AMSACTA MOOREI ENTOMOPOXVIRUS	_							
- 1	CAYSID PROTEIN	SPIROPLASMA VIRUS SPVI-RIAZ B	Т	659-678						
- 1	HYPOTHETICAL GENE ZI PROTEIN	K. I AL URID MERTES VIRUS I	Ē.							
TACO HONE	NATIONAL MALAL CIDAL SI PROTEIN	R. JALUAD IERTES VIRUS I								
1.	MYPOTHETICAL CENE 31 PROTEIN	FEBRESVEIN CAMINICIDATE	315 905		1			+	1	T
	HYPOTHETICAL CENT 19 PROTEIN	ICTALUND REPRESVINUS I	Τ	401.510						
1-	HYPOTHETICAL CENE 21 PROTEIN	HELDES VIRUS SAIMIN (STRAIN !!)	Т	+				\dagger		
Т	HYPOTHETICAL GENE TO PROTEIN	ICTALURID HERPESYIRUS I	1079					l		
П	HYPOTHE HEAL GENE 30 PROFEIN	KCTALUNIO HERVESVIRUS I	166-191					-		
	CEME 32 PROTEIN	VANCELLA-ZOSTER YARUS (STRATIV DURIAS)							<u> </u>	
	POSSIBLE TYROSINE PROTEIN KINASE	HEAVESVIRUS SALMINI (STRAIN 11)	П	346.362						
_	HYPOTHETICAL GENE 37 PROTEDI	KCTALUALD PERVES VARUS I	7	Ť						
VOUS ASY	ATTOLIC ICAL COM TO TROLEM	K. I ALLURUD PRINCES VINUS I	_	10.400	1036-1065					
Т	INTO THE PLAN COME AT PROPERTY	CALLE DE LE					1		1	
PVG-1 THVII	HYPOTHETICAL (#)46 41 MOTEN	ECTAL Chair Library Synatist	Ī,	Ī,	M7-107				1	Ī
T	PROBABLE MAJOR CLYCOPROTEIN	KCTALUNID IERPESVIRUS I	T	Т	T	2		$\frac{1}{1}$	+	Ī
Ī	HYPOTHETICAL CENT AS PROTEIN	KCTALUMU HEAVESYARUS I	Т	Т	T				+	
Ī	PROB TRANSCRIPTION ACTIVATOR EDIT	HELDES VIDIUS SAIMIN (STILATIN !!)	Ī	38-83			1	\dagger	\dagger	
	HYP GENE SI HELGBRANE PROTEIN	ICTALUND IEIVESYINGS I	Γ	14.102				$\frac{1}{ }$		Ī
·	INPOTIE TICAL CENE 52 PROTEIN	ICTALUND IGENES YIRUS I		Г					-	Ī
	INYONE TICAL GENE 55 PROTEIN	ICTALUND KERPESYIRUS I		143.158 201.	361.309					
7	HYPOTHETICAL GENESS PROTEIN	FEUFESVINUS SAIMIN (STRAIN 11)	\$ 18							Ī
PVOX HSVI	HTPOTHETICAL GENE 34 PROTEIN	KTALUKID MIQUESVINUS I	•I	٦	┑					_
T	WAS CENE IN MEMBERNE PROTEIN	KTALINID KE DE CVINS	3	11.	201 110 110 146			+		-
Т	GENE S PROTEDI	SPIROPLASMA VIBILS	T					1	1	1
PVG40 HSVII	HYPOTHETICAL GENE 40 PROTITIN	K'TATINIO IN OFFICE IN	1	11.71	+	+	\dagger	+	+	Ţ
1						1	1			7

PCCENE	Processie	(All Victorial Inclusions Annual Inclusions)									
FILENAME	PROTEIN	YIRUS	ARFAI	ARFA 3	ABEAT	ABFAL	4854 6	4004		7	
PVO61_HSVII	HYPOTHETICAL GENE 6! PROTEIN	ICTALUNID HEAVES VIRUS I	76-102	17:136				_	Т	o vara	4
PVO63 HSV11	HYPOTHETICAL GENE 63 PROTEIN	ICTALURID HERPESVIRUS I	238-259	336-363					†	+	T
PVG44 HSVII	HYPOTHETICAL GENE 64 PROTEIN	ICTALUNID HEAPES VIAUS I	420-445						†	†	
PVO65 HSVII	HYPOTHETICAL GENE 65 PROTEIN	KCTALURID HERPESVIRUS I	117:137	155-173	362-378	118:51	147.1174	1347.1369	\dagger	†	Ī
PVO67 HSVII	HYPOTHETICAL CENE 61 PROTEIN	KCTALURID HEAVES VIRUS 1	108-132	171-118	318.344	332-745	1005-1029	+	1315-1341	+	
WO SPVIR	CENE & PROPER	SPIROPLASMA VIRUS SPVI-RIAZ B	29-09					+			1
PVO70 HSMI	HYPOTHETICAL DENE 10 PROTEIN	ACTALUADD HERPESYRUS I	184.209							-	T
PVQ1 ISVX	HYPOTHETICAL DENS 71 PROTEIN	HERPESYTRUS SAIMIRI (STRAIN 11)	801.68						ı		
FYOR MOVI	IIYYOTHETICAL GENE TO PROTEIN	KCTALURID HERPESVIRUS I	445-471	195-368	730.744	1252-1269		!	:	!	
PVOY HSVIA	G-MOTEIN COUPLED REC HOMOLOG ECRE)	HEAPESVIAUS SAIMIN (STRAIN 11)	124-151						T		Ī
TAC SAN	ODAL 9 PROTEIN	SPIROPLASMA VIRUS SPVI-REAZ B	57.72			 				T	T
PVG I BVG	FIFTOTED	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	1387.1606	1154-1177	2104-2127	2210-2226	2716-2806	2973-2999 30	1073.3090	3120-3145	1174.1199
	_								l		
WHO WORK	~	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	127.178			•				!	:
WOLL CYPIE	EL CLYCOPROTEIN PRECURSOR	PORCINE RESPIRATORY CORONAVIRUS (STRAIN 66/137004/3/RITISII IS	174-193				İ			T	
NO.	ET CL'YCOPROTEIN PRECURSOR	BOYDE CORONAVIRUS (STRAIN FIS)	10-33	133-139	134-180	264.278	101.164	1239.1280	f	t	Ī
TYOU CARE	ES CL'YCOPROTEIN PRECURSOR	BOVINE CORONAVIRUS (STRAIN LY)	123-139	174-190	264-279	651-674	5101-100	1250,1210		1	
TVOL1 CVILY	ES CLYCOPROTEIN PRECURSOR	BOVING CORONAVIRUS (STRAIN LY-138)	Г	135-139	174-190	364.370.	901.1017	1358.1380	\dagger	1	
PVOL2 CVBM	EZ GLYCOPROTEIN PARCURSOR	BOVING CORONAVIAUS (STRAIN MEBUS)	123-139	Γ	264.279	1001.100	1746-1360		1	1	
Was creo	ES CLYCOPROTEIN PRECURSOR	BOVING CORONAVIRUS (STRAIN QUEBEC)	Γ	Т	Т	264.178	1011	1349.1380	1	1	
Was CVIIV	ES OLYCOPROTEIN PRECURSOR	BOVINE CORONAVIRUS (STRAIN VACCINE)	22:139	Т	Т	101.100	1746 1760		†	1	T
PVGL1 CVIDI	E2 CLYCOPROTEIN PRECURSOR	HUMAN CORONA VIRUS (STRAIN 229E)	T	E	1				+	†	
PVOC3 CVA44	ES OL YCOPROTEDI PRECURSOR	DAUTIDE CORONAVIALIS NOIV (STRAIN WILD TYPE 4)	3.111	_	1000	1111111	I	+		+	1
PYCELS CYMAS	ES CLYCOPROTEIN PRECIASOR	MUNUME CORONAVEUS MOTO (STRATO ASS)	Ī	Т				1		1	
PYCE CYNCC	E3 CLYCOPROTED PRECURSOR	MURLINE CORCMAVIRUS MAY (STRADA MOAY / VARIANT C1.3)	T	100						1	
1	ES OL YCOPROTEIN PRECURSOR	MURINE CORONAVIRUS MAY (STRATH HOL)	T	7	-			1	1		
Г	ET CLYCOPADTEN PRECURSOR	PORCING TRANSLESSIBLE GASTROENTERITIE CORONA VIBILE (STRAI	T	Ť	-	1		1	1		
Г	ED CLYCOPROTEIN PRECURSOR	PORCOG TRANSMISSIBLE GASTROENTERITIS CORONA VIBILS (578 AT	T	T		101	174-1797				
Г	ES OL YCOPROTREM PRECURSOR		17	Τ	T		1038-1064	1374-1297			
Г	E2 OLYCOPROTEIN PRECURSOR	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIL	1777	Т	Т		201-100	277:170	1	1	
PVOL1 CVPILI	ES CLYCOPROTEIN PRECURSOR	PORCING RESPIRATORY COROMAVIRUS (STRAIN \$6/1)7004 / BRITISH	316.311	T	T		1030-1002	5621-272	1	1	
PYCELS CYPEN	ES OL YCOPROTEIN PRECURSOR		T	Т	1					1	
PVGL3 CVPRT	EL CLYCOPROTEIN PRECURSOR	BIN CETEAL	T	Τ	7	1030-1073				1	
PVQL3_FBV	EL CLYCOPROTEIN PRECURSOR	(46)		75	٦,		7901-9701	5421-272	1		
PVGL3 BW6	ES OL YCOPROTEIN PRECURSOR	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN 6/12)	Ť	-	-	1000		+		1	
П	E2 OLYCOPROTEIN PRECURSOR	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	Τ	Т	T	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	į	1	1	1	
П	EL CLYCOPROTEIN PRÉCURSOR		Τ	Т	Ť	100		1		1	1
	ES CL'YCOPROTEIN PRECURSOR		T	Τ		200			1	1	T
٦	ES CLYCOPROTEIN PRÉCURSOR	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN KB8523)	Τ	\$17.606	770-796	1055-1040		Ì	1	1	T
WG2 BW	ES CL YCOPROTEIN PRECURSOR		Γ	376.396	Ť	_	1015.1040		\dagger	\dagger	1
7	EJ CL. YCOPROTEIN		176-201		Т	Т		Ì	\dagger	1	
T	EZ OLYCOPROTEIN		178-201					l	\dagger	\dagger	T
	EI GLYCOPIOTEIN	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN UK/167/94)	176-201			Ī			\dagger	\dagger	Ī
-	GLYCOPROTEDY OF 18 PRECURSOR							\mid	+	\dagger	
TVG PONY	OLYCOTAGEN B PRECURSOR				140-777				\dagger	+	T
-	CLYCOTION BY THE LORSON	E)		101.133	111-111			-		\dagger	T
T	G. VOSSOTISM BRECIBEOR	INCOMES SUMPLEA VINCO (117E 1/ SIRAIM 1/)	20							\mid	Ī
T	CA VOCABOTERA BESCHISCOS		2-103						-	-	
Т	CA VIORE DESCRIPTION	410	17:10)						-	-	
Т	CLVCOPROTEIN PARCINCON		83-104						-	-	
L	CLYCOPROTEIN B PRECINCOR		8 2						-	-	
Т	CLYCOPROTEIN B PRECURSOR		M-M	1	1						
	CLYCOPROTEIN B (FILAGMENT)	NDA-11023	Ī	13.144			1	1			
П	GLYCOPROTEIN I PRECURSOR	BOVINE 10 MPE SVIRES 17 PE 1	Τ	689.707	T			+	+	1	İ
\neg	GLYCOPROTEIN IL I PRECURSOR	BOUTHE 10 APESVIRES 1 18 FRAIN BAINT IBOVINE ALCAINILLITIS 179-399	Т	745.767	T	T	T	+	+	+	
PYGLB HSVBC	GLYCOPROTEIN I PRECURSOR	ACUTAGE OF BUILT TYPE, I (STRAIN COOPER)	Τ		†	1	1	\dagger	\dagger	-	1
										1	7

PUCENE	Distrizie	All Virases (Ne Bacteriophages)	П	П	П	П	П	Π	П	П	
FILE NAME			7	3	ARIAL AR	AREAM	ARCA!	OBEA'S	1	4	4
=		V\$25A) (EHV-I)	736-733			+	1	1		1	
			240			+				T	١
Τ.	GLYCOPROTEIN B PRECURSOR	EQUINE HERPESVIRUS TYPE I (STRAIN ABI)	736-757			-					
Т		EQUINE HELVES VIRUS TYPE I (STRAIN AB4P)	736-753			1		1	1		
Г		EQUINE HELD'ES VIRUS TYPE I (STRAIN KENTUCKY D)	736-753			1	1				
L		MANEK'S DISEASE HERPESVIRUS (STRAM RB-1B)	╗			1			1		
L		HELDESYTRUS SALMIÑ (STRAIN II)	Т	384-602	701.716	1	1				
		DESCRIOUS LARYNGOTRACHEITIS VIRUS (STRAIN 6)2)	T	170-/60	200/		1	1	1	Í	
П		INFECTIOUS LARYNCOTRACHEITIS VIRUS (STRAIN SA-2)	Т	100/00	20/20/		1				
PWGLB ILTW		INFECTIOUS LARYNCOTRACHEITIS VIRUS (STRAIN THORNE VIRZ)	T	1007-001	100	+					
2		MUTINE CYTOMEGALOVIRUS (STRAIN SAIITH)	23-136	566-589	731.765	4					
Т	4	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKIIAUSER / HECKER)	207-218			1					
L		VALUCELLA-ZOSTEA VIRUS (STRAIN DURIAS)	538			·					
T		HEAVES SOUTHEX VIRUS (TYPE I / STRAIN 17)	1.22	467.493		•					
Ţ		HEAPES SEMPLEX VIRUS (TYPE I / STRAIN KOS)	1.22	467.403							
T	OR VOOPENTEIN C PRECUTSOR	HERPES SIMPLEX VINUS (TYPE 2)	435-458			•	i		;		•
٦.		STRAIN 3331	436-459			ŀ	i				
	IN VONEOUT IN CAN PRECIMINA	BOVINE HEAVESVIRUS TYPE I ISTRAIN COOMIN)	23.684					.			
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7			444-439			•					
T.		P) AND ISTRAIN KENTICK	427.442			·					
Т	CECRETTIEN CL VOORDOTEIN GPS745 PRECURSOR	MANEK'S DISEASE HEAPESVIRUS (STRAIN NC-1)									
Т.	SECRETORY OF VOOPROTEIN OF 3743 PRECURSOR	MAREK'S DISEASE HENPESTIAUS (STRAIN AN-IN)	169-421								
OWN C PAR	SECRETORY OF YOOM OFEIN CASSAS PRECURSOR	MARKK'S DISEASE HEAPES VIRUS (STRAIN GA)	191-420						į		
PACE C REVIOL	SECRETORY OF YOOMOTEIN GPS 45 PRECURSOR	MAREK'S DISEASE HEAPESVIRUS (STRAIN MD!)	399.421						-		
PVC FIVE	CLYCOPROTEDY CHI PRECURSOR	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKITAUSER / BECKER)	180-197	446-472							
DATE VIVE	CLYCOPROTEIN OPV	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	431-449		,						
PVCC VZVS		VARICELLA ZOSTEA VIAUS (STRAIN SCOTT)	431-449			-					
TYCLE HEVIL	CLYCOMOTEN DIRECUISOR	AND (TYPE I / STRAIN	_								
PYCED HSV2	CLYCOPROTEDY D PRECURSOR	HEAVES SOUTHEX VIRUS (TYPE 2)	7.5							1	
PVOLE HEVIL	GLYCOPROTEIN E PRECURSOR	HERPES SINGLEX VIRUS (TYPE 1/STRAIN 17)	20.10			+				Ī	
PYCELE VEVS		VARICELLA-20STER VIXUS (STRAIN DUNIAS)	1	1970		1		T			
PYCH BASVA		BOVING RESPIRATORY STRUCTION, VIRUS (STRAIN ASSIMA)	103-00	187-687	20.00	1	T				
INCL. BRSWC	FUSION OL YCOPIOTEDI PRECURSOR	BOVING RESPIRATORY STREET I'AL VIRUS (STRAIN CUTEMINAGEN)	100	207-407	200	1			I		
PYOUT BASYR	FUSION OLYCOPROTED PRECURSOR	BOVING RESPIRATION TO STRUCT TALK TIMES (STRAIN NOW)	177.	106.414	43.40	1	T	T		T	
WOLL COW	FUSION OF YCOPROTEIN PRECURSOR	CANINE DISTERNER VINOS (STACKIN CROCKS) EFOCKT)		265.280	484.506	T				Ī	
YOU BOY	FUSION GLYCOPIOTEIN PRECURSOR	WALAN BERBIA ATORY CYNCYTIAL VIRILE (STRAIN A2)		265-280	484-506	Ì	Ì				
PVOL HOSVA	FUSION CL YOUTHIN PIECURON	HINGAN BESTEATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN LO		265-280	484.506	T					
	POSICIONAL DE L'ACCIONATION DE SCHIE COR	HENZAN BESPIRATORY SYNCYTIAL VIRUS (STRAIN RSS-2)		365-280	484-506						
PATE LARGE	FINE OF VENERAL PRECUESOR	MEASLES VIRUS (STRAIN EDMONSTON)MA (STRAIN HALLE)	224-245	286-302	451-477						
PVG LEAS	FUSION CLYCOPROTED PRECURSOR	MEASLES VIRUS (STRAIN IP.)-CA)	227-248	\$06-682	454.480						
Wal Leady	FUSION OLYCOPROTEZN PRÉCURSOR	MEASLES VIRUS (STRAIN YAMAGATA-I)	324-348	186-302	651-477						
TYCE MURE!	FUSION GLYCOPROTEIN PRECURSOR	MUNGOS VIRLIS (STRAIN SBL-1)	2.9	176-292	446-467	1					
PYCL! MUNEM	FUSION OLYCOPROTEIN PRECURSOR	MUNDS VINUS (STRAIN MYAHANA VACCINE)	276-292	446-467		1					
PVOLF MURER		MUNDS VIRUS (STRAIN RW)	176-297	97-99							
PVCU MARES		MUNIOS VIDUS (STRAIN SBL)	5-20	276-797	446-467	1					
PYOLL NOVA	FUSION GLYCOPROTEZN PLECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIANIZ)	273-289			1					
PVOL NOVE	FUSION OLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)	273-289			1					
PVCLF NOVIU	FUSION OLYCOPROTEIN PRECUASOR	MEWCASTLE DISEASE VIRUS (STRAIN HER/JJ)	273-219		1	1	1	T	Ī	T	
PVCL NOVHA	FUSION CLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIXUS (STRAIN BI-HITCHNEIVA?)	273-2119			1	1				
PYOLE NOVE	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIAUS (STRAIN LASVA)	277-2119			1	1	1	T	Ī	
PVOLE NOVA	FUSION OLYCOPROTEDI PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN MIYADERAN)	27.7.289			1	1				
PVCLE NOVO	FUSION CLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN COEFFICIAL)	231.780		+	Ť	Ī			Ī	
NOT NOW	FUSION OF TOP ROLE OF TRECONDER	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B /48)	373.289								
MOD FONTO	FUSION OCTOOR OF EACH PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ULSTEN67)	173-289								
	FUSION CLICATION PRECUISOR	PHOCEME DISTEMPER VIRUS	269-2115	305-326	187-383	331-538					
- A	POSICA OCTIVATION CONTRACTOR				1						

PCGEME	PINCTLZIP	All Virgos (No Bactersonbages)		-	ľ		-			
FULLYAME	PROTEIN	YARUS	AREAI	AREAZ	ARFA 3 A	ZVANV	A D F A G	94.984	1000	
Was rilled	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C39)	456-477	Г		Г	Т	\mathbf{r}	Т	Т
WGD NIH	FUSION CLYCOPROTEIN PRECURSOR	HUMAN PAKAINTLUENZA 2 VIRUS (PIV-2)	450-471					+		
WG NINO	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINT LUENZA Z VIRUS (STRAIN GREEK)	450-471			-		-	<u> </u>	
PVG F NING	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSIUIA)	450-471					-	ŀ	1
	PUSION CLTCUPROTEIN PRECURSOR	BOVINE PARAINFLUENZA I VIRUS	405-426						-	
PVG I PARK	FUSION OF YOMED THE CURSON	HUMAN PAKAIN LUENZA J VIRUS (STRAIN NIII 47815)	e ?	П	453-474					
PVCL RINGE	FUSION OLYCOPROTEIN PRECURSOR	RINDERPEST VIRIS (STRAIN)	20.74	Т	40.47					
PVCJ. SDOS	FUSION OLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN Z / HOST MUTANTS)	107	147.707		1	1		-	
PVGLE SENDS	FUSION CLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN FUSITIALI)	1979		Ť		İ	+	!	
PVGLI SENDH	FUSION CLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN HARAUS)	460-41		İ	+	İ	$\frac{1}{1}$		
PVGLE SENE)	FUSION GLYCOPROTEIN PRECURSOR	SEMDAL VIRUS (STRAIN HV))	200		T	1	1		1	
mar soot	PUSION CLYCOPROTEIN PRECURSOR	SEMDAJ VIKUS (STRAIN Z)	460-411		Ì	T	\dagger	+		
PWGL SV4	FUSION GLYCOPROTEIN PRECURSOR	SDGAN VIRUS 48	453.474			T		+		
PYQU SVS	FUSION GLYCOPROTEIN PRECURSOR	SINGAN VTRUS 5 (STRAIN W))	401-425	446-467		+	T			
WGJ TRIV	FUSION GLYCOPROTEIN PRECURSOR	TURKEY RHINOTRACHEITIS VIRUS	175-191	452-474		-	İ	1		
VGO BOV	SPIKE GLYCOPROTEIN PRECURSOR	INFECTIOUS NEMATOPOIETIC NECROSIS VIRUS (STRAIN ROUND BUT	17.99			•				
_	SPIKE CLYCOPROTEIN PRECURSOR	RABIES VIAUS (STRAIN ERA)	484-474			-				
7	SPIKE OLYCOPROTEIN PRECURSOR	RADIES VIAUS (STRAIN HEP-FLURY)	172.791	454.474		į.		-		
WCC KAN	SPACE CLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN PV)	484.474							
		INCLUS VINUS (STRAIN SAL)	65474						_	
		KABLES VIRUS (STRAIN STREET)	454-474							
	SOLVE OF WASHINGTON TO THE CO.	I UNCET INTRODUCTIONS VINUS	99-216				Т.			
Т.	STATE OF TOO PAINT PRODUCED	MACAL PERCHASHIC SETTICEMIA VIAUS (STRAIN 07.71)	406-428	7						
	CALVODROTIVE M PRICE IN CO.	MEMAN COTOMEGALOVINOS (3 IAAIN ADISS)	T	Т	7	91.712				
-	O VOORACIENI IN PRECINACIA	HERBER CHAN EN WHIR COVE LICERATE IN	Т	364-381	٦	690-71				
1	CLYCOPROTEDNIA PRECURSOR	HERDES SDAPLEX VIRUS (TYPE I / STRAIN HEEM)	707-07	Т	129-621	+	1			
Ι	CLYCOPROTEIN H PRECURSOR	HEAVES SOUTEX VIRUS (TYPE 6 / STRAIN GS)	T	T		1	1		1	
	CLYCOPACTED H PRECUASOR	EQUINE HEAVESVIRUS TYPE 4 (\$TRAIN 1942)	T	814.816	İ	1	1	+		
	OLYCOPROTEIN H PRECURSOR	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP) AND (ISOLATE HVS2SA)	Τ	107-117	\dagger	1			1	
		HERPESVIKUS SADAIRU (STRAIN 11)	Г	658-679	I	+	T			
PYGLH MOAYS		MURINE CYTOMEGALOVIRUS (ŠTRAIN SMITII)	670-690			l	\dagger		-	1
		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	150-180							
TACK TOWN	GLYCUTROIEDNI	HEAVES SINGLEX VIXUS (TYPE I / STRAIN I?)	09-()					L	_	I
Т	GLILLWANDELN I MELUKSOK	LAUNE REJUES VINOS 1 VPE 1	44-63							
-	M POLYPROTEIN PRECIDIOR	BLNYAVAUS CERNISTON	712-761		1	1				
т-	M POLYPROTED PRECURSOR	BUNYAVIRUS LA CROSSE (ISOLATE L74)	1	17.77	116.00	1776	-		1	
	M POLYTROTEIN PRECURSOR	BUNYAYAUS SNOWSHOE HARE	Ī	Τ	T	_	317.1410		+	1
	m polyprotein precursor	BUNYAMWERA VIRUS	_	ş	Ť	_			-	
_	M POL YPROTEIN PRECINSOR	DUGBE VIRUS	Г			\dagger	T	$\frac{1}{1}$		
_	M PCL YPROTEDN PLECURSON			Ť	_	999-1019				
	M PULTINUISM PIECURSON	HANTAAN VIKUS (STRAIN HOIO)	П	Ħ	000-1020					
ALAN TO ESTA	M TOLITIKU I EM TRECUMBON	MARI AND VINUS (STRAIM LEE)	٦		1201-1001					
_	M POLYMONIEM PRECIDENCE	DATE AT TOUR DESTRUCTION OF THE STATE OF	_		\equiv					
Τ	M POLYPROTEDY PRECURSOR	PROSPECT HILL VINIS		200-201	348-367	531-551	15.041			
L	M POLYPROTEIN PRECURSOR	PUNTA TORO PIE EBOVIAUS	T	1000	-	1		1		
8	M POLYPROTEIN PRECURSOR	ALLINAS BI)	T	۳	70(1:(/)	1	1	1		
2	M POLYPROTEIN PRECURSOR		T	1	Ť	1 1 1 1 1 1 1 1	1	1		
_	M POLYPROTEIN PRECURSOR		Τ	Т	+		1		1	
	M POLYPROTEIN PRECURSOR	STRAIN 216-548 MIZ)	T	Τ	Ť	154-1176	1	+	+	
	M POL YPROTEIN PRECURSOR	SEOKL VIRUS (STILAIN 90.19)	П	Г	۲	6101-666	+	1	1	
WOLK SEOUR	M POLYPROTEIN PRECURSOR				П	1000-1020	-	l		
┰	M POLITICO EM PRELORSON	SECUL VINUS (STIAM SR.II) (SAPPONO RAT VINUS)			П					
7	M POLITRUIGIN TRELUASON		%I-585	655-674 824	826-842 92	923-952 96	686-996	H		
		, r								

PCCENE	PUICILZIP	All Viruses (No Bacteriophages)			1		1	ABFAA	ABFA 7	ABEAS	A BFA 9
FILE HAME	PROTEIN	YIRUS	1000	Т	711.000		Т	Т	Г	1	
PVGLP BEV	PEPLONER OLYCOPROTEIN PRECURSOR	BEANE VIRUS		T							
PVGLX HSVEB	GLYCOPROTEIN X PAECURSOR	EQUINE HELPESVINUS TYPE I (STRAIN ABAP)				1				Ī	
PVCLX HSVEK	OLYCOPHOTED GX PRECURSOR	EQUINE HELVESVIRUS TYPE I (STRAIN KENTUCKY A)			Ì	-					
PVCLX HSVEL	GLYCOPROTEIN GX	(EQUINE HEAPESVIRUS TYPE I (STRAIN KENTUCKY D)									
PVGLX PRVIL	SECRETED GLYCOPROTEIN GX	PSEUDORADIES VIRUS (STRAIM RICE)	144.170							T	
PVCLY JUNIN	GLYCOPROTEIN FOLYPROTEIN PRECURSOR	ILMIN ALENAVIRUS ;								Ī	
PVCLY LASSO	OLYCOPROTEIN POLITROTEIN PRECURSOR	LASSA VIRUS (STRAIN GAIR!)		Т						1	
PVOLY LASS	CLYCOPROTED/FOLVPROTED/PRECURSOR	LASSA VIRUS (STRAIN IOSIAM)									
PVOLY LYCVA	CLYCOPROTEIN FOLYPROTEIN PRECURSOR	LYNCHOCYTIC CHONOMENINGITIS VIRUS (STRAIN ARAISTRONG)	3:3			Ī					
WOY I VENN	CO. VCOPROTEIN FOR YPROTEIN PRECURSOR	LYAPHOCYTIC CHORIOMENINGITIS VIRUS (STRAIN WE)	£	101-62							
מושל בי לישובו	CH VENDERATE IN POR VPBOTE IN PRECURSOR	MOPELA VIRUS	13-35	425-447							
	ALL COMPANY DE COMPANY	PUTATION ARENAVRUS	12.38	997-138							
VOLY PARY	CATUMOSEM PALITACIEM PRECORDE	STORY SECTION	15.51			ŀ					
PVCLY TACV	CLYCOPHOTEDI FOLTPROJEIN PRECUASOR	INCOMES TAKES	-			•					
SACEN TACKS	CLYCOPROTEIN FOLYPROTEIN PLECURSOR	TACALIBLE VIRUS (3 FIALITY V.)				1					
PVCI Y TACVI	г	TACARIBE VIRUS (STRAIN VT)	17.2								
A A FAN	Т	TACALIBE VIRUS (STRAIN TRVL 11596)	12:31		٦						
	Т	COWPEA MOSAIC VIRUS	161-161	569-594	157.743	1110-1133	1165-1184				
25	UNIONE PARTITION IN THE	COMPEA MOCAL VIBILE	311.335	741.764							
ACMI COM	CENCHES FULLY AND EAR PR	TEROTERA BARB CORTIC COTS AIN BOC. ST. CL. B.CAN LIFER P.C. VIRGIS 61	657-681			•					
PVCP2 EBV	PROBABLE MEMBRANE ANTIGEN GP220	EVERTICAL VIACE (SINAIN BY) (CONTAINS C				1					
PVGP3 EBV	ENVELOPE OF YCOPROTEIN CP340	EPSTEIN-BALL VIRUS (STRAIN BY)-1) (HUMAN HEATES VIRUS 4)									
VAR ENV	PROBABLE MENDRANE ANTIGEN CP15	EPSTEIN-BARK VIRUS (STRAIN B95-1) (HURIAN HERVESVIRUS 4)	97.8								
VOS SOVE	CTRINCTION AL CO. VOOPBOTEIN PRECURSOR	EBOLA VIRUS	14-52	537-361	653-675	•					
200	STANCE OF VOCABULTED PRECISEOR	MARRIED VIKUS (STRAIN MUSOKE)	538-362	607-627							
MACON SAL	STRUCTURE OF TOWN OF THE PROPERTY OF THE COM	LABBORN VILLE (STRAIN POPP)	538-562	607-627		••					
PVOP MABVE	STRUCTURAL GLYCUPHUIEM PRELUASOR	CONTRACTOR OF STATE AND CONTRACTOR	76.02	105.121							
DOWN IOHINA	PROTEIN-TYROSINE MOSPHATASE.	VACCINIA VIACO (STRAIN CONTINUE)	76.61	104.131							
PUHOL VACCV	PROTEIN-TYROSINE PHOSPHATASE	VACCINIA VIXUS (STRAIN WR.)				+					
PURE VARV	PROTEDA TYROSEME PHOSPHATASE	VARIOLA VIRUS		171-601		\cdot					
PUMBT VACEV	LATE PROTEIN HT	VACCINIA VIRUS (STRAIN WR)	19-61								
VALUE VALVE	LATE PROTECN AT	VANOLA VIRUS	60								
A Labor	PROPARE R HELICASE	FOXTALL MOSAUC VIRUS	182.205			1					
7	PROBABLE HOT ICASE	PAPAYA MOSAIC POTEXMRUS	1133-164			•					
A 100.	PEOTEN II	VACCINIA VIRUS (STRAIN COPENHAGEN)	120-135								
200	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VALIDLA VILUS	120-135								
LANG AWA	TAULEN II	VACCINIA VIRUS (STRAIN COPENHAGEN)	194-220			•					
AVE) VACE	PAULEN D	VACCINIA VIRUS (STRAIN WR)	194-220								
LANG AVEC	TRUEW I	VARIOLA VIRUS	194-220						٠		
PVIO) VARV	Moteuria	VACCEMIA VIBIR (CTRANA WE)	104-128	133-155							
PVTO6 VACCV	PROTEIN 16	CALCALA MACINE	106-178	133-155							
PVIDS VARV	PROTEDY 14	TAKOLA VINOS	7.7	144.147							
PVIOT VACCC	PROTEIN 17	VACUALA VIAUS (STAMP CONTRACES)		100.000							
PV107 VACCV	PROTEIN 17	VACCINIA VIKUS (STRAIM WK)									
PVIOT VARV	PROTEIN 17	VAUOLA VIRUS	•	007-006							
PVIDE VACCE	PUTATIVE KNA HELJCASE IB	VACCIMA VIXUS (STILAIN COPENHAGEN)	7 7								Ì
PVIOR VACCV	PUTATIVE KNA HELICASE 19	VACCINIA VIRUS (STRAIN WR)	717-00								
PVICE VARV	PUTATIVE RNA HELICASE IS	VARIOLA VIRUS	217-00								
PVIET HOWA	35 KD DOGEDIATE-EALLY PROTEIN I	HUNGAN CYTCHEGALOVIRUS (STRAIN AD169)	8	000							
120	SEED DANGEDIATE, EARLY PROTEIN I	HUNGAN CYTOMEGALOVIRUS (STRAIN TOWNE)	17:100	33.350							
1	AS KIN BAGEDIATE KARLY PROTEIN 2	HUNGAN CYTOMEGAL OVIRUS (STRAIN AD 169)	14-33	189-406							
	ALEN DOJETHATE PARLY PROTEIN 2	HUMAN CYTOMEGALOVINUS (STRAIN TOWNE)	14-32	381405							
	DACEMATE EARLY PROTEIN 2	MURLINE CYTOMEGALOVIRUS (STRAIN SMITH)	131-272								
	NO FOR MARTINETE, FABLY PROTEIN 1	HIMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	14.33								
	SACRATE BAR V PROTECTION	HEAPESVINUS SADAUU (STRADH 11)	65.80								
A CONTRACTOR	N. 31 METORS OF STREET	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	911-001	273-290							
PVIEN REVAL	PROTEIN BRATIS	EPSTEIN-BALL VIRUS (STRAIN 895-8)	75-100	135-132	203-222						
1000	┰	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	68-89	190-217							
TOTAL PROPERTY	7	HELDES SIMPLEX VIRUS (TYPE I / STRAIN 17)	83-110	250-270							
200	۳	EQUINE HEAVESVIRUS TYPE I (STIAIN AB4P)	36-49	93.170	145-172	207.763	301-33	33.38			
	T	HERPESVIRUS SAIMIRI (STRAIN 11)	16-101	113-331							
PVOV HSVSA											

WO 96/19495 PCT/US95/16733

MACHINE MACHINA WINGSTRAND MACHINA WINGSTRAND MACHINA WALLA MACHINA	MACTOR M	$\Pi\Pi$	All Viruses (No Bacteriophages)	AREAL	AREA 2	ARTA 2	AREAS	ANEAS	AREA	П	1-1-3	
MOTORNEON PRINCES 1910 1911 1		\Box			7	S PAIN	4	4	ARTA			
MACIONAL HOUSE STAND COPENACED 19-11 19-12 19-12 19-13 19-	MATERIAL VACCION VIRGINIANO COMPANIANO PATES	7	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	10-12	154-121	230-252	•			T		3
ROUTE WACCHA VILLS (TAME VER) FR. 10 FR.	The control of the		VACCINIA VIRUS (STRAIN COPENHAGEN)	89.110								
MODERN WACKERA WILLS STANK COPENACED FIFTS		T	VACCINIA VIRUS (STRAIN WR)	99.110								
		7	VARIOLA VIRUS	89-110			1				-	
		7	VACCINIA VIRUS (STRAIM COPENHAGEN)	07:113	206-334	118.317						İ
		7	VACCINIA VIRUS (STRAIN WR)	87-113	201.214	119:317						•
MACHINET VACCHAN VARISTRAN COPRIAGEN 1944 1	MATERIAL WALLAND STRUCK WALLAND STRUCK WALLAND STRUCK WALLAND WALLAND STRUCK WALLAND WALLA	Ţ	VACCINIA VIRUS (STEAIN COPENNAGEN)	106-133							ľ	
MOTERIAL VACCHAN VARIAS STALAIN WAY 1944 1954 1954 1954 1955 1954 1955 19		T	(VACCINIA VIRUS (STRAIN COPENHAGEN)	19-60								
FOOD BLACK VACCORA VARIS (STAJIN GOVERNACED) 15-54 15-57 15-15 15-57 15-		T	VACCIMIA VIRUS (STRAIN WR)	19-61				Ĺ	-			
WOURSEL WOLDSEL WACCOMA VIRIS STRAIN WAY AND STRAIN CONDINGERS STAIN WAY AND STRAIN CONDINGERS STAIN WAY AND STRAIN WAY		7	VARIOLA VIRUS	19-61	-	-	-	!	•	:		:
HOUTER VALCALA VERUS STAATH WAD STAATH COPERIAGED 167-161 116-201 116-171	High High House High	+	VACCINIA VIRUS (STRAIN COPENHAGEN)	20:05	186-208	292.315	$\frac{1}{2}$					
MOTERIA VACCIOA VAUGA AVAUS FIRE ALL PACTION 18.79 18.75 1	MATTER ID MAGENA WILLS MAGENA WILLS MATTER ID MAGENA WILLS MATTER ID MAGENA WILLS	7	VACCINIA VIRUS (STRAIN WR)	Τ	186.708	3.3.1						
MODIEN M	MACHINE WACKER WILD WARD STRAIN COESTICION LEAS	7	VANOLA VIRUS	Τ	185.207	201.114						
MOTERIA MOTE	MOGNALE IL PROTEIN	┪	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COFENIAGEN)	Τ								
		┪	VARIOLA VIRUS	1			+		:			
	MACHANIE IN PROTECTION MACHAN PATLEGALVINGS TYPE 1 1143 1143 1143 1144		COTTONTAL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	111.00			-					
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MOOGALE LEPOTER MOOGALE PATE 131-34 131-	MORABLE IL PROTECT MORABLE	1	HUMAN PAPILLOMA VIRUS TYPE 41		T							
MOGALE LI PORTEN	MOOABLE ID FOOTEN	٦	REOVINUS (TYPE 3/STRAIN DEARING)	Τ	777. 175		-					
			HUMAN PAPILL OMA VIRUS TYPE B	Τ	8	2,112	+					
			HUMAN PAPILL OMAVIEUS TYPE II	27:20			-					
PROGNALE LI PROTEIN HIGHAN FAPELOGAVINES 17PE 18 19-29			HINTAN PAPIT I DILAVIBLE TVDE									
PROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.218 11.299 11.291 PROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.218 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.218 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FIGACAN FAPIL DOLLAYINIS 177E IA 11.291 FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IF PROTECH FROGNELE IA 11.101 FROGNELE IA 11.10	PROCAZE IL PROTEIN	Г	HIMAN PAPILI DAZA VIBINE 14	86-57							T	Ī
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	PROGNET LI MOTERN HALLAY PATELLOALVINGS TYPE 31 14-40 441-402 14-40 441-402 14-40 14-4	T	MUMANY PAPILLIANIA VIRUS 1 YPE 2A	88-114						Ì	1	
PROPABLE ID FROTEIN HIGHAN PAPEL COLAVIRUS TYPE 11 15-55 14-210 15-55 15-55 14-210 15-55 14-210 15-55 15-55 14-210 15-55	PROMABLE IS ROUTEN	T	HUMAN PAPILLOMA VIRUS TYPE 31		43.462		+				†	
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MORABLE LI PROTEIN		T	HUMAN PAPILLOMAVIRUS TYPE 15	Τ								
PROGRAME LI PROTEIN	PROBABLE 12 MOTERN HIGHAN PARLICALAVERIS TYPE 21 15-56 14-170 4-6 PROBABLE 12 MOTERN HIGHAN PARLICALAVERIS TYPE 21 15-56 12 MOTERN HIGHAN PARLICALAVERIS TYPE 21 15-57 PROPABLE 12 MOTERN HIGHAN PARLICALAVERIS TYPE 21 15-57 PROPABLE 12 MOTERN HIGHAN PARLICAL PROFEEN HIGHAN PROFEEN HIGHAN PARLICAL PROFEEN HIGHAN PARLICAL PROFEEN HIGHAN PROFEEN HIGHAN PARLICAL PROFEEN HIGHAN PARLICAL PROFEEN HIGHAN PROFEEN HIGHAN PARLICAL PROFEEN HIGHAN PARLICAL PROFEE	7	HUMAN PAPILLOMAVIRUS TYPE 41	Τ	14.414	Ì						
MOMENTE LI PROTEIN	MARAN PARLOMANIA 17FE 19 FROGABLE LA MOTERN MARANA PARLOMAVRIS 17FE 51 FROGABLE LA MOTERN MARANA PARLOMAVRIS 17FE 51 FRAGA PARLOMAVRIS 17F	1	HUMAN PAPALOMAVIRUS TYPE 42	Γ	14.170		T			j		
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MOGABEL LA PROTEIN	MONOABLE IS MOTERN	7	HUMAN PAPILLOMAVIRUS TYPE ST	200	T				1			
MONABLE 12 MOTERN MUMAN PARLOMAN'RUS TYPE 69 15:59 10:54	MORABLE IS MOTERN MORAN MARLOMANTRUS TYPE 69 13-59 10-54 10-	٦	HUDGAN PAPILLONIA VIRUS TYPE SE	T	1							
MOOALE LA PROTEIN EUROPÉAN EIR PAPILLOMAVIRUS 16.54	MOOABE LI PROTEIN EUROPEAV EIK PAPILOGALVINUS 105-56 14-71 1	7	HUMAN PAPELDMANTRUS TYPE 68	T			1					
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MONABLE LA PROTEIN MOLAULE LONG STATES 6.28 6.28	MONABLE LD PROTEIN	٦			1							
MUNOR COLE PROTEIN LANGEAL) RECVRUS (TYPE 1/5TRAIN DEAGING) 114-137 111-1316 114-137 111-1316 114-137 111-1316 114-137 114-137 111-1316 114-137 114-137 111-1316 114-137 114-137 111-1316 114-137 114-137 111-1316 114-137 114-137 111-1316 114-137 114-137 111-1316 114-137 1	MANON COLE PROTEIN LANGOA	٦										
JUMOR COLE PROTEIN LANGER 1117-1136	ADDIOR COLE PROTEIN LANGED A RECVRUS (TYPE 11 STRAIN LANGE) 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 111-1136 114-77 114-77 111-77			116.216								
NEWORL CORE PROTEIN LANGE AND NEOVERUS (TYPE I / STRAIN LANG) 114-179	LUMPORT CORE PROTECT LANGED 15 FEATH LANG) 14-171			1								
LOW PROTECH LOW PROTECH MOTECH	LOW PROTECH LOW PROTECH LOW PROTECH LOW PROTECH PROTECH LOW PROTECH PROTECH LOW PROT			Ť	67						\mid	
MOTERN MI	PROTEIN WILLIAM VACCERIA VBUS (STAIN COERNIAGEN) 134-159 177-191 131-103 131-104 131-103 131-104 131-103 131-104 1	Г		7	7	٦						Ī
MOTERN M 17-181	MOTERN M VACCIBIA VILLS ISTAAN WR) 114-154 171-151 171-152 171-152 171-154 171-152 171-152 171-154 171-152 171-152 171-154 171-152 171-152 171-154 171-152 171-154 171-152 171-154 171-	Г		T	٦	٦	45.861		-			T
MATHER ROTEIN WILL PROTEIN ML.1 VALUEL A VALUE STRAIN DEAGING 19-109 134-144 120-231 121-24 121	MOTERN WI MOTERN WI MOTERN WILL MOTERN WILL MOTERN WILL MOTERN ML-3 MOTERN WILL MOTERN ML-3 MOTERN WILL MOTERN ML-3 MOTERN WILL MOTERN ML-1 MOTERN WILL MOTERN WILL MOTERN WILL MOTERN WILL MUTE	Г		7	٦	11-302				İ		
HOWAY VEIGN STRUCTUAL PROTEIN MU.2 FUCUND STRUCTUAL PROTEIN PROTEIN MU.2 FUCUND STRUCTUA	MATHEMORY VERIOR STRUCTURAL PROTEIN MIL. 3 LEGVIRUS (TYPE 1 STRAIN DEARING) 141-164 121-142 121-143 121-	t=		٦		30-251					l	I
MAJOR VULDA STAUCTURAL PROTEIN NO.2 ALCOVRUS (TYPE 1/2 STAIAN) DEALING) (141-164 227-245 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 216-304 217-345 217-345 216-304 217-345		T			Г	21.249			İ			1
MAJOR VENCE STRUCT PROTEIN MULTANULARY 18 TAIN LINE)	MACON VERDOR STRUC PROTEIN ML-1 AND LANGE 141-164 127-245 140-104 141-416	T			Г	Г	L	T	(17.5)		1	
MACON VINCE STRUCT PROTEIN MULIALLIC REOVENUS (TYPE !! STRAIN DEALING) 164-197	MACON VINCE STRUCT PROTEIN MALINAL! C REOVERUS (TYPE 1 / STAIN DEALNG) 164-197	Ť		Γ	Γ	Т	Τ	Τ			1	
MAJOR VILLON STRUCT ROTEIN MJ. IANU-IC REDVIRUS (TYPE J I STRAIN DEARING) I44-193 I44-19	MAJOR VILLON STRUCT PROTEIN MJ. IANU-IC REDVIRUS (TYPE 1 / STAIN DEARING) 164-193 164-19	7		Τ	T	Т	T	,,,,,				
MAJOR VILLOR STRUC PROTEIN MULIAMILIC REOVIRUS (TYPE 1/ STRAIN DS/JONES) (166-197) MAJOR VILLOR STRUC PROTEIN MULIAMILIC REOVIRUS (TYPE 1/ STRAIN LANG) (166-197) MAJOR NOWSTRUCTURAL PROTEIN MULINS (SEOVIRUS (TYPE 1/ STRAIN DEALUNG) (166-197) MATTLUX PROTEIN (166-197) (166-197	MALOR VELOW STRUC PROTEIN MU.I.M.L.IC AEOVRUS (TYPE 17 STRAIN DS/10NES) 166-177	╗		164.103	T	1						
MAJOR VIDLOM STRUC PROTEIN AUJANUJIC REOVIRUS (TYPE JI STRAIN LANG) MAJOR NOWSTRUCTURAL PROTEIN MUJNS REOVIRUS (TYPE JI STRAIN DEALING) MATRIX PROTEIN MATRIX PROTEIN CANDRE DESTRUATORY SYNCYTIAL VIRUS (STRAIN AS1999) JAST	MALOR VIDEN STRIC PADTEIN MU.IAMU.IC REOVINUS GTYPE 1/ STRAIN LANG) 164-177 16			100	1							
MAJOR NOWSTRUCTURAL PROTEIN MILNS (REOVINUS (TYPE 1/ STRAIN DEALING) 104-326 MATRIX PROTEIN 100-00-00-00-00-00-00-00-00-00-00-00-00-	MAJOR NOWSTRUCTURAL PROTEIN ARLAS REOVERUS (TYPE 1/ STRAIN DEALING) 104-316 MATRUZ PROTEIN BOYDRE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A11908) 37-43 MATRUZ PROTEIN CANINE DISTEMPER VIRUS (STRAIN ONDERSTEPORT) 144-165 MATRUZ PROTEIN HUMAN RESPIRATOR Y SYNCYTIAL VIRUS (STRAIN A2) 44-45 MATRUZ PROTEIN LA PERDAGORACIAN-REXICO VIRUS 311-338 MATRUZ PROTEIN REASTES YTRUS (STRAIN EDMONSTON) 311-338				1							
MATRIX PROTEIN BOVINE RESPIRATORY SYNCYTOLI (STRAIN ASSISO) 17-62 MATRIX PROTEIN CANINE DISTEMBER VIRUS (STRAIN ONDERSTERORY) 1442-144	MATRIZ PROTEIN BOVDRE RESPIRATORY SYNCYTIAL VINUS (STRAIN ASSISOR) 10-62-10	Ť		1						-		
MATRIX PROTEIN TOWNS (STRAIN ONDERSTEROORS) 14-04	MATRIX PROTEIN CANTHE DISTEMBER VIRUS (STRAIN OFFICER) 144-165 144-1	-			8						-	
THE PROPERTY OF THE PARTY OF TH	MATRIX PROTEIN HUMAN RESPIRATORY STRUCYTIAL VRUIS (STRAIN A2) 44.63 MATRIX PROTEIN LA PEDAD-MICHOACAN-JEXICO VRUIS 111.335 MATRIX PROTEIN REASTES YTRUS (STRAIN EDMONSTORY 111.335 MATRIX PROTEIN 111.335			Т								T
MATRIX PROTEIN HUMAN RESPIRATORY SYNCYTIAL VIBILS (STRAIN AT)	MATRIX PROTEIN LA PEDAD-MICHOACAN-MEXICO VIRUS 11 CONTROL 111111 11111 11111 11111 111111 111111	PYMAT HOSVA MATRIX PROTEIN		Ţ	6							T
LA PEDAD-MICHOACAN-MEXICO VIRUS	MATRUX PROTEIN MEASUES VIRUS (STRAIN EDWIDNSTON)		(Pulled of the Control of the Contro	7	8	1						
MATTUX PROTEIN					1	1						

PCCENE	PINCTIZIP	All Virger (Ne Beckriophygn)	П	П	П	П	П	п	П	
FILENAME	PROTEIN	YURUS	J	AREAL AS	AREA AREAS	TOWN TO	2 AREA		T T T T T T	ARIAZ
PYMAT MEASH	į	MEASUES VIRUS (STRAIN HALLE)	283 JOA							
PWANT MENSI		MEASLES VIRUS (STRAIN IP.)-CA)	= 12		-	-				
PWAT MEASU	MATRIX PROTEIN	MEASLES VIRUS (STRAIN HUZ)								
PVILLE LABOR		MUMPS VIRUS (STRAIN SBL-1)	191-207	327.250 310	0(0.010					
PVALE LABOR		MUNGES VIRUS (STRAIN SBL)	191.207	227-250	310-330					-
PVACAT NOVA		NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/)2)	135-151	190-201	906-339	_				
	MATRIX PROTEIN	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45)		190-208 309	309-329					
X	NATRIX PROTEIN	HUMAN PARAINFLUENZA I VIRUS (STRAIN C19)	195-217							
	MATUX MOTEIN	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSIIIDA) (PIV-2)	132.184	189-205 301	908-338					
PVICAT PHILA	MATRIX PROTEIN	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSIIIBA) (PIV-AA)	112-332				_			
PYAKAT PYAKE	MATRIX PROTEIN	HEMAN PARAINFLUENZA 48 VIRUS (STRAIN 60:333) (PIV-4B)	112-332	-			-			
TYLAT BOOK	MATUX PROTEIN	ANDEAPEST VIAUS (STRAIN KABETE O)	300-321	117.260 28	283.309		-	L		
WALK LOOP	MATRIX PROTEIN	SENDAL VIRUS (STRAIN FUSHIMI)	195.217	-						
HONGE TANA	MATRIX PROTEIN	SENDAL VIRUS (STRAIN HARJIS)	195-217							
WALK SENEN	MATRIX PROTEIN	SENDAL VIRUS (STRAIN Z.)	13:51	i		-				-
PVALE COVE	MATRIX PROTEIN	SUBACUTE SCLEADSING PANENCEPHALITIS VIRUS (STRAIN DIKI:N)	Γ	314.338		<u> </u>	<u> </u> 			
WAAT EVAL	LA PRINCIPLE	SMEAN VIRUS 41	Γ	1	308.328	-		-		Ī
1	MATERIA PROTEIN	SIMILAN VIEUS S (STRAIN W.)	Τ	ī	308.335	<u> </u> -	-			:
	MATRIX BROTEIN	SPRING VIREMIA OF CARP VIRUS (RHADDOVIRUS CARPIA)	L	Т		-				
Ł	MATRIX PROTEIN	TURKEY NUMOTRACHEUTIS VIRUS	122-143			 -				
ALL CAR	ELCS VCOPROTEIN	BOVING CORONAVIRUS (STRAIN MEDUS)	Γ	137.161	91:17	-	-			-
CALLS	si Ca Vocesotsov	MIDMAN CORONAVIRUS (STRAÍN 229E)	25	T	-	\mid	<u> </u>	-	I	
	to or vocatoren	HIDAAN CORONAVIRUS (STRAIN OCC))	Γ	56.65	137.161	-		-		
The state of the s	ALCONOMICS OF THE PARTY OF THE	LATERAL CORONAVIEW LAIV (STRAIN A CO.	L	I						
VINCE CVINCE	EL CLTCOTACIENT	TO BELLE AND CHEEK LAND STREET HAD		ŀ	1	<u> </u>				
PVACE CYNUN	El GLYCOPKO IEIN	PROBLEM CONCRETE TO STRUCTURE THE CONCRETE STRUCTURE STR		Ì					-	
WAGE CATES	ET OLYCOPROTEIN PRECORDOR	MONTH TO A MANAGE OF THE PROPERTY OF THE PAR	107	174.101		}			I	
PWE! CVPU	ELG. TUMOLEIN MECURSUR	INTERNATIONAL PROPERTY OF THE CONTRACT	134.101						1	
	EL OLT COTTO EL PRECUESOR	TIPLE STATE OF COMMANDERS	T	137.141	171.180				-	I
AND CALLED	EI OLTOMOIEM	LALU REPORT & SENSON TOTAL		T				-		
VACE BY	EL DE CONTROLLERO	AVIAN BEPOTANIS BROACHTIS VIRITS (STRAIN BRAIDETTE)	74.10	ł		-				
	TO CHANGE AND THE PARTY OF THE	AVIAN INSECTING RECOGNITIS VIRIS (STRAIN REALINISTS ALEX	14.101			-				
AND INAM	EI GLI COMO IGN	A CAND THE PROPERTY OF THE CORP. CORP. PROPERTY.	•					 	-	
WAC BY	LECTURAL SING SAN THE SECOND	FEATURE AND CATE AND ROLL	Ţ	178.201	 	+		+		
AND ROMA	-	CAIR BLOWER MAKAIC VIRUS (STRAIN CA. 1841)	T	Ť	111.301	-				
	MOVE MENT PROTECT	CALL PLOWER MOSALC VIRUS (STRAIN DA)		T	107-(0)	-	-			
2007		CALILIDAVER MOSAIC VIRUS (STRAIN BBC)	NE 13X	147-164	12.3	-	-			
WALL CALVA	-	CAULIFLOWER MOSAIC VIRUS (STRAIN NYBISS)	Г	f	107:61	-				
WAS CALORS	MOVEMENT PROTEDY	CAULELOWER MOSAIC VIRUS (STRAIN STRASBOURG)	111-134	147-164	183-201		_			
WAS CANW	MOVEMENT PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN W260)		Г	183-201	L				
PWG CERV	MOVEMENT PROTEIN	CARNATION ETCHED RING VIRUS	393-316	Г		L	_			
PWG DWD	MOVEMENT PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DXS)	18-131	160-191		L				
WAS SOCIAL	MOVEMENT PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-147	273-299			L			Ī
WASA MOBDS	MAJOR SURFACE ANTICEN PRECURSOR	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE SS)		269-295						
PWASA HEBDC	MAJOR SUNFACE ANTIGEN PRECURSOR	DUCK HEPATITIS B VIRUS (STRAIN CHINA)		261-294						
PVICEA HORDO	MAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS IN VIRUS		231-257						
WASA HOBDW	MAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS B VIRUS (WHITE SHANGHAI DUCK ISOLATE S)!)		П			_			
PVMSA HEBOS	MAJOR SURFACE ANTIGEN PRECURSOR	GROUND SQUINKEL HEPATITIS VIRUS	٦	٦	180.395					
PVASA HOBIE	MAJOR SURFACE ANTIGEN PRECURSOR	HERON HEP ATTITIS B VIRUS	<u>_</u>	27:32		+	-			
PVACSA HORBYO	MAJOR SURFACE ANTIGEN	HEPATTHS B VIAUS	7	8	_					
	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIAUS (SUBTYPE ADWZ)		244.270		+	1			
	MAJOR SUMFACE ANTIGEN PRECURSOR	HEPATITIS B VIXUS (SUBTIVE ADIA)	1	244.270		+		1		
PVACSA IPBV9	MAJOR SURFACE ANTIGEN PILECUISOR	METATIFIS BY VICTOR (SUBJETCE ADM/S) INCHAMILY	0.7-17		-	1	1	1		
WASA HUBVA	MAKOR SUITALE AN INCA PARCUASOR	LEGATITICS OF VICTOR (COMPANY AD)	Т	10:10	1	+	+			
PVACA HEBVU	MANCH SAMPACE ANTIOEN PRECURSOR	HEPATITIS B VRUS (SUBTYPE ADW / STRAIN INDONESIA/PIDW420)	Ţ		-	+	+			T
INDIA PARA	MAIOR SIMPACE ANTIGEN PRECINSOR	HEPATITIS & VIRUS (SUBTYPE ADW / STRAIN JAPAN/PIDW2)))	Г	233.259		-	-			Ī
AMIN PERSON	MOON COM THE STATE OF THE STATE		L							

PCCENE	Processie										
FILE MAME	PROTEIN	AN VITAGE (No Declerophoges)		П		L					
PYMSA HOBYL	Г	APPATITIES VISITE AND STATE OF THE PARTY OF	AREAL		AREAJ	AREA	AREA S	AREAG	AREA 7	ABFAS	* 404
PWASA HOBWY	-	HEPATITIC B VIRIA COMPANY CHIMIPANZEE ISOLATE	174-191	233-259		•		1	Т	Т	1
PVNCA HOBVO	_	HEPATITIS IN VIRIAL CAMENDE AND LETENAND CONTRACTOR	2	8.0						1	
PVACA HOBVP	-	HEPATITIS BURILLY SUBTINE ADM STRAIN OKINAWA/PODW212)	174-191	233-259					T		Ī
PWASA HPBVR	М	HEPATITIS B VIRUS (SUBTYPE ADR)	202-581	244-270							T
PVASA HOBVE		HEPATITIS B VIRUS (SUBTYPE AR)	11.70	27.00							
PVASA HOBVW		HEPATITIS B VIRUS (\$UBTYPE ADW)	137-101	211.210							
TAY AND THE PARTY OF		HEPATITIS B VIXUS (SUDTYPE AYW)	Γ	21.259	T				j	=	
PWASA WAVI	MAINS CIREACT AND CONTROL METORSON	HEPATITIS B VIRUS (SUBTYPE ADYW)	L	233-259		-				Ì	
PVALLA WHYSE	MAJOR STREAMS ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS 1	207.334	Τ	178.393					1	T
PVACA WHY?	MAJOR STREAM ANTICEN DESCRIBED	WOLCHUCK NEPATITIS VIRUS 59	212-219	Г	183.399	L	T		1	1	
PVASA WHYS	MAJOR SURFACE ANTIGEN PRECIESCIE	WOODCHUCK REPAIRIS VIKUS 7		274-298	383-398			T	\dagger	1	T
PYACKA WHYE	PROB MAJOR SUNTACE ANTIGEN PREC	WOOD HE VIEW THE VIEWS &			183.398	-				T	T
PVMCA WHYW	MAJOR SURFACE ANTIGEN PRECIESCIE	WOODCHICK HERAITIS VIRUS & (INFIICTIOUS CLONE)	212-239	П	113.37		!		:		•
PYMATZ LAANN	MATRUX (MZ) PROTEIN	INGLITRATA A VIBILE ATTACK A STACK A STACK AS TO THE	125-149	134.249					T	T	Ī
PYMITE LABAN	MATRIX (NO) PROTEIN	DOLLENZA A VIBITO CETALINA AMANICA DALICADA	35.46			-			T	t	T
MOSYS THAN	MATRIX (A2) PROTEIN	INCLUDICA A VIRUS (STRAIN ARORT WARENINGS)	97.6							T	Ī
PYNETZ LAFPR	MATRUX (NO) PROTEDI	INFLUENZA A VIRUS (STRAIN AFOW) PI ACITE VIRISADETACE	23-46			-					
PVMT2 LAFFW	MATRIX (AD) PROTEIN	INFLUENZA A VIRUS (STRAIN AROUN IN ACITE VIRUSAUS VIRUSA)	9.			Ī				T	
PWATZ (ALE)	MATRIX (NO) PROTEIN	INTLUENZA A VIRUS (STRAIN AN ENRICE ADJITACE)	97.6								
PWATE LALES	MATRIX (ND) PROTEIN	DOLUENZA A VIRUS (STRAIN AN FININCIA A MILITARY)	9								
PAPETS LANGEN	MATRIX (NO) PROTEIN	INTLUENZA A VIRUS (STRAIN AMALL ARDANEW YORKATOON)	* 1								
. I	MATRIX (NO) PROTEIN	INFLUENZA A VIRUS (STRAIN APLIERTO RICORDA)		1							T
- 1	MATRIX (AC) PROTEDI	INTLUENCA A VIRUS (STRAIN ASSINGAPORE/1/57)		1		-				-	
אווען דואאי	MATRIX (ND) PROTEIN	DIFLUENZA A VIRUS (STRAIN ALIDORIMOOTI)		1							
TAY CINA	MATRIX (AD) PROTEIN	DIFLUENZA A VIXUS (STRAIN AMICSON-SMITHUS)		T	1	1					
TOWN MEAN	MI-9 PROTEIN	MYXOMA VIRUS (STRAIN LAUSANNE)	226-341	T	T	1	†				
STAN ARVA	16 7 KD PROTEIN	BOVINE ROTAVIRUS (GROUP C / STRATH SHINTOKU)	134-351	T		ŀ	1	1	1	1	1
VNB INBBE	NB CL YCOPROTEIN	POLATO VINUS S (STRAIN FERUVIAN)	21.36			T	Ī	T		\dagger	T
VAR INBHOL	NB GLYCOPROTEIN	THE COURT OF THE STATE OF THE PROPERTY OF THE STATE OF TH	13-39			-		Ī	+	1	1
VNB BYBLE	NB CLYCOPROTEIN	INC. LINCA B VIRUS (STRAIN BIRUNG KONCATT)	13-39				T	Ì	†	\dagger	
VYAB DABLN	NB GLYCOPROTEIN	INTELLERZA B VIRUS (STRAIN BA ENINCIA ANI TRAIN	97.0								T
PVNB DIBIND	NB OLYCOPROTEIN	DATLUENZA B VIRUS (STRAIN BALARYI ANIVIS)	a c	1							T
VAG BROWN	NB CLYCOPROTEIN			1	1						
VN6 INDOK	NB GLYCOPROTEIN				1	1	1				
PWCS ACDEV	MUNICAPED PROTEIN NS. 1		Τ	061-691	T		†	1	1	1	
WHICH PAYED	NONCAPSID PROTEIN NS.1	HOWAN DARWOOTHER WAS	675-690		T		1	T	1	+	
WC PAYIN	NONCAPSID PROTEIN NS-1		575-597					T	\dagger	\dagger	
PVNSI_AHSV4	NONSTRUCTURAL PROTEIN INSI	VIRIS (CEROTYPE 4 / CTB 4 PA U COCKET	40-165						\mid	\dagger	Ī
PYNSI LALA	NONSTRUCTURAL PROTEIN INSI	т	230-272	٦						\mid	T
	HONSTRUCTURAL PROTEIN HS!		1	7	26-192				-	-	T
\Box	MOMSTRUCTURAL PROTEIN NS!	PICOLIANIZA	1	201	107-192						Γ
TVAS INCH	MONSTRUCTURAL PROTEIN NSI		T	114.117	167.103	1	1	1			
	MONSTRUCTURAL PROTEIN INST	(18/49)	T	Τ			1	1	+		
T	MONSTACCIONAL PROJECT NSI		Ī	68-189	\dagger	1	†	1	1	1	
	MONETHING I DECITED IN		05:10	167.192	T	\dagger	+	1	1	1	
L	MONETHIEFT BAT BEOTERN NO		20-47	61:31	1	Ť	1	1	1	1	
L	MONSTRUCTURAL PROTEIN NS	INTELLERYA A VIALIS (STRAIN ARDUCE/URRAINE/16))		64-119 14-119		T	\dagger	\dagger	1	1	1
VNSI_LAFOW	NONSTRUCTURAL PROTEIN NSI			Н	167-192		T		\mid	+	
	HONSTRUCTURAL PROTEIN HS!	INTLUENZA A VIRUS (STRAIN AFONT, PLACIES VIRIGADESCONDA)	1		167-192			r		+	Τ
	NONSTRUCTURAL PROTEIN NSI	ACCOUNT OF THE PARTY OF THE PAR	00:10	167-192					-	-	Τ
PWSI MEN	NONSTRUCTURAL PROTEIN WS!		T	T	167.193	1					T
7	MOMSTRUCTURAL PROTEIN NS!	(TA/11/76)	T	Т	2	1					Γ
			1		1	1				-	-

PCGENE	PINCTIZIP	All Viruses (No Barterlophages)							П	П	
FILEMANIE	PROTEIN	YARUS	ANTA	7777	AREAL	AREA	AREAS	AREA	AREA	ARGA	AREAS
PVNSI IAMAN	MONSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN AMALLARDINE W YOUCK 1997)	8:1	167-192		4					
PWSI IMAO	HONSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN AMALLARIANEW YURKAI/4/18)	X:-	107-192		+					
PVPS1 [AACTA	NOWSTRUCTURAL PROTEIN NS!	INFLUENZA A VIKUS (SIRAIN AMYNAMIANEDA-INAVIO)	14.5	ž						1	
PVIS IATE	MUNICIPAL PROJECT NO.	INCLUDED A VIRIS (STRAIN APPRIATALISENTALISMS)	21.50	167.192	T						Ī
TANK IAPO	MONSTRUCTURAL PROTEIN NS	INTELENZA A VIRUS (STRAIN APINTAL/ALBERTAZOLI)	8:15	167.192							T
PVNS1 LATO	HOMSTRUCTURAL PROTEIN HSI	DIFLUENZA A VIXUS (STRAIN APINTALJALBERTAJSENS)	31.50	167.192	Ī					-	Γ
PVASI LANCE	HONSTRUCTURAL PROTEIN HS!	INTLUENZA A VIRUS (STRAIN APLEATO RICOVIA)		114-137	167-192						
PVNSI JATKB	HONSTRUCTURAL PROTEIN WS!	INTLUENZA A VIRUS (STRAIN ATURKEYBETHLEHEM-GLILIT/1492-B/		167-192							
PVNSI LATKC	MONSTRUCTURAL PROTEIN NS!	INFLUENZA A VIRUS (STRAIN A/TURKEY/CANADA/61)	8	167-192		-					
PVNGI LATKA	HONSTRUCTURAL PROTEIN MSI	DIFLUENCA A VIRUS (STRAIN ATURKEYOREGON7!)	8:			-					
PVMSI LATUS	HONSTRUCTURAL PROTEININS!	INTILIERZA A VIRUS (STRAIN ATERNSOUTH AFRICARI)	27	20.20							
PVNSI LATRI	MONSTRUCTURAL PROTEIN NSI	INSTLUENZA A VIKUS (STRAIN ATERNATURICAENIA/11/72)	X-1	167-192		-					
PWS! AUDO	MONSTRUCTURAL PROTEIN NS)	INCLUENZA A VIRUS (STRAIN AUDORNO)772)	2	14-137	26.	+					
PYNSI IAUSS	HONSTRUCTURAL PROTEIN HS	INCLUENCA A VIRUS (STRAIN AUSSUNGTT)	X-		24:	-				1	T
Wei Wil	NOWSTRUCTURAL PROTEIN MS	DOLLOCKIA A VICUS (STRAIN AS WINESCOWALES)	X:15	74	1						
TANGE BEACH	MONSTANCE UNAL PROJECT NST	INCIDENTAL VIEWS (STRAIN CYCLI PROBNIAND)	222.241		T	•				T	
ALVAN STATE	LINE TO THE ALL PROPERTY INC.	INCIDENCE IN VALUE (SEROTYPE 10 / 1504 ATH 1/5A)	145.161	201.323	Ī	1				Ī	I
NAME OF TAILS	MONSTELLETTE AL PROTEIN NS2	BLUETOWOUS VIAUS (SEADITYPE 17/150LATE USA)	10.10	201-102		 					Ī
WAST STATE	MONSTRUCTURAL PROTEDNING	BILIETOMOUE VIAUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	163:161].				Ī	
YINES BIVIX	NONSTRUCTURAL PROTEIN NS2	BLUETONGUE VIRUS (SEROTYPE 19)			ľ					Ī	
PWED ENDYS	NONSTRUCTURAL PROTECN MS2	EPIZOOTIC HEMORAHAGIC DISEASE VIRUS (SEROTYPE 2/ STRAIN AL	145-161								
PVNS2 LAPUE	MONSTRUCTURAL PROTEIN NS2	INFLUENZA A VIXUS (STILAIN APUEXTO IUCOVIDA)	3-28			١					
PVNS2 LATRS	NOWSTRUCTURAL PROTEIN MS2	IDITLUEIZA A VIRUS (STRAIN ATERNISOUTH AFRICAS)	26-80								
PVNS1 PVM	HONSTRUCTURAL PROTEIN 2	PREUMONIA VIAUS OF MICE									
PVNS) CVPFS	HONSTRUCTURAL PROTEIN 3-1	PORCING TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI				^					
PVINS) CVPPU	NONSTRUCTIONAL PROTEIN 1-1	PORCING TRANSMISSIBLE GASTROENTEUTIS CORONAVIRUS (STRAI	221-122			-					
TANKS CAPEA	MONSTRUCTURAL PROTEIN >-1	PORCHE RESPONTORY CORONA VICES (STRAIN 1984)	2//		T					Ť	
PWS3 USV	NORSH KUCHURAL PROJECT NSJ	HORAM CORONAVEUS (STRAIN 220E)	8 4			-					
1000	MONATURE DE PROPERTO	MATERIAL CORONAVIRUS MITY (STRAIN S)			T	1				T	
200	MONSTRUCTURAL PROTEIN 4	PORCEME TRANSPASSUBLE DASTROENTENTIS CORONAVIRUS (STRAI	42							T	T
PVNS4 CVPPU	NOWSTRUCTURAL PROTEDY 4	PORCENIE TRANSMUSSIBLE GASTROENTERITIS CORONAVIAUS (STRA	15:31		T					Ì	
PWG4 CVPUV	NONSTRUCTURAL PROTEIN 4	PORCEM RESPONTORY COROHAVIRUS (STRAIN RMs)									
PVNSA JOSTV	NONSTRUCTURAL PROTEIN NS4	MAIZE STRIPE VIRUS	¥.÷								
PVNS4 ASV	NONSTRUCTURAL PROTEIN NS4	NCE STREE VEUS	41.56	50-83	132-167						
PWS) CVED	HONSTRUCTURAL PROTEIN?	FELING ENTENIC CORONAVILUS (STRAIN 79-1683)	Į.								
PVM37 FDV	NONSTRUCTURAL PROTEIN?	PELINE INTECTIONS FERTIONIES VIAUS (STRAIN 19:1146)	Ž		1					1	1
PWSC 71178	MONSTRUCTURAL PROTEIN C	HIDAN PARAMETERS I VINE CITATE CIO	10.00		1		1			İ	
WAST HILD	MONETHINETINAL PROTEIN C	HEDMAN PARADYPLUENZA I VIRUS (STRAIN CL-5/1))	26.92	79.197	Ť		T			T	T
WASC MING	NONSTRUCTURAL PROTEIN C	HEMAN PARAMPLLENZA I VIRUS (STRAIN CI-14/1)	76-92							T	
PVNST CVBQ	32 KD NOMSTRUCTÜRAL PROTEDI	BOYDAE CORDINAVIRUS (STRAIN QUEBEC)	11.109								
PVNST DACOL	HONSTRUCTURAL PROTEINS NSI-NS2	DIFLUENZA C VIRUS (STRAIN CKREAT LAKES/1167/94)	222-248								
PWST INCH	NOWSTRUCTURAL PROTEINS NSI-MS2	DIFLUENCA C VIRUS (STRAIN CYOHANNESBURGY186)	122-24								
PANST BOOD	NONSTRUCTURAL PROTEINS NSI-NS2	POLUENZA C VIRUS (STRAIN CARDSSISSIPPUM)	177:24								
PVNST DICYA	NOWSTRUCTURAL PROTEINS NSI-NS2	INTLUMENCE C VICTO (SI KAIN OT AMAGA [Align])	D2-777		Ť					1	
PVNSI PIPV	MONSTRUCTURAL PROTEIN NC.	SANDELY FEVER SICILIAN VIRUS	2		T				1	T	
100	MOMENTALISMAN PROTEIN NS-S	UNKUNDENG VIXUS	52.73	10.00		I	T			T	I
PANAIA BRUKA	PEONANI F MAY I PAR ANTIGEN	PSEUDORABIES VIXUS (STRAIN KAPLAN)	736.777	1801-1801	Ī						
PVACE DHVII	NUCLEOPROTEIN	DHON VIRUS (STRAIN INDIAN/1313/61)	133-139	297-324	T				Ī	T	
PVNUC EBOV	NUCLEOPROTEIN	EBOLA VIRUS	П								
PVNUC LADYA	NUCLEOPROTEIN	DIFLUENZA A VIRUS (STRAIN AVANAS ACUTAPRIMONJE699716)	П	266-287							
PYNUC IAANN	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AJANN ANBONAGO)	171.197		†				1		
PVNUC IABRA	MUCLEOFROTEIN	INTLUENZA A VINUS (STRAIN ABRAZIULITIE)	1173-197	1]	1	1	1	1	7

Port Pare									
5	OTTO	AN VINEE (No Becknopes (1)	1	Т	٦	٦	П		
_	NCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AMITTCERIGARMONE AINCOLD)	TOWN TOWN	4	7	AREAS AR	AREA 6 AREA 2	2 4854	AREAS
_	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN A/CAL IFORMIA/16/19)	131.103		1	1	1		
+-	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/CHICKEN/CERNANA)	133,193	+	1	+	-		
1	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ACHICKEN/PENNSYLVANIA)	11.10			$\frac{1}{1}$	1		
_	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCK/AUSTRALIA/149/10	131.197		Ī				
	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCK/BEIJING/1/78)	133.197	1	T	$\frac{1}{1}$			
PVACC LADCZ NU	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKICZECHOSLOVAKIA/S)	133.193		Ì	$\frac{1}{1}$			
7	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADDICK/ENGLAND/1/56)	137-197		T		-		
PANC IADES	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/DUCK/ENGLAND/IN2)	13.197		ŀ	-		-	
-	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKAHONG KONGANS)	193.197			+			Ī
7	NUCLEOFKOTEIN	INTLUENZA A VIRUS (STRAIN A/OUCKAIEMPHIS/921/14)	117-197		F		-		
_	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKAMANITOBAIUS)	133-197		T				
╗	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKATEW ZEALANDY) (7)	133-197		1	-	-		
П	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKOKRAINEZKO)	133.197		†		-		
7	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN A/ENGLAND/1995)	13.197		+	\mid			
	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AFORT MONMOUTHVIAT)	193-197		1.	+			
	MOLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AFORT WARREN/1/50)	137-197		1				
-	MICLEOMÓTEIN	INFLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUS/DOGSON/DUTC) 13.197	133.167						
PVNUC INFIR NU	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSROSTOCKUM)	133.107		+	1			
	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AGREY TEAL/AUSTRALIA/2/19)	137-197		+		+	-	
	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AGULLARARYLANDVS07)	173-197		İ	-	1		
	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ANGULLMARYLAND/104/11)	133-197		T		-		
-	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AGULLAKARYLANDVISSATS)	173-197		T			_	
-	MICLEOPROTEIN	INFLUENZA A VILUS (STRAIN AGULLANAKYLANDVIBIS719)	13.197		-				
PYNUC INGUA NU	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AGULLASTRAKIIAN223/84)	13:197		F		-		
-	NICLEOPROTEIN	INTLUENZA A VIBUS (STRAIN AGULLARASSACHUSETTS2640)	133-197						
_	NUCL EGRECHEIN	INFLUENZA A VIXUS (STRAIN ACCULACIONESOTAMANO)	13.197		-				
PVNUC IANG	NUCLEOFROTEIN	DNILUENZA A VIAUS (STRAIN AMICROXV40)	13:191			-			
T	NULLEURADIEM	INTLUENZA A VIRUS (STRAIN AEQUINEJIILLINJIA))	133.197			-			
TANK MARA MUSIC	NUCLEURINI ELIN	INTLUENCA A VIRUS (STRAIN AEQUINE/LONDON/1416/1))	173-197						
۲	MANUAL POSSOCIATION	INTEREST A VIXUS (STRAIN ACQUINEMIAMANIA)	173-197		-				
Т	NICE SOPROTEIN	INSTITUTES A VIBIL CONTRACT AND A MONTH OF THE PROPERTY.	173-197		•				
Ţ	NUCLEOPIGIEIN	DATUENZA A VIDUS (STRAIN AROUNE PRACTIE/1/56)	131,107		1	1			
т	NUCL EOFACTEIN	INTLUENZA A VIDUS (STRAIN AROUDIE/TENNESSEE/SAG)	131.107						
	NUCLEOPADTEIN	INTLUENZA A VIRUS (STRAIN ARLEVISATI)	191:11		T	+		1	
	NUCLEOPROTEIN	DIFLUENZA A VIRUS (STRAIN ALENINGRAD/SA/I)	173.197		T	+			
IVAUC LAMA MUC	NUCLEOPROTEIN	DGLUENZA A VDLUS (STRAIN AMALLARDVASTRAKHAN24411)	133.197						
	LEGRACIEDA	DIFLUENZA A VIRUS (STRAIN AMALLARDINEW YORKIN 1978)	193-197			-	-		
7	MUCLEUTAU EN	INFLUENZA A VIXUS (STRAIN AMINIK/SWEDENIA)	173-197					-	
PUNIC LANIE NO.	MULLEUTAULEM	IMPLUENZA A VIRUS (STRAIN ANTWOVA)	193-197				-		
T	MINI EOPLOTEIN	INTLUMENTA A VIBILE (STRAIN AMARBOTAS)	171.197						
Т	NACL EDITEDN	DATE HOLD A VINITE CATE AND A PRINCE TO BUTCH AND	17.19						
T	NUCLEOFROTEIN	INTERPRETATION OF THE PROPERTY	131.187						
۲	NUCLEOPROTEIN	INFILIENZA A VIRUS (STRAIN ASEAL MAKKACHI KETTELIAN)	101 101		1	-			
Т	NUCLEOPROTEIN		131.103		1		1		
г	NUCLEOPROTEIN	T	131.101		†				
PYNUC LATE! NUC	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/TEAL/A/CELAND/29/10)	19:19)		1	1		1	
Г	NUCLEOPROTEIN	=	13.197		\dagger				
	MUCLEOPROTEIN	6	173.107		\dagger				
	MICLEOPROTEIN	INTLUENZA A VIRUS (STRAIN A/TERN/SOUTH AFRICABI)	173.197		T				Ī
П	NUCLEOPROTEIN	INFLUENZA A VIAUS (STRAIN A/TERM/TURKAIENIA/19/7)	173.197		T		+		
-	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ATEXASIITI)	193.197		\dagger	l			
_	MUCLEOFIGUE	(גע	191-197		T				T
PVNUC IAUSS MUC	MOCLEURICIEM		173-197				-		
-		INPLUENCA A VIRUS (STRAIN AVICTORIA/S/64)	173.197				-		
]

171	15 H-218			T	r					
CCENE	PROPERTY		AREAL	2020	AND AND		1	4	1	
Treasure of the same	CONTINUE DE CONTIN	ENZA A YIRUS (STRAIN AWHALEAIAINE) 1244)	173-197			_		-	\downarrow	
7 A		INDICIDIZA A VIRUS (STRAIN ANNHALEPACIFIC OCEANISM)	173-197							
WACC LAWIN	NUCLEURISIN	THE LIFIZA A VIRUS (STRAIN ANNILSON-SALITIVI)	133-197					-		
PVMCC LAWIL	NUCLEOTROIEIN	INCTITIONA A VIRIUS (STRAIN A/SWINE/29/27)	173.197							
- 1	MUCLEOFICIE	INTITIENT A VIBIL (STRAIN ASWINE/11/9)	141-161							
WALL IAZAI	-	INFLUENZA A VIRUS (STRAIN ASWINECAMBAIDGE/175)	173.197					-		
WHICE INCO		MOTUENZA A VIRUS ISTITATIN AS WINE DANDONG WAT)	173-197			4		$\frac{1}{1}$		
WHUC JAZDA	MUCLEUTION	MELLIENZA A VIRIIS (STRAIN ASWINE/GERMANY/2/11)	191-161				-			
WALL LAZGE		INTELLECT A VIETE (CTRAIN ASSWINE/SONG KONDA/6)	133.193			L		-	_	
WALL AZHI	-	THE THOUSA A VIDIL STRAIN AND WINDERSKY KONG/12/22	13.197							į
PVNUC [A2H]	NUCLEOPROTEIN	INTEGRAL A VINCE LEGISLATION AND AND AND AND AND AND AND AND AND AN	171.103	<u> </u>		L	-			
PVNUC [AZII	NUCLEOPROTEIN	INTELLIFICATION OF THE PROPERTY OF THE PROPERT	6			<u> </u>		_	L	
PVNUC IA213	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWINEROWATTOS)				<u> </u> -	-	<u> </u> -	:	:
VORIC IAZE	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWINE/RIVY AND								
14.1	MICLEDING	INFLUENZA A VIRUS (STRAIN A/SWINEATALYA)9419)	1	1		1			-	ļ
11671	Maint Spendten	INFLUENZA A VIRUS (STRAIN A/SWINE/JANESRURG/42)	6			<u> </u>	<u> </u> 	<u> </u>	-	<u>:</u>
AND TANK	MAICH EOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWINGALAY/S4)	131-131	+			1			1
AND TABLE	MICHEOPEOTEIN	INFLUENCA A VIRUS (STRAIN ASWINEMENTHERLANDS 12/15)	13.10	+						1
	-	INFLUENZA A VIRUS (STRAIN ASWINE/OHIO/21/1))	13.167			1	<u> </u> 	İ		1
WALL INCOME		INFLUENZA A VIRUS (STRAIN ASWINE/WISCOMSIN/1/51)	11:11			1	1			1
TANK TO THE PARTY OF THE PARTY	-	INFLUENZA A VIRUS (STRAIN ASWINE/WISCONSIMIA!)	133-197	1		-		+	+	1
PWRUE UALWA		INTELIBUZA B VIRUS (STRAIN BLANN ARBOR/1006 (COLD-ADAPTED!)	234-250				-		1	1
PANUC INITAL	MULEUMOI EIN	MELLENZA B VIRUS (STRAIN BLANN ARBONING [WILD-TYPE])	234-258			-				1
PARIC DOM	MULEUTROILIN	DATIFICA D VINUS (STRAIN DA.E.D.40)	234-258	_						ļ
	MUCLEUMOIEM	TARE LESSON A VIDER (STRAIN BASINGAPORE/722/79)	134-258							1
PVAUC POST		LABBIE WILL CETAIN MUSOKE	16-39	(1.154 /						\downarrow
PVALIC MABVA		LANGE OF CARE AND POPPI	16-39	141-151		-				
PVNUC MABYP		LACTORIA CALIK (CERAIN COPENIAGEN)	- S. S.	342.262 33	136-150					
PVOSI VACCE		VARIOUS A VIRIUS	189-204		334-358				-	4
PVOOI VALV	PROTEIN OI	FOXTAL MOSAIC VIRUS	196-665					-		4
MON! NOW	IN TO THOUSE	NARCISSUS MOSAIC VIRUS		_	_	-	+			1
	THE PERSON NAMED AND ADDRESS OF THE PERSON NAMED AND ADDRESS O	POTATO VIRUS M (STRAIN RUSSIAM)		986-1009	1251-1270 1893-1289	1.000				1
	SALES BOTTEN	POTATO VIXUS S (STRAIN PERUVIAN)	٦	╗	┪					1
	TALKE PROTECT	POTATO VIRUS X	٦	٦	104-322 1010-1030	- 1		+		1
L L	TO SECULIAR	POTATO VIXUS X (STILAIN CP)	٦	╗	٦	1010-1030	S S		-	1
	LAST PARTIENT	POTATO VIRUS X (STRAIN XJ)	╗	٦	106-112 1010-1010	00	+		1	\downarrow
MOR! MOS	IN THOUSAND	OS STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS		188-178				1	1	+
PVORT SATIES	THE POLICE OF TH	WHITE CLOVER MOSAIC VIRUS (STRAIN M)	П			-	-		\downarrow	+
NOW I WANTED	TANK TO PROTECT	WHETE CLOVER MOSAIC VIRUS (STRAIN O)		П	7	1			1	\downarrow
	NAME OF THE PARTY ANTICENS	HEAPESVIAUS SADVIDU (STRADY 11)	424-446	2	551-575 579-595	1031-1072	210		+	1
MACE PLAN	Pio per retail	AUTOCIALIFIA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	4-26	42.59					1	1
TANK MANA	National and a second	ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	_				1		1	1
DAME STAN	PIERCIFO	SPODOPTERA EXIGUA MICLEAR POLYHEDROSIS VIRUS (STRAIN US)	_	7	٦	┪	Т		\downarrow	+
White party	PEOTEN SIB	AICE BLACK STREAKED DWARF VIRUS	\$	1	105-129 195-214	114 260-283	20.000		1	\downarrow
ALM SIEVE	MONETH INTERNAL PROTEDY PYSIO	WOUND TUMOR VIRUS (WTV)	70-107	7		+			1	1
2000	PROMABLE MEMBRANE ANTIGEN P140	EPSTEDN-BALL VIXUS (STRADY 899-4)	694-715	7	1124-1145	1		1		4
Var. 6.000	PROP CAPSED ASSEMBLY AND DNA MATUR PROT			7		1	$\frac{1}{1}$	+	1	\downarrow
100	Т		17.101	122-149	200-216	-		 	1	\downarrow
VANA SISSA	Т	E HELVES VIRUS SAIMIN (STRAIN !!)	136-765		1	1	1	$\frac{1}{1}$	-	+
UA CA SIGNS	FAPETD ASSEMBLY AND DWA MATUR PROTEIN		2			+	$\frac{1}{1}$	+	1	+
1747	STRUCTURAL PROTEIN VPI PRECURSOR	SULFOLOBUS VIXUS-LIKE PARTICLE SSVI	-35	1	1	+	+	+	+	\downarrow
7	CORE PROTEIN PZ	ALTICHOKE MOTTLED CRINKLE VIXUS	37.40		1	+	1		+	╀
200	CORE PROTED P21	CUCUMBER NECROSIS VIRUS	\$6.65	1		1	+		\downarrow	\downarrow
AD ITANA	CORE PROTEIN P21	CYMBIDIDA LINGSPOT VIRUS	3	1		+	1	-		ļ
PVP31 TRSVC	CORE PROTEIN F21		000	696	141.303	+	-		-	ļ
WHI HOW	T	HUMAN CYTOMEGALOVIAUS (STIMM AD169)	101.330	Т	+	-				-
PWP13 H3VII	Г	HEIDER STATES VIKUS (LYTE 1/3 FRANK 1/)	304.113							
		THE PERSON AND ADDRESS OF THE PERSON NAMED IN COLUMN STREET, THE PERSON NAMED IN COLUM						-	_	_

(ACCIONE)	Taxing the second secon										
FILENAME	PROTEIN	All Virgini (No Becterophages)			1	•					
PV721 V2V0	PRIMABILE CAPCID PROTEIN VALL	WALL STATE OF THE	AREAL	ANIA I	CV.NV	ANTAN	AREA S	ARIA	AREA?	ARFAR	ABSA
PVP26 NEVAC	PAR PROTEIN	VAUCELLA-COSTER VIRUS (STRAIN DUMAS)	117-132					_	Т	Т	J
WAS ANKWA	OUTED CANON DECISION AND	AUTOMORPHA CALIFORNICA MUCLEAR POLYTEDROSIS VIRUS	12-31	31-76	117-111						T
100	WIEN CAPAD PROJEIN V72	AFRICAM HORISE SICK NESS VIRUS (SEROTYPE 4/ STRAIN VACCINE)	168-891	974.994						Ť	T
	COLLEG CATSID PROTEIN V73.	BLUETOWGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	361-361	199-424	364.586	679-679				1	
	COLEA CASAD PROJECT VEZ	BLUETOWGUE VIRUS (SEROTYPE 11/15OLATE USA)	361-381	388424	179.149					Ī	T
PVP2 RTV13	CHITES CARRETTE SECTED USA	BLUETOWOVE VIRUS (SEKOTYPE 1) / ISOLATE USA)	362-382	420-438	617-632	657-676				T	1
PVPJ BTVIA	OUTER CAPED PROTEIN VP2	MILITERIORATE VIRIGINALE INTERIORATE USA)	361.381							-	T
PVP2 BTV13	OUTER CAPED PROTEIN VP2	MITHER WATER CARROLLES AND AND THE SALES AND	1000	2							
PV72 EMDVI	OUTER CAPSID PROTEIN VP2	EPIZOOTIC MENOR PLANTO THE PUBLIC STRUCKS	16:31	17.140	Ş	654-681					
PV72 ROTER	RNA-BONDONG PROTEIN VP2	BOVING BOTAVIBLE ACTS AND BEN	33.162	279-252							Γ
PV72 ROTEU	RVA-BRODIO PROTEIN VP2	BOVING BOTAVIBLE ATTENDED	301-317	374-360	32.33	637-69	764-769				
PVP3 ROTHW	NA-BROOM PROFEN VP2	HIMAN ROTAVIRUS (SEROTVE 1 / STEAM WA)	10-101	374-360	ž.	765.790					
PVP2 ROTEC	RNA-ENDONG PROTEDI VP2	MOSCONG BOTAVIEW COLONIA COLON	304-325	342-363	٦	674-700	114-709				
PVP2 KOTSI	ANA-BROOMS PROTEIN VP2	CHATAM II BOTAVIBLE COTA AND A LIN	21:73	301-318	٦	\$14-335	169-599				
PVP 30 MABVP	MINOR MUCI EGRECITED VP16	MARRIED OF REPAIN WHICH	34-57	219.240	302.316	335.36Ľ	523-544	974-700	765-790		Γ
PV732 AGTS!	PHOSPHOPROTEIN P12	APPLIANCE OF THE STREET STREET	2			-					Ī
PVT35 EBOV	-	SECT A VIETE	174-197			-					
PVPJS KABVA	-	MARRITHE VIRILE 1978 AND LANGONES	×			7					
PVP35 KALVP		MARKED VIBILITY AND BOOK	2/2	20		1					
PVP35 VACCC	DAMINOCOMONANT ENVELOPE PROTECN P11	VACCENTA VIETA (STAVITA CORE)	62.4	2							
PVP15 VACEV	BONDWOOMWANT BYVELOPE PROTEIN PIS	VACCIDITA VIETA (STE AND WAY	278-304								
PVPJS VARV	DOADHOOD AND BRYELOPE PROTEIN PL	VARIOLA VIRIK	PO - 10								
PVP38 HSVAG	36 KD PHOSPHOPROTEDA	MANERA Michael Despectable / Para Ant Car	279-305								
П	34 KD PHOSPHOPKOTEIN	MAREN'S INCRACE HERMONISTIC AND AND LOST OF STATES	E 2	1							
PVPJ9 NOVAC	MAJOR CAPELD PROTEIN	AUTOCAANIA CAI ISOBAICA NAICI SAN PAUTOSA VIENA	233-270								
_	MAJOR CAPED PROFIEM	OROMA POPULOTO INATA LAB TICAPED BOX VIENDOSES MADE	i i i			1					
Т	VPJ COAS PLOTEIN	APRICAN MORGE ECCENTED VISITE (CEROT-ME ARTERIO VACCINE)	107.134	I							
	VP3 COAE PROTEDA	BLUETONGUE VIRIS (SEROTVPE 19/150) ATE 11541		1	B	45-462					
Γ	VP) CORE PROTEIN	BLUETONGUE VIAUS (SEROTYPE 17 / ISON ATE 174)	T	177777							
	VP) CORE PROTEDI	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	Τ			+		1	1		
П	VP) COME PROTEIN	EPIZOOTIC HEMORAHAGIC DISEASE VIRUS (SEROTYPE I)	121.162	1		7		1	1	1	
V	VPJ CORE PROTEIN	STRAIN AUG	131.162				1			1	
٦	MAJOR 114 KD STRUCTURAL PROTEIN	ALCE DWALE VIRUS (ADV)	10:08	Ť	107.101	111.007	***				
	DWEA COAL PROTEIN VP)	PORCEDIE ROTAVIRUS (GROUP C / STRAIN CONDEN)	Ţ	T	Т	Т	T	Т	20.00	1	
7	PARA COLE PROTEIN VP)	SDIGAN II ROTAVIRUS (STILAIN SAII)	Т	20144	\$12.516	764.833		+	1		
LANGE EBY	CAPSID PROTEIN PAG		Г	Т	Т		T	T		1	T
T	CASE HATENER	HELDER SINGLEX VIRUS (TYPE 1/STRAIN 17)	66						T	T	T
T	CAPER PROTEIN NA		T	611.6	483-504						T
Т	CAPSID PROTEIN NO	THE SECTION OF THE SE	342-361				Ī				Ī
5	MATRIX PROFESS VP-46	T	200-321								
1	MATRIX PROTEIN VINE										
Ļ	STRUCTURAL CLYCOPIOTEIN PAG	BDADAR VIEW	T								
	CAPSID PROTEIN VP24			7/7	1						
\Box	STRUCTURAL GLYCOPROTEIN GPVI	A POLYHEDROSIS VIRUS		143.374	T	1	1		1	1	
	OUTER CAPSID PROTEIN VPA		T		1		1	1	1	1	
Ť	OUTEA CAPSID PROTEIN YPA	Γ	Τ	£0.00		1	Ì			1	
	VIRAL TRANSCRUPTION REGULATOR P41	AUTOGRAPHA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS	Τ			T		1		1	1
-	PAU PROTEIN	Г	134-137					1	1		T
WALK VALV	MAJOR CORE PROTECT PAR PRECURSOR		117:41					T	1	\dagger	T
7	MANCH CURB PRUIEDS PAB PRECURSOR	ENHAGEN)	131-358			Ī		\dagger	\dagger	\dagger	
Т	MAKOR CORE PROTEIN MA PRECINION	VACCING VIRUS (STACK WA)	31:38							t	T
Т	VM CORE PROTEIN	THIS ASSERDENCE IN VISOR ATTENDED	1	П							Ī
Γ	VP4 CORE PROTEIN		Τ	T	<u>3</u>						
Γ	VP4 CORE PROTEIN	-		7	18-81						
			7		135-55						

PCCFRF	Pricettie	All Virges (No Betierlophoges)		П	П	1	П	П	П	П	
FILE HAME	PROTEIN	VIRUS	ANTA STATE	4854	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	PATE OF	20,100	1	4	4	
PVP4 BTV2A	VP4 CONE PROTEIN	BECETONGUE VIAUS (SEROITTE 27 ISOLATE USA)	193.508	Τ		+		T	Ī	T	
PVP4 MCDV	OUTER CAPSID PROTEIN VY	PAIDWARK VIETS	186-407	693-514 62	626-645						
100	CONTRACTOR DECISION OF	BOVINE ROTAVIRUS (SEROTYPE 6/ STRAIN B641)	483-508								
WAY ROTHE	COUTER CAPSID PROTEIN VP	BOYINE ROTAVIRUS (STRAIN C486)	103.506				+				
PVP4 ROTBU	CUTEA CAPSID PROTEIN YP4	BOVINE ROTAVIRUS (STRAIN UR)	483-508		$\frac{1}{1}$	1		1		Ī	
PVP4 KOTEH	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	226-250	107.(1)	.00	+	\dagger	1	1	1	T
PVP4 ROTHI	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVINOS (SENOTYTE I / STRAIN 1076)	107-101	T	101.101	\dagger	\dagger	T			
PVP4 ROTHS	OUTER CAPSID PROTEIN VP4	HUMAN HOLA VIRUS (SENCITYE AT STRAIN NOTS)	20.	T		†	+				
PVP4 ROTHE	OUTER CAPSIO PROTEIN VP4	HUMAN ROTAVIRUS (SERUITYE I / STRAIN 6/41)	101	276 276	100,100	+	+	T			
MY ROTED	OUTEA CAPSIO PROTEIN VP4	HONGAN MOTAVIROS (SENOTITE 27 STANIN DS)	3	Т	+	+	+			Ī	
PVP4 BOTHU	OUTEA CAPSID PROTEIN VP	MUNICIPAL MAIN COTTO AND MAIN	16.01	T	234.249 482.	487.507		l			
IVN ROTICE	OUTER CAPSID PROTEIN VIA	HUMAN MOLANIA (STRAIN MO)	181.707	Τ	Т	1					
PVM ROTH	OUTER CAPSID PROTEIN VM	THE BOARD STATE OF CORPORATE TO STRAIN MITS	191.707	T	482.507	+					Ī
PVM ROTION	OUTER CASID PROTEIN VIA	THE MAN WORLD VIEW CORNEL OF STRAIN MCN.)	181.204	Τ	463.500	-					
WW TOTHON	GOTER CAND MOTERN VIN	HOMAN BOTAVILLE (SEROTYPE) / STRAIN P)	181-207	Т	462-507	-					
PVM KOTHO	COTES CATES BACTED VA	HEMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST THOMAS 1)	102-181	234-249	482.503	-					
PVP KOINI	WHEN CARE PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4/ STRAIN VA70)	181-201	483.507							
WHITE SAME	CKITER CAPID PROTEIN VP	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	161-207	183-507							
PVP4 ROTPS	OUTER CAPSID PROTEIN VP4	PORCEME ROTAVIRUS (SEROTYPE \$ / STRAIN OSU)	115-250	41)-508	-	1	+	1		T	
PVP4 ROTPC	OUTER CAPSID PROTEIN VP4	PORCEME ROTAVIRUS (GROUP C / STRAIN COWDEN)	487-512			1	+				
PVM ROTPO	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN COTTFRIED)	234-249	100.28	+	+	+				
PVP4 ROTPY	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN YM)	233-230	3069	+	+	1	1			
IVIN KOTRH	OUTER CANSO PROTEIN VP4	AMESUS ROTAVIRUS	2	1	+	1		T			Ţ
PVP4 ROTES	OUTER CAMED PROTEIN VP4	SUGAN II ROTAVIRUS (STRAIN SATI+EM)		\$5,127	+	+	\dagger				
PVP4 ROT\$S	OUTER CAPSID PROTEIN VP4	SINGAP II KUIA VIKUS (SEKURI SAIII-SER)	80.114			†					
PVP4 SBMV	M PROTEDY	WORD TIMOS VIUS	192-215	416-438	498-519 364	165-59					
ALM PANE	CHIEFE CANCID MOTERATOR	BELUETONGLIE VIRUS (SEROTYPE 10 / ISOLATE USA)	195-317	126-345	494.517	•					
1011	CATTER CAPSID PROTEIN VPS	BLUETGNOUE VIXUS (SEROTYPE 11/150LATE USA)	1295-317		94.517	•					
PVPS BTVI)	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 13 / 150LATE USA)	295-317	£ 51.7		+	+	1			
PVP5 BTVIA	OUTER CAPSID PROTEIN VPS	BLUETOMOUS VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	87-102	10.00	+	+	+	1			
PVPS BTV18	OUTER CASED PROTEIN YPS	BUILTONOUS VINUS (SEROTTE 17150LATE SOUTH AFRICA)	366.317		+	†	1	T			
PVPS BTV2A	OUTEA CAPSID PROTEIN VPS	BUELDWOOD VACO (SEACO) TE 17 (SOCK) E COA)	265-284	622-639 6	690-715	T		Ī			
PVPJ RDV	OUTER COAT MUTEUM PS	BLUETOWGHE VIRUS (SEROTYPE 10 / ISOLATE USA)	P.37	Т	261-276	T					
AVEL BIVE	+	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	121-137	438-462							
PVP62 ATVIO	_	BLUETONGUE VIRUS (SEROTYPE 107 ISOLATE USA)	77	157.272		1	1			Ī	
PVP62 MODV	PROB NONSTRUCTURAL 34 3 KD PROTEIN	MALZE ROUGH DWARF VIRUS	30-148	T			+				
PVP64 NOVOP	MAJOR ENV GLYCOPROTEIN PREC	ORGYTA PSEUDOTSUGATA MULTICAPSID POLYHEDRUSIS VIRUS	200	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	716-007	†					
PVP67 NPVAC	MAJOR ENV GLYCOPROTEIN PREC	AUTOCACHIA CALIFORNICA ROCLEAR POR TREUROSIS VIROS	155.172		+	\dagger	-	T			
PVP67 NPVGM	MAJOR ENVELOPE CATCUPACIEIN	IN THE TOWARDS VIRUS (SEROTYPE II / ISOLATE USA)	ž	215.245	257-272						
PVP BIVII	VANDOTED	BLUETOWOUR VIRUS (SEROTYPE 137 ISOLATE USA)	5.13	П	257-272	H					
VIN BTVI	VPS PROTEDN	BLUETONGUE VIRUS (SEROTYPE 17/1SOLATE USA)	\$.33	П	257.272						
PVP6 BTVIS	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1/150LATE SOUTH AFIUCA)	233	٦	261-276		1				
PVP6 BTV2A	VPS PROTEIN	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	204-221	233:248		1	1				
PVP6 WTV	STRUCTURAL PROTEIN PO	WOUND TUMOR VIRUS	374-397		+	†	1	1			
PVP6 WTVNU	STRUCTURAL PROTEIN PO	WOUND TUNCK VEXUS (STROME FU)			+	1	\dagger	T			
PVP74 NEVAC	P14 PROTESM	AUTOGIAMA CALIFORNICA PUCLEAR POLYHEDRUMA VIRUS	27-62		+	1	1				
PVP75 HSVSA	PROBABLE MEMORANE ANTROEN 75	ALTEROPORTES SALMING IS INCIDENT FOR PARTICIONALS VIRUS	274.301	605-470	678-704	T	1	Ī			
PVP79 NPVAC	19 KD PROTEIN	BELIEFONGUE VIXUS (SEROTYPE 13 / ISOLATE USA)	197.111	Т							
PVPT BIVIS	VP1 COME PROTEIN	EPIZOOTIC HEMORAHAGIC DISEASE YIRUS (SEROTYPE I)	205-222	301-323			H				
VOT TOV	NONSTRUCTURAL PROTEIN PNS?	RICE DWARF VIRUS	9] F (00 400			1					
PVP7 WTV	NONSTRUCTURAL PROTEIN PHS?	WOUND TUMOR VIRUS	167-285			1					

PCT/US95/16733

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A	FILE HAME	PROTEIN	All Viruses (No Bacteriophages)	П								
WASTILLIALAL MATIENT	PVPED NPVAC	CAYSID PROTEIN PIO	A I TOCK A PULA CAL ISONO LICE A SECTION AND A SECTION AND A SECTION ASSESSMENT AS A SECTION ASSESSMENT AS A SECTION ASSESSMENT AS A SECTION AS A SE		AREAL	AREAJ	AREAN	П	Г	Т	Т	
WORSTILLY, LALE ADDIEST BLITTONGE TUTI (ESDOTTE 11 11 11 11 11 11 11 11 11 11 11 11 11	PVP87 NPVOP	CAPSID PROTEIN PO	OROYA MEIDOTRICATA LAB TICATA TO THE DECISION		638-660				Г	Г	Т	
NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 10.12 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEIN BILLETONICS VIVIL GEOTOTE 11 150.47 E 50.25 NOSTRACTIONAL PROTEI	PVPE BTV10	HONSTRUCTURAL PROTEIN PS	BLUETONGIE VIELE KEEDTVAE IN 11601 1 4 5 116 11	121-383							T	
NOWTHER COLOUR DOLLERS 10 to 120	PVPI BTVII	MONSTRUCTURAL PROTEIN PR	BI INTOMOTIC VINITA (SEROTVES IN 1800.A IE USA)	20.78			_					
WORTHLEIGHAL WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WORTHLEIGHAL WOTTER WORTHLEIGHAL WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WELD WAS STRUCTURAL FOTTER WORTHLEIGHAL WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILLSCHOTT FILED ALL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WILL GUTLALIN WORTHLEIGHAU WOTTER ALLEGOOGE WORTHLEIGHAU WOTTER ALLEGOOGE WORTHLEIGHAU WOTTER WOR		NONSTRUCTURAL PROTEIN PS	BLIETONGIE VINIE (SEACHTE IN 180LATE USA)	200			l.				 	
WASTILLICHAL POTTER ALLE FOOLE VILLY (SERVING AND		NONSTRUCTURAL PROTEIN PE	BLUETONGIE VIRLIS (SEROTVE 137150) ATE 116.1	R								
MONTHACING A PRITER H BLIEGGOGG WIJG SEGUITES 1100 A 16 A 17		NONSTRUCTURAL PROTEIN PR	BLUETONGTE VIRTIC/GEOTVOET / 1/20LA 12 A 1/2 A 1	02-120			•			ŀ		
MONTEL CAPID PRICE NA BLLEFTORM VALUE AND VALUE AND VALUE		NONSTRUCTURAL PROTEIN PE	BLUETONOUE VIRUS (SEROTYPE L/1504 AVE CAPTU APRICA)	2							ľ	
OVINE LAME DITIONAL FORTERS 1922 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1922 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1922 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1923 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 DANAE WILLS FIRECALLA MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERENCE 1924 MOTERN FOR FERE		NONSTRUCTURAL PROTEIN PE	BLUETONGUE VIRITS (SEROT VPE 9 / 1501 A TELLEA)	8								
OVER LAND MOTION OF REAL MACES MICE GALL MANA PARIS STRUCTIOLAL PARTIENT NY PRECUESCR MICE GALL MACES NY PRECUESCR STRUCTION NY PRE	1	OUTER CAPSID PROTEIN PS (INCH DWALF VIRUS	2 1								
FINACTIONAL MOTERN MELGRASON VACCINAL VIRIG STIGATIN WITH STRAINS 111-121 11-213 11		OUTER CAPSID PROTEIN PS	RICE GALL DWARF VIRIS	7	7							
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NOWTHE CAPER PROTEIN FOR STATE	PVPI VARV	STRUCTURAL PROTEIN VPS PRECURSOR	VARY'S A VIETE	235-242								
MOSTINICTURAL MOTERN PAGE PAGE MOSTINICTURAL PAGE MOSTINI	PVP8 WTV	OUTER CAPSID PROTEIN PE	WORND TRANS VIBER	╗	7							
HOUSE LANGE HAS NICE GOLL DWALD VINUS THE ASSOCIATE DAY OF VIEDNOSS VINUS 151-174	PVP LDV	MONSTRUCTURAL PROTEIN PMS9	RICE DWARE VIRILE	2		121-111	379.405				T	Ī
C. BY DO POLYMEDALL ENVELORE ROTEIN AUTOGRAPH CALLFORNICA NUCLEAR POLYMEDROSIS VINUS 115.140 1 EDOPFOTAGE BANDAL ENVELORE ROTEIN INCLUSIONATIONAL PARTICOLINATA MALTICASSID POLYMEDROSIS VINUS 115.144 1 EDOPFOTAGE BANDAL ENVELORE ROTEIN 10.141 10.141 1 RODALISE BANDA BALLOSTICATA MALTICASSID POLYMEDROSIS VINUS 10.141 1 RODALISE BANDA BALLOSTICATA VINUS STATE I INITIALISMAN BALLOSTICATA VINUS STATE I INITIALISMAN BALLOSTICATA VINUS TYPE BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS TYPE I INITIALISMAN BALLOSTICATA VINUS BALLOSTICATA VINUS BALLOSTICATA	PVP9 RGDV	MONSTRUCTURAL PROTEIN SP	NICE GALL DWARE VIBIR	21:12			-					
12.10	PVPHE NOVAC	29 KD POLYMEDRAL ENVELOPE PROTEIN	AUTOCAAPHA CAI IFORNICA MINT EAR BOX VIETE COSTS	Т								
EROPROTEASE HIGHAN AGENOVILUS TYPE IS ACCUMENTATION OF THE PROTEST 10-111	PVPHE NOVOP	32 KD POLYHEDRAL ENVELOPE PROTEIN	ORGYLA PREI MOTE INTA TA ANT TECARETE NOT THE DROSIS VIRUS	Т	2.53		-				T	T
PROTESSE	PVPRT ADEI2	•	HUMAN ADENOVIEW TYPE 13	23.15								T
PROTESSE STRAIN MAJON-FFLER VIRLS STATE STATE	PVPRT MACTIVE		MOUSE MANAGERY TIEGOS VIETS (478 ATM 59.5)	191			-					Ī
PROTESSE SQUIREE MONKEY RETROUNDS 10-97 PROTESSE STATE STATE STATE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE STATE PROTESSE STATE STATE STATE STATE STATE STATE STATE STATE PROTESSE STATE	PVPRT MONIV		SOGAN MASON PIZE VIBIR		1							
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VAU MOTERN	PVPU HVIBR	VPU PROTEIN	HUMAN MORUNODE PCIENCY VIRIS TYPE I MIRTING ATEN		1		_					
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VVD ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INCSF ISOLATE) 1.31 VVD ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INTISOLATE) 1.31 VVD ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INTISOLATE) 1.31 VVD ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDISOLATE) 1.31 VVD ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDISOLATE) 1.31 VVD ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDISOLATE) 1.31 VPU ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDISOLATE) 1.31 VPU ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDISTER FIET) ALGALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) 1.03 VPU ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) INDIA VPX ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) INDIA VPX ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) INDIA VPX ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) INDIA VPX ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) INDIA VPX ROTEIN HUBALN BOADWOCE KIERCY VIRUS TYPE I (INDIA) I (INDIA) INDIA VPX ROTEIN SAALN BOA	PVPU HVIHI	VPU PROTEIN	HUMIAN INDADMODE FICIENCY VIRUS TYPE I (HXII) ISON ATEL				-		-			
VAU ROTERN HIGHAM DOURNOGE KIENCY VIRUS TYPE (AAL ISOLATE) 3.30	WPU HVIII	VPU PROTEIN	HUMAN INDAINODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)		Ì]	F					
VAU ROTEN	AND HAINS	VPU PROTEIN	HURIAM DIGITION PICTURE TYPE I (RIAL ISOLATE)	177	T		1			1		
VAU MOTERN	WED HINDS	VPU PROTEIN	HIMAN DOMINODEFICIENCY VIRUS TYPE I (NIN ISOLATE)	2.30	T	1	•					
VYD MOTERN	ONIAN PLAN	VPU PROTEIN	HUMAN BOMUNODEFICIENCY VIRUS TYPE I (NDK ISOLATE)	1738	\dagger	Ī						
VPU RIGITEM	ALIAN DAN	VPU PROTEIN	HUMAN BARUNODEFICIENCY VIRUS TYPE I (PV12 ISOLATE)	1.29			Ī		1	1		
VAY MOTERN VAY	JAN MAN	VIOLENCE IN	HUMAN DAUMODEFICIENCY VIRUS TYPE I (SF162 ISOLATE)	3.28					T	1	1	
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VPX PROTED HIGHANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE DEP NO.) 10.23 VPX PROTED HIGHANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE DEPA). 10.23 VPX PROTED HIGHANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE DISO.) 10.23 VPX PROTED HIGHANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE DISO.) 10.21 VPX PROTED HUBANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE DISO.) 10.21 VPX PROTED HUBANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE DISO.) 10.21 VPX PROTED HUBANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE SBLISY) 10.21 VPX PROTED HUBANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE SBLISY) 10.21 VPX PROTED HUBANN BOGINGOENCERACY VIRIOS TYPE 2 (150LATE SBLISY) 10.21 VPX PROTEDN HUBANN BOGINGOENCERACY VIRIOS (150LATE SBLISY) 10.21 VPX PROTEDN SUBANN BOGINGOENCERACY VIRIOS (150LATE SBLISY) 10.21 VPX PROTEDN SUBANN BOGINGOENCERACY VIRIOS (150LATE) (150LATE) (150LATE) (150LATE) (150LATE) (150C		VPU PAOTEDN	SIGEP PERMONARY AND NOVATIONS OF THE COLUMN SIGNATES	22							\dagger	
VPX PROTED HTGALAN DEGINGEENCY VILLIS TYPE 2 (1904, HE DEA) 10-13 VPX PROTED HTGALAN DEGINGEENCY VILLIS TYPE 2 (1904, HE DAS) 10-13 VPX PROTED HTGALAN DEGINGEENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTED HTGALAN DEGINGEENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTED HTGALAN DEALNOGEENCIENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTED HTGALAN DEALNOGEENCIENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTEDN HTGALAN DEALNOGEENCIENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTEDN HTGALAN DEALNOGEENCIENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTEDN HTGALAN DEALNOGEENCIENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTEDN SALAN DEALNOGEENCIENCY VILLIS TYPE 2 (1904, Ar.) 10-13 VPX PROTEDN SALAN DEALNOGEENCIENCY VILLIS (1804, Ar.) 10-13 VPX PROTEDN SALAN DEALNOGEENCIENCY VILLIS (1804, Ar.) 10-13 VPX PROTEDN SALAN DEALNOGEENCIENCY VILLIS (1804, Ar.) 10-13 VPX PROTEDN SALAN DEALNOGEENCIENCY VIRLIS (1804, Ar.) 10-13 VPX PROTEDN SALAN DEALNOGEENCIENCY VIRLIS (1804, Ar.) 10-13 VPX P	Г	VPX PAOTEIN	HOMAN DAMINODESICIENCY VISUA TYPE 3 ARM A TE SELA								l	T
VPX MOTERN	П	VPX PROTEIN	HRACAN BORGNODEFICIENCY VIRUS TYPE 3 (1904 ATE CALC)	25.0	1						T	T
VPX PROTEIN HABAJN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE DDS.)7 15.31 VPX PROTEIN HUMAN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE GHANA-1) 16.32 VPX PROTEIN HUMAN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE RIHZ) 16.32 VPX PROTEIN HUMAN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE SBLISY) 16.32 VPX PROTEIN HUMAN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE SBLISY) 16.32 VPX PROTEIN HUMAN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE SBLISY) 16.32 VPX PROTEIN SURLAN BAGINGOEJ KIENCY VIRUS TYPE 2 (1SGLATE SBLISY) 16.32 VPX PROTEIN SURLAN BAGINGOEJ KIENCY VIRUS (1SGLATE SBLISY) 16.31 VPX PROTEIN SDGAN BAGINGOEJ KIENCY VIRUS (1SGLATE SBLISY) 16.31 VPX PROTEIN SDGAN BAGINGOEJ KIENCY VIRUS (1SGLATE) (SIV-MAC) 16.31 VPX PROTEIN SDGAN BAGINGOEJ KIENCY VIRUS (1ST 1SGLATE) (SIV-MAC) 16.31 VPX PROTEIN SDGAN BAGINGOEJ KIENCY VIRUS (1ST 1SGLATE) (SOGTY M. 16.31 VPX PROTEIN SDGAN BAGINGOEJ (1ST 1SGLATE) (SOGTY M. 16.31 VPX PROTEIN SDGAN BAGINGOEJ (1ST 1SGLATE) (SOGTY M. 16.31 VPX PROTEIN SDGAN BAGINGOEJ (1ST 1SGLATE) (SOGTY M. 16.31 VPX PROTEIN SDG		VPX PROTEIN	HUMAN BORGNOOEFICIENCY VIRUS TYPE 2 (1908 ATE DISA)	77.0	1							
VAX ROOTED FURANN DAALNOOE KCIENCY VIRUS TYPE 2 (ISOLATE GHANA.) 16-33		VPX PROTEIN	HUMAN BARCHODE/ICIENCY VIRUS TYPE 2 (ISOLATE D205 7)		1	1						
VPX ROTELN	1	VPX PROTEIN	HUMAN DOMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE GHANA.))	1	1		1		1			
VFX ROTEIN HUMAN BAADNOEF KIENCY VIRUS TYRE 2 1850.ATE 80D) 16-33 VFX ROTEIN HUMAN BAADNOEF KIENCY VIRUS TYRE 2 1850.ATE 58L1SY) 16-33 VFX ROTEIN HUMAN BAADNOEF KIENCY VIRUS TYRE 2 1850.ATE 58L1SY) 16-33 VFX ROTEIN SALAN BAADNOEF KIENCY VIRUS BALL CLONE GRUIN (8-44 SPATROFEN) 16-33 VFX ROTEIN SALAN BAADNOEF KIENCY VIRUS BALL RESPONSE OR 18 SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SIV-MAC) 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SIV-MAC) 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SIV-MAC) 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SIV-MAC) 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SIV-MAC) 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SIV-MAC) 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SOLATE (SOOTY MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW SPATROFT MA 16-33 VFX ROTEIN SALAN BAADNOOF FICIENCY VIRUS RAW		VAX PROTEIN	HUMAN BARRODEFICIENCY VIRUS TYPE 2 (ISOLATE NIH.Z)	100	\dagger	1	T		1		1	
VYX ROTEIN	1	VFA FROTED	HOMAN INDAUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	10.22		1	1		1	1	1	
VAR MOTERN	T	VANTALIA	HUMAN INONUNODE FICIENCY VIRUS TYPE 2 (ISOCATE SBLISY)	0.32	\dagger	1	T	1	1	1	1	
VY R TOTEIN		VEXTROILIN	HUMAAN BARUNODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	27.0	\dagger	1	1	-	1	1	1	
V. X. PLOIEIN SUMAN PAGNAOEE CHENCY VILUS (190.A.T.E. ACIA/ CLONE GAL-1) (194.14	T	VYA PROTEIN	LACTATE DEHYDROGENASE-ELEVATING VIRUS	145-165	t	1	T	+	1		1	
10.25 10.2	T	VYA MOJEIN	SIMILAN INDAMPODEFICIENCY VIRUS (ISOLATE AGM / CLONE GRU-1) (S		\dagger	T		\dagger		1	1	
VY R ROTEIN SALAN BARINDEFICIENCY VIRUS (KAW 1901-ATE) (19-33 VY R ROTEIN SALAN BARINDEFICIENCY VIRUS (F38-SACI 150-ATE) (500TY M 16-33 VY ROTEIN SALAN BARINDEFICIENCY VIRUS (F38-SACI 150-ATE) (500TY M 16-33 ALPIA-A PROTEIN BARLEY STAUE MÖSAC VIRUS (FBIACT) 150-ATE) (500TY M 16-33 MONSTRUCTURAL PROTEIN NCV72 BOVINE ROTAVIRUS (5 TAJIN IL) 140-137	Т	US Y PROTEIN	SMUAN BANDNODEFICIENCY VIRUS (ROLINZ-B) ISOLATE) (SIV-MAC)	10-33		T				1	+	
VPX PROTEIN SPACAN ENGINENCY VINUS (F3 ISOLATE) (SULA	Τ	ON PROTEIN	SOUTH INDICHOLICIENCY VIRUS (KAW ISOLATE) (SIV-MAC)	10-33		T	T	\dagger	\dagger	+	+	T
VPX PROTEIN SEGLAN BOOTH INC. THUS (FIREICT) ISO. TEST (SOOTY MI (19.33) ALPHA-A PROTEIN BAALEY STRUE MOSAIC VIRUS (BSMV). MONSTRUCTURAL PROTEIN HCVP2 BOVINE ROTAVIRUS (STAJIN ID)	T	VEX PROTEIN	SMACH INDICIONAL PRINCIPAL (K) 150LATE) (SIV-MAC)	10.32				T		\dagger	\dagger	T
ALPHA-A PROTEIN MONSTRUCTURAL PROTEIN MCV72 BOVINE ROTAVIRUS (STRAIN IS) (100.157	T	VPX PROTEDY	SPACE INVOINTING TO THE STATE OF THE STATE O	10-32				\dagger			1	
MONSTRUCTURAL PROTEIN MCVP2 BOVINE ROTAVIRUS (S FIXAIN IS)	Г	ALPHA-A PROTEIN		Т						-	-	T
140-137	П	NONSTRUCTURAL PROTEIN MCVP2	(August)	Т	676						-	Τ
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POGENE	PISCTULIP	All Vivers (No Beteriopheges)	ARFA! ARF	A J ARFA J	AREAN	AREAS AR	AREA AREA! AREA!		AREAS
PILEHAME	PROTEIN	MRUS	140-137 428-450	Т	Г	Γ			
PVS65_ROTID	HOWSTRUCTURAL PROTEIN NCVP2	HUMAN ROLLAVIRUS (STRAIN TOVING)	T	Ţ	<u> </u>	•	-		1
PVS0S ROTPC	MONSTRUCTURAL PROTEIN MSSS	FORCINE RUI AVIAUS (CHRISTIN CATE)	399.416	:	:				
PVS65 ROTSI	NONSTRUCTURAL PROTEIN NCVP2	SIMILAR II ACIA VIRUS (STANIN ST.)	201-125	_					
PVSO6 ROTBR	VP6 PROTEDI	BOVING BOTAVIRUS (GROUP C/ STRATA SHINTOKU)	SB-83					•	-
PVSOG ROTES	VP PROTEIN	BOVINE BOTAVIRUS (STRAIN UK)	201-115			+		-	
PVSO ROTEU	VI TRUITER	EQUINE ROTAVIRUS (STRAIN FI-14)	103-113			<u> </u>		<u> </u>	1
THE PARTY	VAN PROTEIN	EQUINE ROTAVIRUS (STRAIN II-2)							
100	OF BATER	ROTAVIAUS (GROUP B / STRAIN ADRV) (ADULT DIAUNHEA ROTAVIRU				+			
	VICTOR DE LA CASA DE LA CASA DE LA CASA DE CAS	ROTAVIRUS (GROUP B / STRAIN IDIR)		1					T
200	We have the	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN 10%)	202-203					1	
THE STATE OF THE S	We pentrin	HUMAN ROTAVIRUS (GROUP C/STRAIN BRISTOL)	25.53						
THE ROLL	NOT PEOPLE IN	HUMAN ROTAVIRUS (SEROTYPE 1/STRAIN S2)	202-228		-				
STATE OF THE PARTY	TOTAL PROJECTION OF THE PROJEC	KIMANN ROTAVIRUS (SEROTYPE 1/STRAIN WA)	٦				-		
PASS ROLL	VAL MOUTE DA	PORCEAU ROTAVIRUS (GROUP C/STRAIN COWDEN)	314.340	9	+				
THE PERSON	VALPROTEIN	PORCINE ROTAVIRUS (STRAIN COTTINIED)	201:23	1	-		-		
THE POLICE	CE VCOPROTEIN VP?	BOVINE ROTAVIRUS (STRAIN KN-4)		+			-		
evtre acritic	CLYCOPROTEIN VP? PRECURSOR	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)			+				
PVCM BOTTS	NONSTRUCTURAL PROTEIN NCVP4	SIMAM II ROTAVIRUS (STRAIN SAII)	27.5.03		+				
PVCO 10Ths	GLYCOPROTEDI VP?	BOVINE ROTAVIRUS (SEROTYPE 6/ STRAIN 61A)							
PVS09 ROTBA	Т	BOVINE ROTAVIRUS (STRAIN A44)						-	
PVSOP ROTBE	Г	BOYINE ROTAVIRUS (SEROITTE 107 STRAIN BLLS)							
PVSOF ROTBK	Г	BOVINE ROTAVIRUS (STRAIM R.R.)	1		-				
PVSOP ROTES	Т	BOYING ROTAVIRUS (SEKOLYTE IV STRAIN 1447)	114.198	ļ	 -				
PVSOP ROTC!	Т	CHOKEN ROTAVIRUS A (SERO) TTE // STRAIN CHA	11:133		-				
PVSOP LOTEL	Г	EQUINE RUTAVIKUS (STRAIN LANS)	205.232		-				
PVS09 ROTG	_	KOTAVIKUS (GRUOT B.) STRAIT (DIN)	Ť	197-213					
PVSOF ROTH	_	RUMAN RULA VINCE (SENO) 112 C 1 STEAM RUS	197.212		-				
PVSOP ROTHA		MANAGED AND CONTRACTOR OF THE STRAIN DS.)	197-212						
PVSOP ROTHD	_	HIBAAN ROTAVILUS (SENOTYPE 1/STICAIN HN126)	П		7				
PVS09 BOTH	GLYCOTION VI	HUMAN ROTAVIRUS (STRAIN L26)	T	197.212	-				
PVSOB KOTHE	_	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN MI))	7	97:312	\downarrow				
OHOU POAN	_	HUMAN ROTAVILUS (SEROTYPE I / STRAIN MO AND STRAIN D)	21-12		1			-	
PYSON ROTHER	Т	HUMAN ROTAVIRUS (SEROITTE 37 STRAIN PL	131-185		L				
PVS09 ROTHER	GLYCOPROTEIN VP1	HUMAN MOLAVIMOS (SENOT PLEST STRAIN S)	197.213						
PVSOP ROTHS		KINGAN KOTAVIRUS (SEROTYPE 4/ STRAIN VA70)	П						
PVS09 ROTHY	OLYCOPIOLISM VEV	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	П	197-212				$\frac{1}{1}$	
PVSON ROTHW	_	PORCTING ROTAVIRUS (SEROTYPE \$ / STRAIN OSU)	٦	197.212				+	
100	_	POACING ROTAVIRUS (SEROTYPE \$ / STRAIN TFR-41)	21-13		1				
PVCO BOTTE	Т	PORCINE ROTAVIRUS (SEROTYPE 4 / STRAIN BEN-144)	717.70		1			-	
PVSOF ROTPIA	T	POACTIVE ROTAVIRUS (SEROTYPE 4/3TICAIN BNII-1)	11111		1		-	-	
PVSOP ROTEH	Ť	RAESUS ROTAVIRUS	131-133						
PVSOP ROTS!	П	SOCIALITY OF THE STRAIN ADEN (ADULT DIARNER ROTAVIRUISE 153	1136-133						
PVS11 ROTOA	7	MINAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	<u> </u>						
PVSH HOSVA	SMALL HYDROPHURE, PROTEIN	MARGES VIRUS (STRAIN SBL-I), AND MUNITS VIRUS (STRAIN SBL)	7.29						
PVSH MORO	7	MIDAPS VIRUS (STRAIN EDINGBURGH 2 & 4)	1.79						
TVSH MOROZ	7	MUNOS VIXUS (STRAIN EDINGBURGH 4)	1.29					+	
PVSH MABO	Т	MUNOS VICUS (STRATM MATSUYAMA)	10.29			1	+	\downarrow	
ANA PEROV	Т	MUNDS VIRUS (STRAIN BELFAST)	7.23						
NA.	Т	MOROTS VIRUS (STRAIN ENDERS)	2.2	1					
TANK TO SERVICE	Ť	MUMPS VIRUS (STRAIN JEAYL-LYNN)	2.		1				
SOUTH WAY	7	MUND'S VIRUS (STRAIN KILHAM)	2.		\downarrow			-	
PVSH MAROL	1	MUNGS VIRUS (STRAIN BRISTOL I)	20,70		-				L
PVSH MUMPH	1	MUMOS VIRUS (STRAIN MIYAHARA VACCINE)	****						
	۱								

PCCENE	Principle	IAN Warm MA Desiration								
FILE MAME	PROTEIN	VIETS		Т	7	П	П	П		
PVSH MUMPR	SMALL HYDROMIOBIC PROTEIN	MUMPS VIRUS (STRAIN RW)	27.00	200-10	100	Z V	ORGA	NEW Z	AREA (OREA.
PVSH MUMOT	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN TAKAJÍASÍII)	200	<u> </u>	 -		1	İ		
WSH MORON	SHALL HYDROPHOBIC PROTEIN	MOMOS VIRUS (STRAIN URABE VACCINE AM9)	10.79		<u> </u>			1	1	
PVSII REOVE	SIGMA I PROTEIN PRECURSOR	REOVINUS (TYPE I / STRAIN LANG)	8191	+	-				1	Ī
LASID MEDICAL	SIGMA) PROTEIN	REOVIAUS (TYPE 1 / STRAIN DEAUNG)	152-170	-	-			T	Ť	T
TVSD MEDV	SIGNA J PRGILLY	REOVIAUS (TYPE 27 STRAIN DIJONES)	152-170					1	1	1
LASID MEON.	SIGMA J PLOTEIN	REOVIRUS (TYPE I / STRAIN LANG)	193-170	-			T	1	Ť	
LAND MEDIN	SIGNA I'S PROTIIN	REOVILUS (TYPE 1/STRAIN LANG)	79-101					T	1	T
CASTA HEVBO	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN BURNÁ)	116.595		-			1	1	T
TASES NEVAGE	STRUCTURAL PROTEIN 3 PRECURSOR	HEPATITIS & VIRUS (STRAIN MEXICO)	116.292	-	-			T	1	T
1000	STRUCTURAL PROTEIN 3 PRECURSOR	HEPATITIS E VIAUS (STRAIN MYANMAR)	112.241		-				Ì	T
FVST1 MSVPA	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN PAKISTAN)	292-311		1					
PVST FEVE	STRUCTURAL PROTEIN 3	HEPATITIS & VIRUS (ISOLATE PUESUS)	21.09	-	-		1			1
PVT3 MYXVI.	TUMOR MECROSIS FACTOR SOL RECEPTOR PREC	MYXOMA VIRUS (STIAJIH LAUSANNE)	261.283				1		1	
PVT2 SFVKA	TUMOR NECESSIS PACTOR SOL RECEPTOR PREC	SHOPE FIBROMA VIRUS (STRAIN KASZA)	3.W. 280		+		1			
PVTJA CAPVI	PROTEIN TJA	CAPAPOXYIRUS (STRAIN INS.1)	11711		1		1			
PVT4 SFVKA	T4 PROTEIN	SHOPE FIDROMA VIRUS (STRAIN KACZA)			-			Ī		
PYTER EBY		EPSTEIN-DARK VIRUS (STRAIN BOS.B)			·	-	:			
PVTER HOMYA		MINAN CYTOMEGAL OVERTR (STRAIN AD1AS)	1	Т	4					
PVTEA HSVII		MEDBER Charle by Walls From 1 2572 A. 19.	T						-	
PUTER HISVAU		WEBPER CHAPTER VIOLENTIAN A STRAIN INCAME A STATE	363-380 673-686	=	-					
PVTER HSVEB	PROBABILE DNA PACKAGDAO PROTEIN	FOR THE DESCRIPTION TO SEE A SERVICE OF THE SERVICE	200-278							Γ
PVTER HISVII	PROBABLE DNA PACKAGINO PROTEIN	KTALIMIN INTERCONSING I	ī		-					
PVTER HBVEA	PROBABLE DMA PACKACING PROTEIN	THE PARTY OF THE CANADA	76.71	=					;	!
PYTER YZVO	PROBABLE FINA PACE ACOUST PROTEIN	VARIATION ACCESS WITH A STATE OF THE PARTY O	218.241		•					
PX INTEGS		CHOLDER CORREST LIKE A THIS CHAIR COMAS	372.389							
PX WHV		MONOCHINE AND	1							
PX WICKS		WOOLD THE STATE OF	3		, i					
PX WATER	PROTEIN X	WANTER THE VIEW OF THE STATE OF								
PX WHY	PROTEIN	WOODCHING THE VISITE OF	SE-23						l	
PX WHYE!	PROTEINX	WOODOOGER KEPATITIS VIBILS & CARECTIVALE CO CARE	2 2							
SWYN X4	PROTEINX	WOODCHETTE HEPATITIE VALUE WAS ARE BRUCESS	6		•					
PY104 ADEa7	HYPOTHETICAL 164 ED EASTY PROTEIN	MAKAN ADEMOVIER TORES	2							
PYIOG SSVI		SIE FOLDBUS VIRILET ING PARTICLE REVI	27.73							
PYIOK MSVS		MAIDE CTREAK WHITE COURTS ARBICAN ISSUES	R							
PY119 \$5VI	HYPOTHETICAL 11 8 KD PROTEIN	SULPOLOBUS VIRUS-LIKE PARTICI P CEVI	1							
PYLIK PASV		PANICIA STREAK VIRUS								
1	OTEN	REET NECROTIC YELLOW VEIN MOSAIC VIRILS GOOR ATP GIT								
		CYMBIDITAL MOSALC VIXUS (STRAIN SINGAPORE)								
PY137 ADERS		HUMAN ADENOVIRUS TYPE 1	5							
		CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	377	+			1			
		CASSAVA LATENT VIRUS (STRAIN NIGERIAN)							1	
		TOWATO YELLOW LEAF CURL VIRUS (STRAIN MAJUKANDE)	10.33				1		1	
7		TOWATO YELLOW LEAF CURL VIRUS	14.55		1		1	1		7
1	ROTEIN	HUMAN ADENOVIRUS TYPE 1	132	-					1	1
		HLONIS STUATE MOSAIC VINUS	34.80	-			T		1	Ī
T		SULFOLDBUS VIXUS-LIKE PARTICLE SSVI	100-125 141-162	27					1	Ī
T	ALL LINEOTHERES. S.	50-73				T	T		T	
A PACE ACCURA			163-188				l			T
T		A POLYHEDROSIS VIRUS	90-106	_			t		\dagger	T
T	THE IS	SOTBEAN CALCACITE MOTILE VIKUS	65.90				T		\dagger	T
T			122-142						 	Τ
2			34					T	\dagger	T
T			31:36						\mid	T
T			553							
PYESK SSVI	OTEIN		J	7						Ī
1			10-105	3 343-365	657-675 764-784	764-784	Н			Γ
										1

TILENAME PROTEIN HOTEN I PYR SOCIV HYPOTHETICAL PLOTEIN I PYRT ADER HYPOTHETICAL I TO EAULY PROTEIN I PYRT I SEV HYPOTHETICAL I STOP PROTEIN I FYALI I ISBV HYPOTHETICAL BALLI I FYALI I PROTEIN I F		VIRUS SOVREÁN CIGOROTIC MOTTI E VIRUS	102201	रप्राप्त रप्राप	AVIET	विष्टु रुप्रध्	ABEA 6 ABEA1	ABEA 8	AREA
		MANAGE AND THE MEDIT OF STREET	-	_				-	
1	EIN 8			+	+	+		-	
,	DEALLY PROTEIN	HUMAN ADENOVIRUS TYPE 7			†			1	T
7	PROTEIN	SULPOLOBUS VIRUS-LIKE PARTICLE SSVI	T	11:79	+	1		+	T
Г	1 PROTEIN	EPSTEIN-BARK VIRUS (STRAIN B95-1)	203-220		+	1			T
7	HE-ORE I PROTEIN	FOWLYOX VIXUS (ISOLATE HF-438(MUNICHJ)			+			+	1
	H-CHET PROTEIN	FOWLYOX VIRUS (ISOLATE HP-434(MUNICHJ)	77.	1				+	Ī
	HE-ONLY PROTEIN	FOWLPOX VIXUS (ISQLATE HP-4)IJIMUNICHJ))	1		1			
	HE CALFID PROTEIN	FOWLPOX VIXUS (ISOLATE HP-4) UMUNICHI)	1		+	1		1	Ī
	H-ORFIZ PROTEIN	FOWLPOX VIRUS (ISOLATE HP-4)4(MUMCH))	7	£ 132		+	1		T
PYRLL SFVIL BELAPROTED		SINGAN FOAMY VIRUS (TYPE 3 / STIVAIN LK3)	100		+		1		T
_		HUMAN SPUMARETROVIRUS	32-76		1	1			1
YOR! HSYSC KINP 24 7 KD PROTEDY DI DIGTA SPECION	IN DAGA SPECTION	HEXPESYTAUS SADADU (SUBGROUP C / STILATN 488)	206-230				-		
Т	N DIER TREGION	HEXPESYTRUS SADATA (SURGROUP C./ STRAIN 411)	06-69						
т	PA PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 1993-8)	200-222		•				
+	A MANTEN	MARRY PRICEACE HERPSYMEN (STRAIN BC.)	081-561		-	_			
	A PROJECT	MARKET INCRACE MERPECVILLE (STEATH MDS)	175.190		-	-			
-	C TOTAL	IN A LANGE AND A CORPUS AND A PARADA	161-101			-			T
╗	EUN HOU.F4	RUMAN CTI UMCALLO VIANO (SI MAN ADIEN)				+		†	T
	KD PROTEIN	VACCIPIA VIAUS (STINAIM WA)		1	1	+		†	T
	LEOCAPS® ORF	MURIDAE CONCONAVERUS MAY	2		1	+		+	
PYIOR CYMI HYP PROTEIN IN MUCLEOCAPSID ON	LEOCAPSID ONF	MUNIDAE CORONA VIRUS MAYA	× -					1	I
	LEOCAPSID ON	MUMBER CORONAVIRUS MAYA	2						
Γ	72 PROTEIN	EPSTEIN-BARR VIRUS (STRAÎN B95-4)	67.90						
PYLI2 ADEA! HYPOTHETICAL 10 KD PROTEIN	D PROTEIN	HUMAN ADENOVIRUS TYPE 41	٦	٦	٦				
EBV		EPSTEIN-BARR VIRUS (STRAIN 895-1)		128-155 215-241	330-350				
	CD PROTEIN	SUADLIDA DEDESCENT VIRUS (INSECT INDESCENT VIRUS TYPE 23)	_						
L	EN	AVIAN ADENOVIRUS GALI (STRAIN PIELL'S) (FOWL ADENOVIRUS I)	-		1		1		
5	PROTEIN	CONOMITION YELLOW MOTTLE VIRUS	Ç,		<u> </u>		-		1
г	D PROTEIN	THEIDWORKOTEUS TENAX YARUS I (STRAIN KIAI)	290		1	1			
Ş	Р Котем	CONDICELINA YELLOW MOTTLE VIRUS	\$ Y 2						
	D PROTEIN	EQUING ARTERITIS VIXUS	165-192		1			+	
PYON LELV HYPOTHETICAL 28 4 KD PROTEIN	CD PROTEIN	LELYSTAD VIRUS	212			+			T
PYOU LYX HYPOTHETICAL II & K	CO PROTEIN	LA Y VACUS X	22.17			+		\downarrow	T
П	PROTEIN	NARCISSUS MOSAIC VIRUS			+				T
	PROTEIN	POTATO VIXUS A		1	-	+			T
	PROTEIN	POTATO VICUS A (STIANIN CP)				1		+	T
_	PROTEIN	WILLIB CLOVER MUSALV VICUS (SIRVIN M)		1	-	+			Ī
٦	PROTEIN	WHITE CLOVER MUSAUL VICTOR IS INAUN U)	1000		1				Ī
5	U TAULEIN	AVION ADDITION OF THE CONTRACT	10.161					+	Ī
٦	Droien	SAVER ANTENNES TAND						1	
	PROJECT	TANCELSON MOSTER TENAN VIBILITY LETT AND ME ALL				+			
1	A LEGITICAL DE LA CONTROL DE L	THE BLOOD TELE TENAY WHILE I AT A AN KEAL			 	+			I
1	D TROITER	THEFT CONTROL OF THE WATER LATER AND REALLY		311.746	-	+	-	+	T
YOUN TIVE HAYOUR INCAL SEED THOUSING	D MOTERA	Tribandeenffile fenax vinis i (strain keal)	T		+	+		-	Ī
T	Mame	RICE TIDICAD BACKLIFORM VIRUS	T	104-126					Γ
TITLE KIBY HIPOTHETICAL PARENCES	POLEDI	RACE TINCALO BACTILIFORM VIRUS (ISOLATE PHILIPPINES)	T	104-126					
1.	TO MOTEON	ALITOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIXUS	311-234						
SYNC SERVICE REPORTED TO SECTION OF THE STATE OF THE STAT	CD PROTEIN	ORGYLA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OP	+-		-				Γ
Τ	CD PAOTEDY	ORGYLA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OP	27.54	215-230	-			L	
Т	ROTEIN	TOBACCO NECROSIS VIRUS (STRAIN D) (TNV)	16:31						
厂	D PROTED	LYNANTRIA DISPAR MOLTICAPSID PUCLEAR POLYHEDROSIS VIRUS	16-35						
Т	EMILI	HEAVES SDUPLEX VIRUS (TYPE 6 / STRAIN GS)	99-21						
Т	TEN 1872	HEADES SOUTEX VIRUS (TYPE 6/ STRAIN CIS)	35.74						
Г	ENVI	HERPES SDAPLEX YOLUS (TYPE 6 / STRAIN GS)	× 2						
П	130	CHILO DIDESCENT VINUS (CIV) (INSECT INDESCENT VINUS TYPE 6)		$\frac{1}{1}$	-				
	0654	CHILD INDESCENT VIOLIS (CIV) (INSECT INDESCENT VINUS 1 TPE 6)	5	\exists					
PYRES TRV6 REPETITIVE PROTEIN ORDS	ORES	CHILD INDESCENT VIAUS (CIV) (INSECT INDESCENT VIAUS LITE OF	78-123	179-204 200-483					7

9710000	Taxable data									
FILE WALL	FISC LESIF	All Virgini (No Becteriophages)		П			Г		-	Γ
PYRU EBY	HYPOTHETICAL BREE PROTEIN	FPSTEIN BARB VIBILS (STBAIN BOLE)		ABEAL ABEAL	AREA	DAKA 3	१ रुप्रचर	OF CARRA	ARCA! A	AREA C
PYNU EBY	HYPOTHETICAL BRAET PROTEIN	EPSTEIN BARR VIEWS (STRAIN POLA)	177	+	1			İ	+	-
PYSK! EBV	HYPOTHETICAL BSRFI PROTEIN	EPSTEIN BARR VIBILS SCHALL BOLD	11.00			-		j	1	
PYTRI EBV	HYPOTHETICAL BIRE! PROTEIN	FPCTENCEANS VISITE (CTEAN DOC DA	616-77							
PYUB2 NPVOP	HYPOTHETICAL 34 8 KD PROTEIN	ORGYNA PSEUDOTSUGATA MALTICAPSID POLYHEDANSIS VIRILS (OF	107-101	1	+	\downarrow		1	-	
PYVAL VACCC	_	VACCINIA VIRUS (STRAIN COPENHAGEN)	1	100	+			1	1	1
PYVAF VACCC	HYPOTHETICAL 8 4 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	T	27	1			1	1	
PYVAL VACCY	INVOINETICAL () ICO PROTEIN	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE	T		-	1	1	1	1	I
PYVAT VACCV	HYPOTHETICAL 19 KD PROTEDI	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STIARIN COPE	20.46	<u> </u>					1	
PYYBE VACCV	HYPOTHETICAL 18 SKD PROTEIN	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE	9-28	+		1		1		
PYYBO VACCC	HYPOTHETICAL II 2 KD PROTEDA	VACCINIA VIRUS (STRAIN COPENHAGEN)	73.11							
PYYCA_VACCC	HYPOTHETICAL 10 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	25.3	1	1					
PYYD2 VACCY	HYPOTHETICAL 8 6 KD PROTEIN	VACCINIA VIRUS (STRAIN WE) AND VACCINIA VIRUS (STRAIN CORE	T							
PYYDA VACCC	HYPOTHETICAL 9 2 KD PROTEIN	VACCINGA VIBING STRAIN COPENIA CEN		;;	-					
PYVDA VACCY	HYPOTHETICAL 9.2 KD PROTEIN	VACCIDA VIIII (CTI A IN WE)	T	1	†					
PYMEA VACCO	APPOING TICAL 9 I ED PROTEIN	VACTORIA URILIA ATTA A DI CORENIA CENA	T	17:77 RC-77						
PYVEP VACCE	HYPOTHETICAL 11 KB PROTEIN	VACCIDA VIETE (STRAIN CONTAINS CENT	10-10		-					
PYYOA VACCE	HONOTHER ROAT 14 1 KD DECOTERA	VACCINA UTILIS (270 A DI COREMIA CIA)	77-17		-					
PYVER VACY		VACCEMENT VIEW (STRAIN CONTINUED)	62-62		7					_
794 6 144		TACAMA VINUS (SIRAIM CUTEMIACEM)	24-19					-		
ATT ATT AN		CESTELLINGACK VINUS (STRAIN BPL4)	20.166		•			-		
	DITCHESTAL 143 AD PROTEIN	CHUMUS STRUKTE MOSAIC VIRUS						-		
TANK SOL	HTPUINE INCAL 11 0 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	13	141-162		L				
r row ALDES!	HTPOTHER HEAL 70 & KD EARLY PROTEIN	HUMAN ADENOVIRUS TYPE 1	11-05			_				
PT25K BNTVP	KNA.3 KTPOINE TICAL 24 7 KD PROTEIN		163-148		-	L				T
TANK MENAL	HYDING IKAL WAND PROTEIN	A POLYHEDROSIS VIRUS	PG1-06			L				I
T2 SOCHV	HYPOTHETICAL PROTEIN 2	SOYBEAN CHEOROTIC MOTTLE VILUS	63.90		ŀ			T		Ī
TOTAL SSVI	HYPOTHE TICAL 11 1 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	122-142					İ		T
Toko Savi	HYPOTHETICAL 60 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	23-44						\mid	Τ
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MITOTHER PART AND PART OF THE	VACCINIA VIRUS (STRAIN WIL)	21-36		ŀ				-	T
Τ	UNIVERSITY OF THE PROPERTY	MEASURES VICTOR (STRAIN MALLE)	3.28							
T	INVAMENTAL TRANSPORT	SOT BELOW CHECKED IN THE VIKUS		╗				-	-	Γ
NA CONTRACT	DOMESTICAL IS TAUTHOUGH	SOLUTION VIXOS-LIKE PAKTICLE 35VI	_	155-173 543-565	657-675	764-784			-	
Ver ANEON	INVESTIGATION OF THE PARTY OF THE PROPERTY OF THE PARTY O	MANA AND AND THE TRUE	10-27							
Weet Sevi	INPOTITETICAL 63 KM BEATEN	STATE OF THE VALUE OF THE PARTY							_	
YALI EBV	HYPOTHETICAL BALFI PROFEIN	PPSTEINTERE VIRIE (STEAN BELL)	2.7	-						
	HYPOTHETICAL BANGGORF! PROTEIN	FOWER DAY VILLE ALCO ATE UP A STRUCTURE	077-507	1						
Т	HYPOTHERTICAL BANGE ONLY PROTEIN	FOWEN VINIT GOLD ATE UP A SIGNATURE AND								
	HYPOTHETICAL BANGE ONLY PROTEIN		17.0					1		
PYB10 FOWPM	HYPOTHETICAL BANGGORF TO PROTEIN		4.100					1	+	T
	HYPOTHETICAL BAMBGORFIZ PROTEIN	FOWLPOX VIRUS (ISOLATE HP-1) HAUNICH))		12.169 12.169	-			†		T
╗	BEL-1 PROTEIN		113-128					1		
	BEL-1 PROTEIN		53-78					l		
7	HYPOTHETICAL 21 7 KD PROTEIN IN DHFR TREGIO	HERPESYTRUS SABARN (SUBGROUP C / STRAIN 411)	106-230		-			t	\dagger	
Z.	HTPOTHETICAL 9 S ND PROTEIN IN DIGH. STEGION	/ STRAM 418)	06-69						\mid	T
7	HTPOINE ICAL ECAUTION		200-222					t	\dagger	
_	HTFORKERCAL 23 6 KD PROTEST		175.190						+	1
FTUAL REPORT	NTFOIREIRAL 23 6 KD PROTEIN	5	175-190		_				-	
-	HINDING TAULTH MALE	STRAIN ADIGO	121-101					-	-	T
7	T		10-102						-	
PTIOS CVIMAS	HITOING IN AL MOJEIN OF MCCLECCAPSID ON	MUTURE CORDINAVILLS NATV	41-156						-	
T	MITOINE IN ALTHOUGH IN MULLEUCASID ONE		141-156					\mid		Ī
T	Т	1000	7.33							
Т			07.40							
PYNOU EBV		1 205.81	34 100	T						
Т	15 9 KD PROTEIN	THIRECENT VIBIG TVAE 335	J	187-(17	200			1		
1			97.57							

PCCEME	Priscrizir	UNCH (ING BACKETIONING)		Τ	1		т	Τ	Т	
FILERAME		т	o de la constante de la consta	TOTAL TOTAL	7	Poppor	1	200	1	707
PYORI ADEDI	HYPOTHETICAL PROTEIN	IECTS) (FOWL ADENOVIKUS I)	2		1		Ī			
PYORI COYMV	HYPOTHETICAL 13 KD PROTEIN		200		+					
PYORI TTVI	HYPOTHETICAL 19 KD PROTEIN	RAIN KIAI)	3.40		1				1	
PYORE COTAN	INNOTHETICAL IS KD PROTEIN	TTLE VIRUS	23-49						-	
PYORE EAV	HYPOTHETICAL 23 6 KD PROTEIN	EQUINE ARTERITIS VIRUS	165-192		-					1
PYON2 LELV		RUS ,	196-212							
PYON LVX			11.92							
WOR I NOV	HYPOTHETICAL MICE PROTEDY	MARCISSUS MOSAIC VIRUS	7.30							
1900			1.74							
2000	INSECTION OF AS IND PROTEIN	(STANCP)	7.:							
		SISTRAINAN	9.29		-					
	The Assessment Assessment		12		-					
	HITCHE IN THE PROJECT	CLECOW ADENOVIBLIE IN	70.07		ŀ					
PYORS ADEC		+								
PYOUS EAV					1					
PYORE NAIV			97-51		<u> </u>					
PYORU TIVI	HYPOTHETICAL 16 6 KD PROTEIN		27:72							
PYORL TIVI			6.70							
PYORM TTVI			12-102	233-256						
PYORE TIVE	HYPOTHETICAL 30 3 KD PROTEIN	STRAIN KRAI)	91-113							
VATA ATTE			3.25	104-136						
PV534 B TE V7			3-33	971.701						
Total Control	WASATUR THE ALL ALL AND PROTEIN IN PASTILEGION	S	211-234		ŀ					
	HYPOTHER TO A 12 3 KD PROTEIN IN PR 5 STEGION	_	13.100							
	NOTICE OF THE PROPERTY IN PACKAGE OF THE CHANGE OF THE CHA	1	27.55	215-230						
	7	+-	15.0		-					
A COLONIA	7	POLYHEDROSIS VIRUS								
	AND THE PARTY BANKS OF THE		47.50			-				
THE REAL			55.74							
2			2.2							
WAS HOW		ECCENT VIRUS TYPE 61	500							
S I		-	977							
PYRA RV		_	94-123	179.204 266.285						
PTES BY	THE STATE OF THE S	7	18-23	Т		-				
A STATE OF THE STA		PPCTETALBABB VIBIG (STRAIN BOLD)	164-182							
A COLL			23:13							
			183-401							
PTIRI DV		PSID POLYHEDROSIS VIRUS (OF	133-152							
	WOOTH THE ALL IS NO PROTECT	VACCINIA VIRUS (STRAIN COPENHAGEN)	¥.2	140-156	_					
SWALL VANCE	HYPOTHETICAL 64KD PROTEIN		17-40	89-15						
A VAN	HAYOTHETICAL 9 KD PROTEIN	CIPITA VIRUS (STRAIN COPE								
	NAME OF THE REPORT OF THE PROPERTY		¥.		L					
A DYO HAVE	-		6-21							
TOWN OWN	HYPOTHETICAL II 1 KD PROTEIN		17-SH							
AND A VACO	MANOTHETICAL BOILD MOTERA	I	19-33							
PYVD2 VACCV	HYPOTHETICAL S & KD MOTEDI	CINIA VIRUS (STRAIN COPE	5-26	15-50						
PYYDA VACCC	HYPOTHETICAL 9 2 KD PROTEIN	ENHAGEN	22-38	19-11						
YWDA VACEY	HYPOTHETICAL # 3 KD PROTEIN		91:	12:38 44:64	Ц					
PYVA VACO	HAYOTHETICAL 7 I KD PROTEDY		41-67							
PYYTY VACCE	HYPOTHETICAL 1 3 KD PROTEIN		13-41							
PYYOK VACCE	HYPOTHETICAL 143 KD PROTEDI	VACCINIA VIRUS (STIVAIN COPENHAGEN)	105-127							
PYYES VACCE	HYPOTHETICAL 9 0 KD PROTEIN	SEN)	25.70							
	National Service Management	FORTERLEADED WINDS AND MAIN BOLDS	771 031		-	_				

WO 96/19495 PCT/US95/16733

TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MQTIF

PCCONE	PERTILIF	All Virges (no betierlaphages)	Т	7	AREAS	AREA 4 AR	AREAS AREAS	Г	AREAL
TANT.	PROTEIN			100	Т	l	Г	i	1
PRUL 1 18RVS	ANAL POLYPROTEIN		ī					L	
5	BAAT POLYROLFIX	1	ŀ	1001	İ	1		<u> </u> 	
200	ALSO SELECTION OF THE PROPERTY		- ;					<u> </u>	1
	CENONIE BOX YEARING		1			1	1	1	
	SECOND IN THE PER YEAR OF THE	US ISTRAIN SO-1)	67:13	390-138				1	
	2230000		6.5			-		<u> </u>	İ
2010	THE PARTY OF THE P		20-1132			1	1	$\frac{1}{1}$	
10000	CERCINE TIAL TROUBLE	A 21 (ECHO 9 VIRUS) (1 (9.V)	87.80			-		1	
10000	GENOME FOR FYROLISM		1601-1611					1	İ
77CI C COX4	GENONIE FOR YTHOU IN		1587-1614					1	
FOI G COXBI	GENOMI FOLYFIOLIN		1315.1617				<u> </u> -		
POI G COXB)	GENOMIE POLYPROTEIN		1317.1615					_	
PPOLG COXDA	GENOMIE POLYPROTEIN		19.00	1585-1617					
Prot G COXBS	GENOAIE POLYPHOTEIN.	100000000000000000000000000000000000000	1111	1485.1419	2401.2434				
SING C TOR	GENOAGE POLYPROTEIN							<u> </u>	İ
3000	NI STEED OF VEHICLE							<u>!</u>	l
TACLE OF IN			61.95				1	1	
PPOLG DENZE	GENONE FOLITION		61.95	1113.1146				1	İ
PPOLG DEN11	GENOVIE POLYPROTEIN		56.19					_	
PPOLG UENZO	GENOMIE FOLYFROTEIN		10.14						_
PECH C. LIFERIA	CENONE POLYFROIT IN	THE VIRIS INTE 2 (STRAIN JANIAR A)							<u> </u>
12	CENONIS PCE YPROJETS	THE MOUTE VINIUS TATE 2 (STRAIN NEW GOINT A C)						<u>l</u>	
200			6-19	9			-	<u> </u>	-
200	מבשמעוד ענער וו שנו בייבי		ş					1	i
FULC DENT	GENORIE POLITICAL DE LA COMPANION DE LA COMPAN			1390.2012			<u> </u>		-
PPOI G DENJ	CENORIE POLYFROILIN		FO.09						
	_		174.806				<u> </u>	<u> </u>	
FINE 11 116	ATTITUDE OF A PURCHASE			100					
1	A THE PARTY OF THE	1	07	1001				1	Ī
	THE PART OF THE PA		20.00	1001-1001				1	Ī
E LEVE	SENGRIC TO LIVE STATE OF THE ST	_	1196-1211	1465-1503				1	
POIG ENCYD	GENOMIE FULL TEROTEIN		1036-1064	1001-1133	1167-1199	100:100		1	
200	GENONE FOLTEROITIN	Г	1036-1074	1091-1133	100	1465-1501		-	
FIDVA	GENONIE POX YFROTEIN	LOGI AND MINISTER DISEASE VIRUS (STRAINS OIK AND OID) SI	100	1167.1199	1463-1501			_	
MDVO	GENOME POLYPROTEIN	Ī	1640-1670						
PPOLG SICVI		Ī	361.1393	1360-1311	1131.3150				
<u>۲</u>			1	1000	1111.1159			<u> </u>	
	i					!	-		:
III VIK						-	<u>!</u>	1	l
.5		!	1040-10/0					1	
			256.291			-	1	1	
			11.12				1	1	1
200	The state of the s	THE TIMES C VIRUS HISOLATE HC-14) (HCV)	111-143	1693-1924		-		1	1
170.0	CLINCKIE TALL LANGE IN		1640-1670			1	-	-	
PPCIFIC INCVIA	CEPACINE TALVENCIN	:	1840.187E					- !	_
FURCE IN ALL	בין היכורון לנון או אינון וויי	A THE PARTY OF VIRING THE BANA AND THE V	1640.1670						
1111 G 1R V W	CO MINT TON VINCILLIN	THE PARTY OF THE P	1314-1550	1066-1099					
PPOLG HPAV2	GENOME POLYFROTEIN	THE PARTY A CHIEF OF PARTY AND THE PARTY AND	1314-1530	3068-3099					
FPOI G HPAV4	GENOME FOLVFROILIN		1514-1550	2069-2099					
PPOLG IIPAVI	GENOME POLYPROTEIN		1817.1831	2069-2100					
PPO 0 1PAVI	GENOME POLYPROTEIN	III PALIFIE A VIALID STRAIN THE TANK TH		100			! 	<u> </u>	!
IN C. LITAVI	AL HOURA DE LA CALLES	THE PAINTY A VIETNA CALLE AND A STATE OF THE PAINTY AND A STATE OF THE	1					-	
	NI III AND AND AND AND AND AND AND AND AND AND		33.131	2007			-	1	
1	Z-1-0407 200 10 12 12 12 12 12 12 12 12 12 12 12 12 12	SIMIAN HEPATITIS A VIRUS (STRAIN AGNI-27)	31.16	1313.1333			-	+	
	NEL CONTROLLER	INDMAN BURNOVIAUS 14 (HRV-14)	1004-1133	2003-2041				\dagger	
TOTAL STREET	NISIORAL TOR STOCK	INDIAN RUIMOVIRUS ID (MXV-1B)	1653-1415	1816-1849	1913.2019		-	+	
TOTO IN A SE	THE PARTY OF THE P	HINTAM BILINOVIAUS 1 (IIAV-2)	1646-1475	1809-1142	1976-2012			1	1
<u>.</u>		HENCEN BICKLYINGS SP (118 V. 09)	1460-1492	1823-111.6	1970-2026		-	1	i
PPOI G HKY 12		LINGAN ME BOVIETIC 2015 TRAIN 167071	1108-1145					- <u> </u>	
FFOI G HULVI	CHINDAIL FOR YTHININ	ACIALINA LETRONG MIRKAL DISEASE VIRUS (STRAIN ON)	223-260						
FOLG INDVO	STRUCTURAL POLYFROTLIN		61-99	1333-1269	1316-1349	2179-2813	1374-3311		
PPOLG JAEVI	GENOME POLYPROTEIN	INVANCES CINCENSIS CINCENSIS CARRAIN CARNIS	81.19	1333-1269	1316-1549	2779-2413	3274-3311		
PPOLG JAEVS	GENOME POLYPROTEIN 2								İ

PCGENE	P13C71.21P								
ILL BAME	PROTEIN	VIRUS	-					П	
Prot G IAEVI	_	IAPANESE ENCEPHALITIS VIRUS (STRAIN JAOAR S912)			3	3	ABIA 2	AREA	ABLAL
PEG G MEVN	GENONIE POLYTROTEIN	JAPANESE ENCEPLIALITIS VIRUS (STRAIN NAKAYANA)	101	107.170		11.6	1274-1311		
PPOLG KUNDA	GENOME POLYFROIEIN	KUNIIN VIRUS (STRAIN AIRAIGIC)		747					
PROJECTANY!	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN TP21)							
FFOLG MCFA	GENORIE POLYPROJEIN	AIOSQUITO CELL FUSING AGENT ICTA FLAVIVIRUS	74.1304		1230-1284	2,000.2,001.2	1085-3133		
L.I	GENORIE POLYTROIEIN	NIAIZE DWARS AKUSAIC VIRUS (ATDAIV)	137.181	1000					
MVEV	GENORIE POLYPROIEIN	HURRAY VALLEY ENCEPHALITIS VIRUS	191	1104.1149					
POLG OMV	GENONE POLYPROTEIN	ORNITHOGALUM MOSAIC VIRUS	144.376						
Proto PENVC	GENOME POLYPRUICIN	PEPPER AIDT ILE VIRUS (CALIFORNIA ISOLATE) (PENIV)	636-659	1016-1124					
TOIC TOICE	GENONE POLYPROTEIN	POLIOVINUS TYPE I (SIRAIN MAJIONEY)	1121-1158						
	CENCRIE FULTIFICATION OF THE PROPERTY OF THE P	FULIOVIRUS TYPE 1 STRAIN SABIN)	1123.1130					Ī	Ī
	CENONIE POLYTROJEIN	POLIOVIALIS TYPE 2 (STRAIM LANSING)	1130.1157						
	CENONIE POLYTROIE IN	POLIOVIRUS TYPE 2 (STRAIM W.2)	1130-1157						
	CENONE POLITICIEN	POLIOVIRUS TYPE 1 (STRAIN 21127)	10.156						
	CENTRAL TOLITICAL	POLITIVIRIUS TYPE J (STRAINS POLEONI)? AND POLEON (24) (II)	1119.1136						Ī
	CEMONIE FOLITIFOLIEIN	PLUM POX POTVIRUS (STRAIN D) (PLV)	1960.2991	3064-3113				Ī	1
	GENOME FOLYFROILIN	FI UNI POX POLYVIRUS (STRAIN EL ANIAR) (PFV)	1337-1361	1461-1490					
	GENORIE POLYPROTEIN	MI IMI FOX POLYVIRUS (ISO), ATE NATI (FFV)	2044-2075	1066 3007				Ī	
2000	GENTALE FOL TERCOLON	FLUM POX FOTYVIRUS (STRAIN RANKOVIC) (FPV)	2959.2990	2116-1901				Ì	
NOS O DO	DENIME FOLTFROIEIN	P.C. A SEED HORNE MOSAIC VIRUS ISTRAIN DEDIT	997.16	1011-1445	3149.3178			Ī	
	OFFICIAL POLITICAL PROPERTY AND A PR	PUTATO VIRILS Y ISTRAIN ILLINGARIAN) ITVVI	1303-1336	1001-1001				Ī	
1000	CENTRAL FOLLTROILER	FOIAIO VIRUS Y ISTRAIN N) (FVY)	1107-1136					Ì	
2010	CENTRAL FOR CARCILLE	PARSMIT VI 11 0W 11, FTK VIRUS (1501, A IT, F. 121) (PV) V)	110.362	110.113	1401.1061				
2000	CENONIE POLICEPINA	SOUTH AN AIDCAIC CIRIT (STRAIN N)	245.234						Ì
Project Control	SERVICE POLICE CONTRACTOR STATE OF STAT	ST LOUIS EM. FILIALITY VIRUS ISTRAIN MIST. 1)	61.03	101.131				Ì	İ
יייטיים הייים	THE PARTY OF THE P	SUCARL AND ALL VIRUS (VIRAIN SC)	307.336					İ	
Prot G SVDVI	7:3:044, 104 3:VOX30	SWINE ALVIOLAR MISCASC VIRUS (STRAIN 10) 76)	1385-1617						
PPOLG TBEVS	7,51047,104 37,0835	SWINE VEST (ILVA INSLAND VINUS (STRAIN UKG/2012)	1305.1617						
Proi G Ingva	CLEAN OF POST PROGRAM AND	CALL CONTROL OF THE PROPERTY O		1137-1111		3003.1130			
PING IIV	プロロスのことに	; ;	-:	3166-2198	1011.111			İ	i
FRONG TAREND	-EMONE POLYPROTTIN	1	_	_ :					
PROIG TAREND	Ì				1770.108	904-1910			:
FRING TAIEVG	SENSON PROPERTY.		Bi		_	38.14			
Philo IUNV	PONTE NA YPROJECT	HIMNIP AIDSAIT VIRUS (TUNIS)	201.169		≕	161.00	j		
7 Y 1 2 KH	THE MAN AND THE PARTY OF THE PA		14.98.3711				i		:
	ALL LA ALEGA A	NAME VIRING II	111.01	1			-	1	!
AND SELECTION	CARONIE TO THE TIM			13.500	1172.1109		Ì	Ī	
		VILLOW EVEN VINIS (VINA)	=	220-1266	-	3108-3140	1003-1133	Ì	<u> </u>
T	CENOR PLA VENCETA		<u>; </u>	_	1405.1337	2301.3140	1001.117	Ī	
1-	Will for Ventilla	THE HIGHER AND	111 14		:			İ	!
	GAMBAGE MALYFRONLIN	_	122.114						
PHIN FEVV	HONSTRUCTURAL FOLVFROTEIN	_							į
_	AON STRUCTURAL PULYTROTI IN	_	Ť			1		j	
N CAL	HON STRUCTURAL POLYPROTEIN	-	100	Ī		Ī	Ť	1	Ì
	MON-STRIKE THE POST APROLETY	_	101.00	İ	T		İ	İ	-
	ALCOHOLD ALCOHOLD AND ALCOHOLD	IN PATILIST, VIRUS (STRAIN (ILLRAIA) (III. V)	1618.1612	-	İ		1	İ	-
_	NAME OF THE PARTY	_	616 1650	i				İ	
NOW HEVE	NON-STRUCTURAL POLYPROTEIN	TEPATITISE VINUS (SIRAIN MYANNIAR) (ILEV)	1618.1653				-	Ì	
•	HONSTRUCTURAL POLYPROTEIN		1617-1651				-		
117	HONSTRUCTURAL POLYPROTEIN		-+		İ				
RIGOV	ON-STRUCTURAL POLYPROTEIN		011111	606-16.30	1	j			
Sf V	ONSTRUCTURAL POLYFROTEIN		T.	177	1	Ī		1	
CENT	MOMSTRIKCTURAL MY YEADILIN I	SINDINS VIRUS (SUNITYPE OCKEL NO / STRAIN EDSNYN 82:5)	Ť			T	1		Ī
PECH N CININ	MINSTRIKTIERAL FOI YERUTIEN		1414.1486		1	Ì	İ		
							1		

PCC.INE.	PLOCI ZIP	All Vieurs (no besterney heggs)	AREAL	ABEAI	ANTAL	AREAS	SKAL	ARGAE	BELL
	CANAL DE AL POR VPROTEIN	EASTERN EQUAME ENCEPTIALITIS VIRUS	П						
1	CHILDRAN POLYPROTEIN	EASTERN EQUINE ENCIPITALITIS VIRUS (STRAIN VAD) TEN PROFICK II	135.53				Ì		
	STRIKE LITE AL POLYTROICIN	(1 NEZUELAN EQUINE ENCEPTIALITIS VIAUS (STRAIN 1C.0.)	201-130						i
1.4	SINIK HAL POLYPROTEIN	LENEZIPLAN EQUINE ENCEPHALINS VIAUS (STRAIN TRINIDAD INDIRECY)	-				Ì		;
DINIO	SIRIK HIRAL POLYPROTON	ONYTHE SY ONG VIRIS (STRAIN GULU) IONN)	200	20.02					
Pro S BYN	SIRIN IIMAL POLYFROITIN	BOSS BIALD VERSING NEW AND CONTRACTOR	100					1	:
٠	STRUK TURAL POLYFROTI IN	ROSS BIVIE VIRTS (STEAM TOP) (BEV.)	200						į
2	SIER LIEAL PRIVING	SI MULKI IORI ST VIRUS	2						i
CANA	SCRIP LINEAL PON VPROTEIN	SINDDIS VIRUS (SUB) YFF OCKEL BO / SI RAIN EDSNYN 13:3)	1197-1333						-
200	CENTRAL POLYPROTEIN	SINDRIS VIRUS (STRAIMS LIRSP AND HALP)	1197-1333						
	STATE OF CHECKEN	WESTERN BOUINE ENCEPHALITIS VIRUS	11811.1224						
, M. C.	SINO IONE TO THE STATE OF THE S	BOOLING INITIATION OF FICTORICY VIRUS 11501 ATE 106) (DIV)	141.111						
110	TOL THOUSING	DOCUME AND ACTIVE BY VIETER (INC.) ATE 1331 (INV.)	101.111						
	POL POR YPROJEIN	AND THE PROPERTY OF THE PROPER							
	POL POLYPROJEIN	BOVING LEUKERIIA VIRUS (AUS) KALIAM ISUILAIED (IIILA)							!
	MIL PIN Y PROTEIN	CAPRINE AR HINTIS ENCEPHALITIS VIRIUS (STRAIN CORK) (CAPA)	20.7.00	60.77					
	PUTATIVE POLYPROTEIN	COMPLETINA VILLOW MOTHE VIRUS (COYMIV)	100		1730-178	100			1
	NI POS YPEO IS IN	EQUINE INFECTIOUS ANEALIA VIRUS (CLONE 1169) (ELAV)	166-198	306-519					
	20 POLICE 20 POL	EULINE IN ECTIONS ANEMIA VIRUS (CLONE CL22) (FIAV)	106.198	\$06-539					
ł	7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	FOUNE IN ECTIOUS ANEMIA VIRUS (ISOLATE WYOMING) (1 (AV.)	166-198	103.501					
		INDIAN SPINSARE TROVINUS (FOANT VIRUS)	36.136						
- 1	יייי איז די אין די איז	CHROOM ARE ENVIOUS VIRIA							
יואר.	POL POLYPROTEIN	TO THE PARTY OF TH	417.466	-					
- 1	POL POL YPROTEIN	TO THE SAME TO THE SAME THE SA	417.411						
מרוונוכ	POL PULVFROIEIN	HINIAM I CELL LEORENIA VIRIJO I I VE I CAMINOLAIN ISOLAICI (INIC. 1)		111					
ł	POL POLYTROILIN	HERITAN BEREINODEFICIENCY VIRUS 1 YFE I (ARVIVIVI 1500.ATI) HILLY I)	100	1					
N N	TOL YOU YEAR IN	III AIAN INIMUNODE FICIENCY VIRUS TYPE: I (DITIO1SOLATE) IIIIX-1)	2	446.716					!
1	POL POL YPROTEIN	IIUNIAN INIMUNODEFICIENCY VIRUS TYPE I (BITS ISOLATE) (111V-1)	343.376	36.216					-
	NEW POR VALUE	HUNIAM INTRIUMODEFICIENCY VIRUS TYPE I (MRU ISOLATE) (HIV-I)	30.1%	912-549					
	N. S. C. S.	HUNIAM ININIUMODEFICIENCY VIRUS TYPE I (ELI ISOLATE) (IIIV-I)	130.363	499.936					ļ
	Nie od voe	ILUMAN INFILMODEFICIENCY VIRUS TYPE I (IIXB2 ISOLATE) (1114-1)	331.164	105.005					
	NISIONAL POR POR	HIMIAN HANDMONTHCIENCY VIAUS TYPE I (IRCSF ISOLATE) (HIV: 1)	135.368	204.50					
Į	NEW POLYMENT	III BIAN BAILMODE FICIENCY VIAUS TYPE I (MAL ISOLATE) (HIV-1)	130-361						
١	POLYPROTEIN	III MIAN INDICHODEFICIENCY VIAUS TYPE I (NIN ISOLATE) (IIIV-1)	334.363	903-540					
N	PUR PUR VIEW	HINAM IAMIUNODI FICIENCY VIRUS TYPE I (NEW YORK-5 ISOLATE) (IIIV-	=	\$00.513					
1	MI POI VPROTEIN	ICILINCY VIRUS TYPE I	130.363	474.536					
Ł	NISCOULA FOR	INITIALAN BARADMOINFECTINGY VIRUS TYPE I (OVI ISON ATL) ITHS: 1)	131.364	100-311					
	2	HILITAN INKLINGING ICH NCY VIRUS 1979: 1 (FV22 15/N.A.1.) (111V-1)	103.176	312.540					
		HINTER BARINOISEICH NCY VIRUS TYPE ((REALAT ISOLATE) (111V-1)	330.363	490.516					
2 2 2	FOIL POLITICIA IN THE PROPERTY OF THE PROPERTY	TA ICA CACAMINE MINERAL PARTY OF THE PARTY O	-	13.536					
2	AND POR VERNING	1. \cdot\cdot\cdot\cdot\cdot\cdot\cdot\cdot	_	1116					
	MA TONIA WAS A STATE OF THE STA	10 VIII VALANTA TAY TO SEE A SECTION OF THE PARTY OF THE SECTION O	_						
IV2CA	TOWN THE PROPERTY OF THE PROPE	THE PARTY OF THE PARTY OF THE PARTY AND PARTY OF THE PART	Ξ	-					
14347		THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TO THE PERSON NAMED IN COLUMN T	_	!		•	:	:	i
THE INTRO	MALEN VIRGINIA	THE PROPERTY OF THE PROPERTY O							
FF(M IFIIA	FITATIVE PULTON YEADTIN	III ANDII A IMI AALIDII KAAL AARAMIKI ENAMININ							
V X	ALLICE ALEGICIES	ALVERTAGE AND THE PROPERTY OF		1	: :	:	:	1	! !
7	FOR ALMOND IN	OVING I FAIRVILLE COLLAIN CA ONIVE	80.18	101.110	182.216	398.331			
ONIVS	FOR FORTHOUSING		70 00	616.168	199.141				
>=	NI SIGILA EC		714.074		100		:		: !
	N'INTERIOR	CALLED BOARD CIPIES DATE AND AND CONTRACTOR AND	111.161						
- 1	FOR THOSE IN	CHILDRANTE BARINGAN TICIEM VINITAGENTO	144.111	24.56					
	FOR FOR THUSING STATES AND	CONTRACTO CHOIC PROFILE VINUS	17.35			:	-		
ı	IN/ WITH ILL THE VITE IN THE		410.401						
PPOL SRVI	POL POLYPROTEIN	CHANGE OF THE STREET STREET	10.113	201.235	317.350				
١	POL POLYPROTEIN	CIETA SECTION SECTION SECTIONS I VI. 18613	1110	13.150					
1	POL VAROTEIN	VICENTIFICATION OF THE COLUMN TO THE COLUMN	10117	301-335	113.38				
- 1	FOL POLYTRO IEIN	MERPE SUMPLEX VIRUS CTYPE 67 STRAIN GS)	16-09						
PP41 HSV6C	PROSTRUCTURE STORES	ATTICONALITY TAT ISONITA MACI FAR POR MISDROSIS VIRUS	3.63						
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PALV CIAVE	ACV PROTEIN	CHINE IN LOCALISM WINDS (INCIDATE 17) (IIIV)	8						
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PREV SIVAT		SIMIAN INITIANOPERICIENCY VIEW COOL TOOL ATTENDED ACTION	8						
FRIR! ASFM?	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LANGE CH	APRICAN SWINE PEVER VIRUS HSOLATE BIALAWITH JOHN FACELS							
FRIRI HENDA	RIBONUCLEOSIDE.DIPHOSPHATE REDUCTASE LARGE CHI HI	HUNIAM CYTOMEGALOVIRUS (STRAIN AD169)	270.00	917 191					
PRINCIPLE OF STREET	RIBONUCLEOSIDE DIPIOSPIIATE REDUCTASE LARGE CIT	EQUINE HERPESVIRUS TYPE I (STRAIN ANAT) (EHV-1)	19		464-6)	7			
	PROMICTEDSIDE DIPLICATE REDUCTASE LANGE CH	VACCINIA VIRUS (STRAIN COPINIACION)	20.233					Ì	
	PROMOCLE UNIDE-DIPHOSPHATE REDUCTASE LANGE CH	VACCINIA VIRUS (STRAIN WR)	100			·			
PRIRI VZVD	RIBONIET ENGINE DIPLOCEULTE REDUCTASE LARGE CH	VARIOLA VIRUS	£ 102						
PRIMIL AVEVR	ANDL. SERINE / HOLDONING - PROTEIN EINAGE TO A LICE CALL	VAUCELLA-ZOSTER VIRUS (STRAÍN BURIAS) (VZV)	2:3	100	11:316			1	
PRAIR AVIII	RAMIL SEATHER THRE OWINE - PROTEIN KINASE TRANSFORM	A VIAN RUUS-ASSOCIATED VIRUS TYPE I	149.133					T	
PRIMA VACCV	_	VACCINA VIBILS ASSESSED.	_					T	Ī
PRPM VARV	CRUPTION SPECIF	VARIOLA VIRUS							
PRPOI VACCV		VACCINIA VIRUS (STRAIN WR)	14.0						
THEO CAPAK	D POL YPEPTIDE	CAPRIPOXVIRUS (STRAIN KS.1)							
PRPO COMPX	D POL YPEPTIDE	COWPOX VIRUS (CPV)		90.79					
ATTO ATTO	DIVA DIRECTED RIVA FOLYMERASE 111 KD POLYPEPTIDE	VACCINIA VIAUS (STRAIN WA), AND VACCINIA VIRUS (STRAIN COPENTIAGE	-		1				
PRPO) VACCV	DNA DIRECTED BYA PAY WAS ARE 10 VA BAY COTA 11.7	ARIOLA VIRUS		115.51	1	T	1		
PRIOS VARY	DNA DIRECTED BNA POLYMERACE 19 ED BOX VALUE	ALLINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENIAGI			İ	Ť	İ		
PAPOL FOWPI	I KO POLYPETINE	VARIOLA VIAUS	3			T	Ť	\dagger	
PRPOA LELV				-		T	İ	†	T
PRPOL EAV	Ī		3	3133-3163	3426-3457		\dagger	\dagger	T
PRATI DEIVE				J041-J072					
TAKE TAKE		100	57	117.6				-	
FREE LAND	MANA DIRECTED RIVA FOLYAGRASE SUBLINIT PI		20.00	1					
PRICE INDICE			Т	115.16		1	1		
Ĺ			Т			\dagger		\dagger	
	Ī	MELIEW A VIEW (STRAIN AFOWL FLAGUE VIRUSAOSTOCK))	416-311			İ	Ť	\dagger	
			116-518					l	
PRRP2 (AHTE	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI		# C 31				+	İ	Ī
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Т	2	A A VIRUS (STRAIN ABUDGERICAR/IOKKAIDOVIN)	Ť	+	+	1			
$\overline{}$		K/343	Ť		+				
1	RAA DIRECTED BAN PO VALERACE CINIES.	MA A VIRUS (STRAIN AN OWL PLACIUS VIRUS/WEYTH (KAIL)			+	<u> </u>	1		
PARPY IAGUA		Ī			\dagger	+			
1	The state of the s	Γ	119:505		+	\dagger	1		
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NVNVI 14 88		A 150/78)	\$18.613					
	ALA DISECTED BUY POLYKO BAG SUBINIT P.	A VIRUS (STRADY ARUDDOY TURNSTONE/NEW JERSEY/47/85)	213:613					
1	BLA DISECTED BLA BOL WARRACE CIRCUMIT P.	Т	19:53					
19	TANA TABETTER BUY POLYTREAMS CONTROL PI	INFLIENZA A VIRUS (STRADA A/TURKE YAITANESOT A/13/1/0)	3.63					
	BMA DIRECTED BMA POL YAGERASE SCHOOL PT		119:55					
ŀ	BANK MEETING BANK POLYMERACE SIMINIT PI	וונשנו	35.61)					
١.	ANA CARECTED MAN POLYMENACE CORPORT 91	INTELENZA D VIRUS (STRAIN BYANN ARBORING ICOLD ADAPTED)	35.76					
	THAT CHECKED HAN TO THE MASTER COMMITTED	INTERNAL BY VIETS ISTRAIN BY BONING WILD TYPE II	735.769					
	THAN DIRECTED AND FOLLERANDE SUBURITOR	INTERPRETATION OF THE PROPERTY	604.661					
1	KINA-UIKELIEU KINA YOL TRIKKASE SUBONII YA		137					
	KNA-DIRECTED HNA POLYNERASE SUBUNIT P	(SI KAIN CILINA)						
	ANA-DIRECTED RNA POLYNGRASE SUBUNIT P.)	THOGOTO VIRUS (THO)	5	374-336			_	7
PRRPA CVH22	IRNA-DIRECTED RNA POLYMERASE			112.745	1262-1295	1963-1999	2078-2112 2474-2508	1183-3191
PREA CVAIN	BNA.DIRECTED BNA POLYNGRASE	שעו	708.740	3544.3577	1157.1785	1931.3961		
200	THE DISERTED BUY BOX VACE AND		Т	2133-2160	1111.2304			
VARTO DEV	HUNA-UIKEL I EU RIYA PUL I MEMASE	A STATE OF COLUMN STATE AND STATE AND	Ī		100	V166 3076		
PRRP CVAIAS	MANDIMECTED HIM POLTMENASE	MICHING CURCANINGS PITT (SIRVING AN)	Ī					
PRAFE CYMEN	RNA-DIRECTED RNA POLYNERASE		Ī	200	27/1-1	4130-419	6717-MG	
PRAFB CVPS	ANA DIRECTED ANA POLYNGRASE	ALITIS CONUMAVIAUS		111.150	417-313			
PRRPB CVPR	RNA DIRECTED RNA POLYMERASE		10-113					
FRAPB IRVB	RNA-DIRECTED RNA POL YMERASE	IONCILLIS VIRUS (STRAIN BEAUDETTE) (IBV)	616-670					
FREE BURNY	RNA POLYNERASE	_	101-111	1096-1128				
PREM HANTV	RNA POLYNERASE	HIANTAAN VIRUS (STRAIN 16-118) (KOREAN HEMORRHAGIC FILVER VIRUS)	1611-161					
PRESI LINGVA	-	INJUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	111.913	1111-1213				
			Ī	694.736	1042-1074	1797-1632		
THE PARTY IN	-	MARRIED VIRIOR COTRAIN POPPI	T	608.736	1042.1074	1221.2251		
. 1.	ANA-UNACLED ANA TOUT MENASE	NETONI	T	647.613	744.625	1160-1192	1436.1914	
	MAN POLITICANSE BEIN SUBDINI	Tisse	1					
31	KNA POLTMERASE DE LA SUBUMI		+	1011				
2	MAA POLYMERASE BEIN SUBURI	THE WASTLE COSENSE VINCO (STRONG SENDER IN THE CAST AND ASSESSEDANCE ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESS	T			1	100 100	
- !	MAA POLYMERASE BETA SUBUM!			236.325		***************************************	Ť	
FREE FINA	RNA POLYMIRASI: III: TA SIRRINIT	VINUS (NIRAIN MILL CHIRA)	1	113-764	784-2114	111.111		
FREM. RABVE	RNA POLYMERASE HETA SUBUNIT		1	104-317	X(1-40)	1930-1762		
FRRPL RABVS	INA POLYMERASE BETA SUBUNIT	(0.019)	7	104-133	1365-1394	1930-1962		
FREE ROV	ANA-DIRECTED ANA POLYMERASE		-					
FRRPL RVFVZ	ANA DIRECTED ANA POLYMERASE		2	1009-2044				
FRRM. SENDS	ANA POLYNITASE DETA SERITME	SI NDALVIRLIS (STRAIM Z / HOST MILITANTS)		233.269	235.764	786-814	3140.3177	
	TAN IN AND BANK HILLA CARINI			43.89	141.181	1927-1955		<u> </u>
FREIT, SI-M32	ANA MY VAICHASII NETA STRIUNIT		16.39	337.769	135.704	784-814	1140.2177	
PREP. SEGUI	ANA-DIRECTED ANA POLYMERASE		196.631	938-1978.	2081-2119			
PRAPIL SVSWR	RNA POLYMERASE RETA SUDUNIT	_	337.580	94-1122	1020-2051			
FRRPL SYNV	ANA POLYMERASE BETA SUBUNIT	SONCHUS YELLOW HET VIRUS (SYNV)	136-164	603-634	Т	918-951	404-1517	
PRRFI. TSWVD	RNA-THRECTED RNA POLYNIERASE		_	43.440	126A-1298	3169.2403	2481.2511 2005.2840	ç
THE CAN	BNA FULVAMBASI:		1017.1051	1147.1177	1261-1911	2000-2005		
PREPL VSVIII	ANA POLYMERASE BETA SUBUNIT	VESICULAR STOMATIFIS VIRUS	_	313-369	1011-1039	1662-1697	1954-1919	
FREE VSVIO	ANA POLYNGRASE BETA SUBUNIT		1011-1019	954-1919			-	•
PARPL VSVSJ			111.80	98.746	97.71	961.99	1011-1019 1739-1772	73 2051-2087
PREPO RWYVE	PLITATIVE ANA DIRECTED ANA POLYMERASE		146-174					
PREFO DYDVI	FILE TIVE RIVE DIRECTION AND THE PASSE	HARD LY YELL TOW DWARF VIRIS (INMANIE MAVIESI) (HYDV)	33.355					i
WIND HANGE		1	2011					
	PITATION DISCOSTING TO VALE ACE		23.35	Ī			 -	Ī
AND STATE	POLYTICE NAT MARCHED BNA BOT WARRACE			Ī				
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PRINC CCMVS	PUINTY MAY DIRECTED MAY FOLT MERCASE	T	Ť					
NO CAR	PROBABLE RIVA-DRIFECTED RIVA POL TMERASI:	CAA)	T					
TANFO CRI	FROUABLE RNA-DIRECTED MAA FOLTMENASE	Ī	7	Т	470-301			
PARTO IBDVS	PUTATIVE RNA-DIRECTED RNA POLYNGRASE	STICKIN ST/0) (IRDV)	T	1				
PRATO IBDVA	PUTATIVE RINA-DIRECTED RWA POLYNIERASE	AVIAM IN ECTIOUS BURSAL DISEASE VIRUS	160.711	311-343	347-621			
PERO PRV	PUTATIVE KNA-DIRECTED KNA POLTMERASE		Т	144:178				
FRRIO IFNVS	PUTATIVE RNA-DIRECTED RNA MILTMERANE		٦	2/1-1/2				7

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PARACHICE DE NAT OLIVELASE STUDIES 19-101 19-10	_	PUTATIVE RNA. DIRECTED ANA POLYMENASE	FIFTER MILLIO MOTTLE VIRUS (STRAIN SPAIN) [FFAIV)	Г	102.330	169.65	1069-1106	1337-11365		
MAY OFFICE TO BAY OF VERANE KINDER VI 100 VIET DIALY OF VERANE KINDER VI 100 VII	Τ.	PUTATIVI KNA DIRECTI DANA MY YAIFRASE	AFD CLOVI'R NICROTH KUSKAIC VIRIUS (RCINALV)	П	130-353					
MAY DIFFERED BAY OF THE LAKE MUNDEN VIEW	1		RI:UVIRUS (TYPE 2/STRAIN PS/JUNI:S)	384.313						
NATE DESCRIPTION OF THE ACT OF THE STATE	_	-	NOVINE ROTAVIRUS (STRAIN RF)		200.231	141.116				
MAY ADDRECTED BANK POWERASE STROWNER TO INCREME VOLUME STRAIN COLUMNIC STRAIN	_		DOVINE ROTAVIRUS (STRAIN (IR.)		247.276					
15.00 15.0	_		PURCINE ROTAVIRUS (STRAIN GOTTFRILD)		247.276					
TOWART IN CAPACING TO BEAT POLYTERASE TOWARD TO BEATS BY THE WILLS TOWARD TO BEATS BY THE WILLS TOWARD TO BEATS BY THE WILLS TOWARD	Г		SIMIAN II ROTAVIRUS (STRAIM SAIT)		20:33	347-276				
The NAME OF THE PART OF THE ALEST TO ALL OF THE ALE ALE ALE ALE ALE ALE ALE ALE ALE AL	Ī	RHA POLYNIERASE	TACARINE VIRUS	17-51	109-138	2078-2112				
THE PROCESS OF THE WASTERN OF THE WORLD OF	T	PROBABLE NAS DIRECTED RNA POLYMERASE		670.501						
THE TITLE WAS DIRECTED BAY FOUNDATION THE TITLE STATES THE TITLE WAS DIRECTED BAY FOUNDATION THE TITLE STATES THE TITLE WAS DIRECTED BAY FOUNDATED THE TITLE WAS DIRECTED BAY FOUNDATED BAY FOUN		PROBABLE RIMA-DIRECTED RIMA POLYMERASE	TURNIP CRIMALE VIRUS (TCV)	Γ				İ		
UNIT UNIT		PUTATIVE ANA DIRECTED ANA POLYNERASE		Г	120-159	209-244	176-406	180.050	155.00	1327-155
		PUTATIVE ANA DIRECTED ANA POLYNERASE		Τ	76-406	300.728	1313-1369	Ī		
		PUTATIVE ANA-DIRECTED ANA POLYMERASE		Π	76-406	700-728	1533-1565			
1000 1000	Т	PUTATIVE RNA-DIRECTED RNA POLYMERASE		Γ	76-406	700.728	۴	1313-1165		
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The color of the	Т	ANA POLYMERASE ALPHA SIGNINIT		215.202			İ	Ì		
The part of the first and th	1	NA PON VAICEACE ALPITA CLIRIDALI		100.111				Ì		
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NAME PARTICLE AST A PARTICULAR NEWCASTIE DISEASE VILLS (STACH AUGITECOSINATION) 100319		15		2				Ì		
MAY DOLYMEASE AT PIA SUBLINIT		WA FOLYMERASE ALPHA SUBUNIT		220-255				İ		
				310-355						
MAY POLYMEASE ALPIA SUBURIT INDAMA PARING LIERAZ A VRUS (STAMN TOSSURA) (TV 2) 151-151 151-154 1		INA POLYMERASE ALPHA SUBUNIT		116.233						
MAY POLYMERASE ALPHA SUBUNIT MALANE LLENA AN ANDS (STAMM 4-2) 120-211 131-344 MAY POLYMERASE ALPHA SUBUNIT MANIE VILLS (STAMM 4-2) 110-111 131-344 MAY POLYMERASE ALPHA SUBUNIT AND		INA POLYMERASE ALPIIA SUBUNIT		Т						
MAY POLYMERASE ALPHA SUBUNIT PROPERTY VALUE		WA POLYMERASE ALPHA SUBUNIT		П	33-364					
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NAM POLYMERASE ALPHA SUBUNIT A A A BASE OF STATING	╗	INA POLYMERASE AL PILA SUBLINIT		16.16						
AND POLYMERASE ALPHA SUBUNIT A CABIES VIRUS (STAMP RAY) AND POLYMERASE ALPHA SUBUNIT A CABIES VIRUS (STAMP RAY) AND POLYMERASE ALPHA SUBUNIT A CABIES VIRUS (STAMP RAY) AND POLYMERASE ALPHA SUBUNIT A CABIES VIRUS (STAMP RAY) A CABI	╗	UNA POLYPIERASE ALPINA SUBUNIT		16.24						
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NAME POLYMERASE AL PILA SIGNAMI 1 SECONDARY OF THOST RULTANES 100-566		THA POLYMERASE ALPHA SUBUMIT								
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MAN POLYMERASE ALPIA SIGNUMI SEEDIA VIRUS SISAMI MANINA 100-160	Ţ	POLYMINASE AI FIIA SIMIIMI	:	3			:	:	:	
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KUIT BUNKTIN KINSKALI AN TIKE PROTEIN SUFFRANCINE DISAULTASE LIKE PROTEIN SUFFRANCINEN SAFERNI SERRA PROTEINAN SERRA PRO	Ť	THE POST OF PARENTS AND PARENTS	_	207-24						
SUFFICIENT SELIKE PROTEIN VARIOUS (STRAIN VR.) SUFFICIENT ANS CLIKE PROTEIN VARIOUS STRAIN VR.) SPREADITH AND STRAIN CAUSANDES STRAIN CAUSAN		ALL BOYLEN MACANIA AND BASE PROBLEM			_ 	:	Ī		!	;
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FILE STATES	GENE 21 PROTEIN	FOUNE HEAPESVIRIS TYPE I (STRAIN AND) [ENV.1)	103.333	178.812			İ	Ī
FIR 37 HSVSA	GENE 6) PROTEIN	HERICESVIAUS SAIMBRI (STRAIN II)	209.995			 -		
11.11 7270		VARICELI A.ZOSTER VIRUS (STRAIN DURIAS) (VZV)	598.629	106.736	176.806			
THE PERMAN	T	HUNIAN CYTONIF GALOVIALIS (STRAIN AD169)	137-188					
0070	INDST STOLES VINCENTAGES	VARICELLA ZOSTER VIRUS (STRAIN DURIAS) (VZV)	24.307					
	MENINAME TRUILIN ULT	HERTES SIMPLEX VIXIS (1775, 1751AAIN 17)	1.70					
AND THE PERSON	DECK. IS MENISTAN. TROIL IN	VARICE C.A. ZOSTER VIAUS (STRAIN PICKIAS) (VZV)	76.64	27.70				
NI STATE	OF ED AF PILA TRANS INDIFFING PROTEON	FIGHTINE LEGISTECALUVINUS (STICALINATION)		741.77				
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1200	DAY BOD IN A TION PROFESSION IN CO.	TERRET STATE OF STRAIN HOT BUILDING THE RELIEVE OF STREET	382.617					
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	-	HI KIES VIAUS SAINIIKI (SIRAIM II)	279.767	174.411				
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PVIJK JRVPL	16 KD PROTEIN	IOBACCO RATTLE VIRUS (STRAIN PLN)	34-62						Ī
PVIAL NOVAC	IR LKASE	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	113.342						
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PVALJ CLVK	1 .	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 044)	77:113					
PVALJ CLVP	7	CASSAVA LATENT VIRUS (STRAIN INCENIAN)	13:11			-		
PVALJ TYLCM	. 7	TONIATO YELLOW LEAF CURL VIRUS (STRAIN MATRIANDE) (TYLCV)	31-16					
VALI TYLCV	ALI PROTEIN	TONIATO YELLOW LEAS CURL VIRUS (TYLCY	2 2 2			1	1	
	A PAIN TO A PAIN	CAIR IS DWE MOTAIC VIRIL (STRAIN DAIL)	1	0.1.0				
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PVAT CALIVI	_	CAIR IFLOWER ANDSAIC VIRUS (STRAIN NYRISS) (CAMV)	25.5	91:18			-	
PVAT CAMVP	_	CAIR IFLOWER MOSAIC VIRUS (STRAIN PVIAT) (CAMV)	10.51	91:18				
PVAT CAMVS	_	CAULIFLOWER NOSAIC VIRUS (STRAIN STRASPOURG) (CANIV)	10.53	91:10				
PVBON VACCC		VACCINIA VIRIIS ISTRAIN COPENTIAGEM)	134.156	419-525				
PVB04 VACCV	_	VACCINIA VIRUS (STRAIM WR)	134.136	419.525				
PVBO4 VARV	PROTEIN B4	VARIOLA VIRUS	419.525					
PVBIG COWPX	INTERLEUKIN-I BINDING PROTEIN PRECL	COWPOX VIRUS (CPV)	19.126					
PVB16 VACCV	INTERLEUKIN-I BINDING PROTEIN PRECURSOR	VACCINIA VIRUS (SIRAIN WR)	89.126					
PVB19 VACCC	_	VACCINIA VIRUS (STRAIN COPENTIAGEN)	¥ .					
PVB19 VACCD	SURFACE ANTIGEN SPRECIASOR		11:20					
PVB19 VACCV	SURFACE ANTIGEN SPRECURSOR	VACCINIA VIRUS (STRAIN WR)	2					
PVBIS VARV	SURFACE ANTIGEN S PRECURSOR	VARIOLA VIAUS	7					
PVBRI BGMV		DEAN GOLDEN MOSAIC VIRUS	66.19					
PVC03 SFVKA	G-PROTETH COUPLED RECEPTOR HOMOLOGICS	(XI V)	9			$\frac{1}{1}$		
PVCO VACCC	PROTEINCE	VACCINIA VIRUS (SI KAI)	2	113.216				
PVCG4 VACCV	PROJEINCA	VACCINIA VIRUS (STRAIN WR)	8	\$12.0				
PVCO VARV	PROTEINCA	VARIOLA VIRUS	26.34					
ŀ	PROTEINCE	VACCINIA VIRUS (STRAIN COPENIACION)	76.67					j
PVC06 VACCV	PROTEIN CO		2 :			1		İ
- 1	PROTEIN CO					+		_
PVC01 SPVKA	INTOINE HEAL PROTECTION CO	SUPPLY THE CONTRACT OF THE CON	200				<u> </u> 	-
ALCO AVEC	PLACE STATE OF THE PARTY OF THE		11.40					İ
PVC10 SFVKA	HYPOTHETICAL PROTEIN C10							
PVC10 VACCC	PROJEIN CIO	VACCINIA VIRUS ISTRAIN COPENHACIAN	111	Ī		-		
1.	PROIFINCIS							
1	PROTEINCIO		<u> </u>				_	
برا	PROTEIN CZI/BZI		1.74					
PVCAP FBV			10.10	П				
PICAP IKMVA	MINIOR CAPSILIPACITIES	HINDAM (YTOMICALOVINIS (STRAIN ADIM)	-	19:181	346.2Rh			
LYCAP IISVII	MAION CAPAIN THE IN		2	٦				
LI CAP LISVAN	MAJOR CAPSIDARDILIA	COLLINE TITLES OF STREET STATES AND AND STREET STREET		969 909	M :			
1	THE REPORT OF THE PROPERTY OF			ī	Ť			
NAME OF LAND	MADE CAPUS PROFILE	IANA SICRAI	16.9	360.310	Ť	901.786		
PV CAP VZVID	1	l'A	13.15		Ī	<u> </u>	<u> </u> 	
PVI UNI AIN BY	ALINEM CONT PROTEIN.		86.113			<u> </u> 		Ī
PVCOSI ADEOS	NEWOR CORF. PROICIN	N ADT MOVIRUS TYPE S	13:114					
PVIND VACCC	PROTEINDI	I NI I VIEW I	05.21	146-112				
Primi VACTO		NIA VIRIUS (NIA) SAN	9.0	14.112				
LVIN VA		VARIATION VINITALIAN	9	211-49				
PV[XX]	WE AND PROTEIN	1230458	20.50			<u>: </u>		
אנונר אנונר	TRUE LA LA		2		1	1		
1	Policino.		9	Ì		-		
	PECIFICATION		19:31			-		
rvros vacco	PROTEINES	VACCINIA VIRUS (STRAIN DAIREN I)	T		T			
	TOTAL STREET		į.	E S	311.540			
FVI OF VACCV	PROTITINI 6			_	311.500			

18.0.0.0	17.17.17.19	All Vicaires (no hocteriophapes)	Т	Т	1 1 1 1 1 1	ABFAGAR	AREA 9 AR	AMEAG	AREA?
THE REAL PROPERTY.	72-1-12-1	VIRUS	3		T	Т	ı	I-	
100			ī	2	1	1		+	
PVEDS VARV	PROJEINES		=			-	1	1	
PIT 10 VACCC	PROJECT		=				_		
2012	TROUGH IN								
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	2 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7	╗		1		1			
	TACAN TACAN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACAINTY)	45.77				1		
	EARLY 18 3 NO PROTEIN	_	£.5						-
PVE. 145.05			151.291						
PVE 10V11	EI PROTEIN	HIGHIAN PATH. UNIA VINOS CONTRACTOR	36.381						
11.101			Ī		†		1	- -	
			1	2			+	1	
	I.I FROITING		230-263			-			
			141.271					_	
1	23102413			160				-	
ı	F. PB. CT. F. S.							-	
1		THE DATE OF THE STATE STATES	231.267				1		
P1E1 11PVS	EI PROTEIN		\$6.3			_		_	
	EPROTEIN		100.000					-	
۱	6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 -	IIIWIAN PAPILLOMIAVIRUS TYPE 68			1				
1	CI FRUIT I	LICER DADE I DATA VIRIS	161.201	į				1	
PLEI PAPUD	EIPROIEIN	1	337.790						
	201612	ī		Ì					
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P. C. S. S. P. A.C.	EARLT 25 TO FRUIT	THE STATE OF A VIET OF TYPE OF	21:15						
P. L. 117.57	ENPROTEIN	ī	13.13					_	
	211111111111111111111111111111111111111	7			Ī				
		EAR POLYHEDROSIS VIRUS (ACNINPL)	4-37					+	
PIEZ MPVAC	EARLY 40 YND PROJECT	=	9.36						
PUT IN IIPVII	PROBABLE ESA PROTEIN		,			-		_	
1	2131516 15 21 21 15 15 15 15 15 15 15 15 15 15 15 15 15							H	
	FROM SECTION OF SECTIO	TANA TANA TANA VIRILIS TYPE OC	3.5						
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	PRODABLE ES PROTEIN			İ		-			
	N. I. C. S.				1	1		1	
	TRIMININ IS IN MARKET TO THE PROPERTY OF THE P	INUS TYPE I	= : E						
	PROBABLE ES FROILIN		09.140						
Indita Valle	PROBABLE IS PROTEIN								
1							1	İ	İ
. ;			33:30					Ì	
١	I TROUGH		55.90						
	ETPROTEIN		1				_		
ĺ	ET PROJECT						_	_	
i									
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F.: 2 H.C.14			1						
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	E. PROIETH	THE PARTY CALLACTER TYPE AT	M-19					_	
PVET INVA			61.80					_	
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			11.11						
LAI MILAN		_	25.90						
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BUE 1 MP VAR	E) PROIEIN	23 1175 00				l			
C. 0 4 0 10	CHENTEN					1		İ	
	1100000	_	60.43		Ì				
PVE) PAPVE	ETPROTEIN	M. YHEDROSIS VIRUS (ACAINFV)	133-153	650-678					
PVER NPVAC	EARLY 94 KD PROTEIN	ī				-			
2150	VIBAL ENHANCING FACTOR	TAICHOFLUSIA NI GICANOLOSIS VIRUS (1 PR.V.)	7				-		
130	70.000 000.000		16-31	17.117					
FVERV III.Y	I NATI OF L'ACTION	IN INDIANTITION DISCO	201.185				_		
PVENV DICELL	ENVELOPE GLYCOPROTEIN PRECURSOR		201.314				-		
PVENV MCVI	MAJOR ENVELOPE PROTEIN	MOLLUSCUM CUNIACIOSOM VIAUS SOULTEE LIFECTI		I	Ī	+	-	T	
	-		201-136			1	+	Ť	
PVENV MC	-	VACCINIA VIRUS (STRAIN COPENIAGEN)	201-241			-	1		
PVENV VACCO			304.341			-			
PVENV VACCI									
STATE OF THE PERSON							1	1	
	11 11 11 11 11 11 11 11 11 11 11 11 11	VACCINIA VIRUS (STRAIN VR)	701.741			1		1	
PVI:NV VAC. V			181.881	104.141					
FVENV VARV	MAJOR ENVELORIS FROIDING							!	

	r					-		-	Γ
PCGENE			AREAI	ARFA?	AREAS	AREA . AP	ANEA! AREA!	6 AREAT	
	LEGITATE .	VACCINIA VIBILE (618 ATM CINERALIACIEM)	Т	Г	Т	Т	Ī	Т	Ī
			Ī			1			Ī
PVE03 VACCV	_	VACCINIA VIRUS (STRAIM WR.)						1	Ī
PVFP1 FOWPV	_		207-330			1			1
PUTPA FOWPV	PROTEINFR		237-367					1	1
PVP CAVK	PROTEIN F7	CAPRIPOXVIRUS (STRAIN KS-1)							1
PVFUS VACCE	14 KD FUSION PROJEIN		19-61						1
PVFUS VACCV	IN KO FUSION PROTEIN	JS (STRAIN WR)	3						٦
PYFUS VARV	14 KD FUSION PROTEIN		28-41			_			1
PVODI HEVEL	HYPOTHETICAL GENE I PROTEIN		317-346						1
PVCD HVVFR	HYPOTIGETICAL GENE 2 PROTEIN		961-19			-			
PVC03 VACCV	ISATIN. BETA. TIINSENUCARBAZONE DEPENDENT PROTE	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPTINIAGE	92.130						
		VARIOR A VIRIL	92.120						ļ
700	SATINGE AT MICHELLANDALMS DESCRIPTIONS	ICTALIBID MEDDECURIS I ICHANNEL CATERII VIRUSI (CCV)	162.136						
MACH (B)	HINDING INC. JANIEN		14.61						Ī
PVC06 HSVII	CAL GENE 6 MEMBRAME PROT	ICIALCINO REPUES VIROS I (CRANCE CATTES VIROS) (CCV)				1			Ī
PVCO6 VACCC	PROTEIN GA					1			Ī
PVCO6 VARV	PROTEIN G6		0 N						Ī
FVG01 VACCC	PROJEIN G7		51-12						Ī
PVG07 VARV	PROTEING	VARIOLA VIRUS	113-148						_
PVC00 VACCC	PROTEINE	VACCIMA VIRUS (STRAIN COPENITAGEN)	101-101						
VICTOR VICTOR	121010		106-301					_	1
2847			303.338						
	STATE OF STATE OF SING HINDING PROTEIN	INFOVINCE LICHAMME CATHERN VIRUSI (CCV)	130.183			-			Γ
rvcII) IISVII			306.341			l			Ī
٦	2					t		-	ı
٨	HYPOTIETICAL GENE 12 PROTEIN		3	1		1			Ī
	CAPSID PROTEIN		T	T	414-452	+	-		1
Ī	IIVPOTITETICAL GENE 12 PROTEIN	ICTALUND HERPESVIRUS & (CHANNEL CATFISH VIRUS) (CCV)		647.678				1	Ī
FVG23 JISVII	JIYPOTHETICAL GENE JI PROTEIN		50 o			1			1
	HYPOTHETICAL GENE 26 PROTEIN	NEL CATFISH VIRUS) (CCV)	94-123			1		1	1
PVG17_HSVSA	IIYPOTHETICAL GENE 29 PROTEIN		36.74						
PVG28 HSVII	,		49.52						Ī
2		`	180-217						-
PVC2 SPV4			100.144						
rvcjs lisvii	CHENE IS FROILIN	NEL CATHISTI VIRUS) (CCV)	15-46	190-226					
PVGJ6 IISVSA	POSSIBLE TYROSINE-PROTEIN KINASE		151-185						
Г	IIVPOTIRETICAL GENE 19 PROTEIN	ICTALURID HERPESVIRUS I (CITANNEL CATFISH VIRUS) (CCV)	10.57	641-682					
Т	IIYPOTITETICAL GENE 40 PROTEIN		٠						_
ī	HYPOTHETICAL GENE 41 PROTEIN			202-233					
1	HYPOHIETICAL GENE 43 PROTEIN		91-125						
PVC43 HSVII	HYPOTHETICAL GENE 41 PROTEIN F			157.185					
Γ	PROBÁBLE MAJOR CLYCOPROTEIN	NEL CATFISII VIRUS) (CCV)	111.925						
PVG48 IISVSA	IIYPOTITETICAL GENE 48 PROTEIN ;		18:12						
PVGS0 IISVSA									
PVGSI_IISVII	IIYPOTHETICAL GENE SI MEMINAME PROTEIN	(CCV)		14:1% 14:1%					
PVG32 HSVII	HAPOINELICAL GENE 32 PROTEIN		3					-	1
	HYPOTHETICAL GENE SS PROTEIN							-	1
1	HYPOTHETICAL GENE SAPROTEIN	ILLIALUNU REFESVINUS I (CIIAMBEL CATRISA VIRUS) (CCV)	Т	29-119	1001-1120			+	Ī
╗	HYPOTHETICAL GENE 31 PROTEIN					+		+	Ī
PVGSB HSVSA			204.7	103-633					1
rvast ilsvii	HAPOHIE H.A. GER, SYNEKBRANI PROHEN						1	1	1
7	HYPOTHETICAL GENE 61 PROTEIN	-	76-109	٦					
П	INPOTIETICAL GENE M PROTEIN	ICTALUAD REPORTED FOR A CHANNEL CATERIA VIRUS) (CCV)	22.63	Т		+	+	+	T
PVG65 HSV1	HYPOTHETICAL GENE 65 PROTEIN			2	9771-XZ	+		1	Ī
PVG61 HSWI	INPOTIETICAL GENE 67 PROTEIN	MEL CATPISH VIRUS) (CLV)				1		1	1
PVC6 SPVIA	GENE 6 PROTEIN	SPIKOTLASMA VIKUS SFVI-KIAZ B	4				1	+	Ī
ار	HYPOTHETICAL GENE 71 PROTEIN		Т					+	
٦	HYPOTHETICAL GENE 72 PROTEIN	CONTRACTOR IN CONTRACT PARTIES IN THE CONTRACT PARTIES PARTIES PARTIES	٦			1	1	$\frac{1}{1}$	٦

	PINCTIZIP	All Viruer (na Decirelophoges)	П	1 1		Т	П	
11.5.263.6	PROJEK			A PORTO	77/10	2552 05102	24.5	198
Т	HYPOTHETICAL GENE 10 PROTEIN		97.0					
	GENE 7 PROTEIN	IN BEAUDETTERAIN)	E	-	3103-2146	1601-1633		
יייייייייייייייייייייייייייייייייייייי	CLYCOPROTEIN 11101 PRECISESOR			137-183				
	GLYCOPROTEIN PRECURSOR		129-1294					
2	ET GLYCOPROTEIN PRECURSOR		199159					
7	GLYCOPADI FIN PAECUASOR		28-28		1			
FVGL 2 CVBN	ET GLYCOPROTEIN PRECURSOR		129-1294					
7-	ET CLYCOPROTEIN PRECURSOR		129-1294					
78.7	ES GLYCOPROTEIN PRECURSOR)	1359-1394					
CAIN	ET GLYCOPROTEIN PRECURSOR		1053-1018					
3	ET CL VCOPROTEIN PRECURSOR	D TYPE 4) (ANIV.4)	1267-1304					
	CATION OF THE PROPERTY OF THE ACTION OF THE		1315-1352					
Т	CO COLORD LEND BECT IN SOR	V / VARIANT CL-3)	1267-1304					
Т	CI CLOSED SEIN PRECIESCO		1136-1163					
Т	TO TO THE PARTY IN COLUMN TO THE PARTY IN COL	IS CORONAVIRUS	632-665	116-74	1338-1363			
Т	ELOCACIENT PRESENTATION			78.35	1311-1361			
1	GLYCOPROTEIN PRECURSOR	SCHOOL TO A MACHINE CONTRACTOR OF THE STATE OF THE SCHOOL AND A VIET OF	Ī	134.742	1326-1361			
٦	EJ GLYCUTAGE IN PRECUMBUR		Ī	114.743	136.1361			
	E3 GLYCOPAOTEIN PRECURSOR		Ť		Ì			
	GLYCOPROTEIN PRECURSOR	FORCING RESPIRATION TOROGRAPHOS	T		9111			
PUCLE CVPRM 620	GI.YCOPROTEIN PRECURSOR	POLCINE RESPIRATORY COROSAVIRUS ISTRAIN MISTERLY	ī					-
	ET GLYCOPHOTEIN PRECURSOR	PORCINE TRANSMISSING GASTAGEN FRITIS CORONAVIRUS ISTRAM NET	Ī	70/-10	10011-076		 	
PYCL FIPV EN	GLYCOPROTEIN PRECURSOR		Ī	9	8			
18VB	E) GLYCOPROTEIN PRECURSOR	RAIN BEAUDETTE) (IIIV.)	٦					j
S	GLYCOPROTEIN B PRECURSOR		٦	25.20		-		
	YCOPROTEIN B PRECURSOR &			707.144				
1_	YCOPAGIEIN B	. 6 / 51 RAIN UGANDA-1102)	73-110					
	YCOPAGIEIN I PRICURSOR	NOVINE HERPESVIRUS TYPE I	234-2116					
PVGL B BISVBY GLY	GLYCOPROTEIN ILI PRECURSOR	BOVINE MAMMILLIUS VIRUS	745.774					
PVGLB HISVING GL	YCOPACTEIN I PARCURSOR 1		237.117			Street		
PVGI B II. TV6 GE	YCOPROTEIN II PRI CURSOR		42.472					
Fren H.TVS Ca.		1	127-123					
יימום ווזייו מו	GLYCOPROTEIN II PRICORSOR	RAIN THORNE VARY (II. TV)	٦			-		
PIGLE MCNIS GL	YCOPROTEIN II PRICURSOR		Ì	31:376				
PVGLC HSVII GLY	PCOPROTEIN C PRECURSOR	TEMPER SENIE EX VINUS (TYPE I VINUS 13)	8	1				
v	PCOPROTEIN C PRECUASOR		8	1	Ì			
FVGLE 115V2 GL.	YCOPROTEIN C PRICTINSOR		013.465					
PVCIC IISV21 CA.	CA. YCOPHOILIN C PRI CUMSOR		130-466		Ì	-		
_	GLYCOPROJEIN GILL PRECURSOR I		ī					
_	CH.YCOPROTEIN CFV		T	3	1			1
	GLYCOPROTEIN GPV		ī					
	CLYCOPROTEIN DIRECTINSOR		2	i	i	1		!
			T			-		
T	GLYCOFROIEIN D FRI CURSOR				Ī			-
HSVEA	GLYCOPROTEINE		T	1		-		1
-	GLYCOPROIFIN F PRECURSOR		T		Ť			-
	GLYCOPROTEIN E PRI CURSOR		Ţ	77477	Ì	<u> </u>		
PVG F PRVRI (14.)	CHANDLE OF THE CHANGE		_	-		:		-
_	LINES CLYCOTECH IN THE LUNCH	1	ī	15.51		1		
PVCLF BRIVE FU	FUSION GLYCOFRUIEIN PRECURSOR	N) (IIM))	44-913					
-	FUSION GLYCOFROTEIN PRECURSOR	2	11.513		1		-	
ī	FUSION CLYCOPROTEIN PRECUASOR	٦	262-58					
PVGLF ICK VI	PUSION GLYCOPROTEIN PRECURSOR	7	42.53					
Т	FUSION OF YOURDIFIN PRECURSOR	IIIMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN AT)	3					_
	FUSHING CITYCOTROLLIN PRICURSOR	4	404-313	1	1			
	FUSION GLYCOPROTEIN PRECURSOR		Т					
PVGLF MEASE FU	SION GLYCOPROTEIN PRECURSOR		7		1			

CULE KANE N'GLT NEASI				3	4854.2	AREAS	AREAS IA		
VGLF MEASI	PROTEIN		Г	Γ					١
VICE BIEARY	FUSION CLYCOPROTEIN PRECURSOR	ATA-II	324-356	181-184					
	FUSION CLYCOPROTEIN PRECURSOR			446-474					١
VGLF MUNSPI			446-474					1	
VOLF ARMITAL	FUSION (A. YCOPRIDIT IN THE CURSON	AILMIPS VIRUS (STRAIN RW)	174					1	
P. C. L. BIUNITA	PUSICA CLICOTACITIA PRECINSOR		T	46474			1		
NOT E VINE	FISHON CLYCOPACIEN PRECURSOR	Sev.	3.6					T	
NON I PA	FINION CLYCOPROTEIN PRECURSOR	(STRAIN LASsé) (MOV)							
VCI F PIODV	FUSION GLYCOPROTEIN PRECURSOR								
VOLE PINE	FUSION GLYCOPROTEIN PRECURSOR	(STICAIN COS)	2002						
ALL PITE	FUSION CLYCOPROTEIN PRECURSOR							Ī	
MIN DAY	FUSION GLYCOPROTEIN PRECURSOR	HUNIAN PARAINT LUENZA 3 VIRUS (STRAIN MH 4711)	T	441 480					
VCz F RINDK	FLISTON GLYCOPROTEIN PRECURSOR (T	41.4				Ī	
VC F PROF	FLISTON GLYCOPROTEIN PRECURSOR		T						
PVCI E CENTS	FLYION GLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN Z / HOST MUTANTS)							
VCI F CENDS	FUSION GLYCOPROTEIN PRECURSOR							Ī	
	FISSION GLYCOPROFEIN PRECURSOR	us)	200						
5	EINTON CLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN HVI)							
1.	FIISION GLYCOPROTEIN PRECURSOR							Ī	
	FISION GLYCOPROTEIN PRECURSOR								
VCI F 181V	FUSION GLYCOPROTEIN PRECURSOR								
VCI C HSVEB	GLYCOPROTEIN G PRECURSOR	EQUINE HERFESVIRUS 1 YPE I (STRAIN AB47) (EIIV-1)	100						
VC2 C VNV	SPIKE GLYCOPROTEIN PRECUTSOR								
מנו כי מניאט	SPIKE CLYCOPROJEIN PRECURSOR		2000						
9/3/2	SPIKE CLYCOPROTEIN PRECURSOR	VESICULAR STORIATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN COULM)							
2012	CHIKE GLYCOPROJEIN PRECURSOR	_	430-486						
אטוט אנאנו	SPIKE GLYCOPROTEIN PRECURSOR	_	200						
Т	GLYCOPROTEIN H PRECURSOR		916 007						
-	GLYCOPROTEIN II PRECURSOR	HUNIAN CYTOMEGALOVIRUS (STRAIN TOWNE)	16.30	640.437					
т	GLYCOPROTEIN H PRICIASOR		57.67	105					
PVC4 II MSVE4	GLYCOMOTEIN II PRECURSOR		200						
PVGLII HSVEB	1 1	EOUINE HERPESVIAUS TYPE	148.194					T	
PULL HENVA	INMEDIALI: LANLY GLYCOPROTEIN PRIX URSON			419.460	917.1070	1049-1084		Ī	
PVGIM DUNGE	M POI. YPROTEIN PRECURSOR	MINYAVIRUS CERNISION	1						
FVERN MINET	N PAR YEAD IN PRI CHRIS		20.270	144.181		•	:	:	
TV(# A) DUINSIB		HINTANIA STATE OF THE STATE OF	101.10	034-472	100				
rvisi ii libiyw	M POLYTRUITH PRICEIRSOR	HUNTANIM AN VINIS	14.23	17.613		218-34.5	1401-1441		
AUCH IN BIA		THAT AND AN VIETNAME OF THE REPORT OF THE PROPERTY OF THE PARTY OF THE	910 e4i	tori.iii	:	 -			
PVIN NI CIAMIN		HANTAAN VIRUS (STRAIN HOLO)	111.222	(13-64)	1083-1130				
PVGLM HANTE	A VICTOR OF THE CONTRACT OF TH	HANIAN VINIS (STRAIN LT.)	111.23	13.641	2	!			j
TACHER HANGE		HANIAAN VIRUS (STRAIN 76-118)	11.22	(\$\frac{2}{3}\)	<u> </u>				
ACE NO INCA	LE POR VEROTEIN PRECURSOR	INFATIENS NECROTIC SPOT VINUS (INSV.)	200.303	1028-1062					
ALC: N PIC	ALPON YPECULISIN PRICUESOR	FROSFI CT HILL VIRUS (MIV)							
PVGLM PTPV	M POLYFRUIGH PRECURSOR	FUNTA TORO FILEBOVIRUS	784-644	600					
PVGLM PURMIT	M POLYPROTEIN PRECURSOR	PUUKA) A VIRUS (STRAIM HALLINA) III)	1000						
PVGR.NI PULINIS	NI POR YPROTEIN PRINTINGER	FUUNIALA VINUS INTERNATIONALIA	5	10.01					L
FVGLNI RVFV		MINT VALLET PENER VIRUS (APPAR)	039.079	130.863	1136-1185				
PVGLAI RVIVZ	NI POL YPROTETN PRECURSOR		410.64	9					
PVCLN SERUE		SECOND CHEST AND DESCRIPTION OF THE PROPERTY O	173-609	061-130			•		
PVGLM SEOUR	N. POC. YPROTEIN PRECURSON	COLUMN CO	17.0g	1081.13					
PVCI.N. SEDIIS	_	THE CONTRACT CHARGE CHARGE	97-10	\$6.85					
PYCH NI UUK		DIENE CIPITS INC.	100						
PUCLE BEY	PEPLONER CLYCORROTEIN PRICORSOR.	ILVIN ARENAVRUS	13.43						
PVGLY JUNIO	CLTCORDITED FOLVER PRECUREDA	LASSA VIRUS (STRAIN GAIN)	111.265						
VGLY LASSE	COLUCIA SELECTION CONTRACTOR SELECTION SELEC	I ACCA VIRUS (STRAIN RISTAIL)	218.34A						

FULL KAPIE PVGLY PIARV PVGLY TACV PVGLY TACVI	GLYCORDIEN POLYPROTEIN PRECINSOR	VIRUS	9.5					_	
FVGLY TACV	Т							ł	1
PVGLY TACVI		TACARIBE VIRUS	1					+	1
PVCA.V TACVI	Т	TACARINE VIRUS (STRAIN VS		22.51				+	١
, A. C.	CHICOTOLISM OF VEDIEN PRECISOR	TACARINE VIRUS (STRAIN VT)		2				+	
- A - A - S	<u> </u>		_	Ž				+	
PVGNO CPAIV	 -		٦					H	
PVGNALI CPMV		COWPEA MOSAIC VIRUS (CPMV)	1	15.60				+	
PVGNA! CPSMV		COWPEA SEVERE MOSAIC VIRUS (STRAIN DC)	Į,					-	
PVCMA RCMV	_	AED CLOVER MOTTLE VIRUS (RCMV)						\vdash	
PVGP3 EBV				T				<u> </u>	l
PVGPJ EBV	ENVELOPE GLYCOPROTEIN GP)40	MIAN HERFESVIAUS -					<u> </u>	-	
PVHOS VACCC	LATE PROTEIN HIT	ENITAGEN						╁	
PVHOS VACCV	LATE PROTEIN HIS	VACCINIA VIRUS (STRAIN WR)						ŀ	l
PVINE VARV	LATE PROTEIN HI	VARIOLA VIRUS	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					\mid	١
PV1103 VACCC	PROTECNIS	VACCINIA VIRUS (STRAIN COPENIAGES)						-	
PUSIOS VACCV	PROTECNIIS	VACCINIA VIRUS (STRAIN WR)						+	l
PUTIOS VARV	PROTEINIIS	VARIOLA VIRUS						+	l
PVIIEL LSV	PROBABILE IN LIK ASI	LILY SYNITIONAL PSYNINGS (1.5v.)						-	
P. 101 VACCC	ROHINI	VACCINIV VINES ISTRAIN CONTRIBUTE A						+	Ì
PUBLICARY	PROTEIN	VARIOLA VIRUS						+	
P. 106 VACCV	PROTEIN IS	VACCINIA VIRUS (STRAIN WR)							l
PUTOS VARV	FROIEIN H	VARIMA VIRUS						<u> </u>	
PY INT VACCE	PUTATIVE RICA MILICASE 18								
	PATENTINE BUY HIS CITAGE IS					I		1	
	STATE THE PLANT PICACE IN	VARIOLA VIRUS	2					†	1
1101 111	THE PARTY OF THE P	HUNIAN CYTONII GALOVIRUS (STRAIN AD169)	241-271					\dagger	
- NEW 18	THE PARTY CAN IN VENTER IN	HUNIAN CYTONII GALOVIRUS (STRAIN TOWNE)	141.27					+	
	TO TO STATE OF THE PARTY OF THE	- NOVINE INMUNICATION OF CHARLS CISOLATE 106) (BIV.)	42.71					+	1
2 1	THE PARTY OF THE P	BOVINE ININGROUP FICH NCY VIRUS HISOLATE 1271(RIV)	42.78					+	
		CINITAN INVITINGIBLE IN THE SECTION OF STATES CAND	66.7A	İ	-	1		<u> </u>	•
		i	=					+	j
WI SHALL		[FSILIN-HARR VIRUS (SIRAIN 095-6) HIUNIAN HERPESVIRUS 4)	25.1%					1	
A NO. ILLUSTRA		HUNIAN CYTONI GALOVINUS (STRAIN ADIES	Ī					1	
11.751		HINN'S SINITIL'S VINUS (IYTE I / STRAIN 17)	Ī	136-171	230-32			+	
ULASII ANIXA		I QUINE HERPLSVIRUS TYPE I (STRAIN ANAP) (EHV-1)	1	123		132-361		+	
PUND HEVER	INTEGRAL MENIDRANE PROTEIN	HERFESVIRUS SAINIMI (STRAIN II)	76.111					 	
120	PRINAIL PATTCHASE	SUITUREMUS VIRUS LIKE PARTICIL, SAVI	133.74					+	
בי ומן השכנה		VACCINIA VIRUS (STRAIN COPENIAGIN)						\dagger	l
PUBLICACO	PROTEIN 15	VACCINIA VIRUS (STRAIN WR)						1	١
PV BY	PROJEIN 15	VARIOLA VIRUS						+	
PANO VACCO	-	VACCINIA VIRUS (STRAIN COPEMIAGEN)	17.120					\dagger	1
PLKON VACCV	+-	VACCINIA VIRUS (STRAIN WR)	2					\dagger	
FIX 03 VACCC	-	VACCIPIA VIRUS (STRAIN COPENITACIEN)	10.5					\dagger	
PVK03 VACCV	+-	VACCINIA VIRLIS (STRAIN WR)						\dagger	
PATES VACCE	1	VACCINIA VIRUS (STRAIN COPENIIAGEN)	20.46					+	
FUT 62 VACCV	1	VACCINIA VIRIJS (STRAIM WR)	2					\dagger	
PVIOL VARV		VARIOLA VIRUS	11.10					t	
PVI 6) VACCC	1	VACCINIA VIAUS ISTRAIN COPENITACEN)	1				-	+	
PATON VACCV	4	VACCINIA VIRUS (STRAIN WR.)	777.77				1		
PVI 03 VAR	T	VARIUS -	121.31				1	\dagger	
VIEW VACCV	1	VACCIPIA VIRUS (STRAIN WR), AND VACCIPIA VIRUS (STRAIM LOI EMINOL						+	l
PVI OS VARV		VARIOLA VIRUS.	Î					+	l
	PROBABLELIPROTEIN	HENLYN PAPILL CALAVIAUS TYPE SB	377.40					1	١
PVL2 CRPVK	PRODABLE LI PROTEIN	CHILLIAM BABRIS (SHOPE) PAPILLONIAVIAUS (STRAIN KANSAS) (CRPV)	_					\dagger	1
PVL 1 IDVOS	PROBABLE LY PROTEIN	THE STAN PART CHANGE I VALLE						\dagger	l
PULL HOVOR	PROBABLELIPROTEIN	IN MAN PUT COMMANDS TYTE I		ŀ				\dagger	ı
VIAM C INC	PROBABLE LT PROTEIN	IN STAND BUT CHANNING I THE IA	120					1	ı

	PROTICE PROBABLE LI PROTEIN	AIBUS HIJANA PAPILLOSIA VIAUS TYPE J9	145	ANTA!	AREAL	AREA!	45543	AREA	AREAL
	ELI PROTEIN	HUNIAN PAPILLONIA VIAUS TYPE 19			Г	Г			
	National Parties			717-207			1		
		TO THE PAPER ON A VISIT TYPE AZ	344.379						
	THE PROPERTY OF THE PARTY OF TH	INTERIOR PAPER ONLY VIRIOR TYPE 47	36-57					-	
	N 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	INDIAN PAPEL ONIA VIRUS TYPE SI	39.50						
	E 1 PROFEIN	HUNIAN PAPIL LOMAVIRUS TYPE SB	17.57						
	2.310.24 C. 2.310.25 C. 2.310.	INTERN PAPILLONIAVIRUS TYPE ME100	39.39						
	N. S. C.	PYGNY CHIMPANZEE PAPILLOMAVINUS TYPE 1	19-59						
	2	TIPULA IRIDESCENT VIRUS (TIV) (INSECT IRIDESCENT VIRUS 1YPE I)	144.177	111-919			Ì		
	MINOR VIRION STRUCTURAL PROTEIN MU-2	REDVIRUS (TYPE 1/SIRAIN DEARING	180-318	124-361					
REOVE	MINOR VIEWN STRUCTURAL PROTEIN MU.	REDVIRUS (TYPE 1/STRAIN LANG)	310-316						
_	NAME OF STREET OF A PROPERTY OF STREET	REDVIRUS (1 YPE) / STRAIN DEALING)	661.191						
-		REOVINUS (TYPE 1/ STRAIN DEARING)	168-199						İ
		REDVIAUS (TYPE 1/STRAIN DENOMES)	168-199						
1		DEDVIAUS (TYPE 1/SIRAIN LANG)	161.199						
TABLE DATE TO THE PARTY OF THE		REDVINUS (TYPE) / STRAIN DEARING)	133.364						
T	POTEIN	SIMILAN VIRUS S (STRATH W2) (SV5)	308-342						
٦,	DOTEIN	TURKEY AHINOTRACHEITIS VIRUS (TRTV)	123-150						
Ī	NIE1084	BOVINE CORONAVIRUS (STRAIN MEBUS)	64-103						
	ZUICES	HUBIAN CORDNAVIRUS (STRAIN OCA))	101.49						
Т	NI SI COL	INDINE CORONAVIRUS AINV (STRAIN AS9)	101.59						
Т	PROTEIN	ATURINE CORONAVIRUS MILY (STRAIN MIM)	63-103						
т	PROTEIN	TURKEY ENTERUC COROMAVIRUS ITCV)	84-103						
	NISTON	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTELLINV)	101-01						
T	PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE NIAT) (IUV)	11.101						
T	PROBABLE MENBRANE PROJEIN	EPSTEIN-BARR VIRUS (STRAIN BYS-8) (HUNIAN HERPESVIRUS 4)	178.213						
T	ANDVENTENT PROTEIN	CARNATION ETCILED RING VIRUS (CERV)							
Ŀ	MOVEMENT PROTEIN	SOYDEAN CHLOROFIC NOTTLE VIRUS	П						
1	NAJOR SUMFACE ANTIGEN PRECURSOR	DUCK HEPATITIS B VIRUS (BROWN SHANGHAL DUCK ISOLATE SY) (UHBY)	3i-33	269.702					
т	MIAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS D VIRUS (STRAIN CHINA) (DHBV)	I	20.70					
₹	NAJOR SURFACE ANTIGEN PRECURSOR,	DUCK HEPATITIS B VIRUS (DIBV)	I	2					
Ţ.	NAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS II VIRUS (WINTE SHANGHAI DUCK ISOLATE S) I) (MINV)	Ī	26.70					İ
-	MAIOR SURFACE ANTIGEN PRECURSOR.	GROUND SQUIRREL HEPATHIS VIRUS (GSHV)	1	100					
	MAJOR SURFACE ANTIGEN PRECURSOR:	HEAON MEPATITIS & VIRUS	24.63	136-209					
Г	NACE ANTIGEN	ICPATITIS D VIRUS	70.08						
г	MAJOR SURFACE ANTIGEN PRECURSOR:	IEPATITIS D VIRUS (SUNTYFE ADWZ)	246-277						
	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATHIS B VIRUS (SUBITYPE ADRA)	740-217						
	MAJOR SURFACE ANTIGEN PRECURSOR.	HEPATITIS B VIRUS (SUDITIFE ADIV / STRAIN WT)							l
	MAJOR SULFACE ANTIGEN PRECURSORI	HEPAILLIS B VIKUS (3 I KAIN ALTIIA)	107:07						
	MAJOR SURFACE ANTIGEN	HEPAILIES BY VIKUS (SUBITOR AD)							۱
П	MAJOR SURFACE ANTIGEN PRECURSOR	TEPATITION OF VINES (SUBJECTED AND A STRAIN INCOMESTIMATE)	36.16					Ī	
_	MAJOR SURFACE ANTICENTACIONSON	INCOMPRESENTATION OF THE PARTY	333.36						١
7	MAJOR SURFACE ANTICEN PRECUNSORS	HEPATHES B VIRUS (SUBTYPE ADR./ STRAIN MC.)	20.00						
PARISA IIFBVII MAJOR 30	MAKON SURFACE ANTIGEN PRECIPEROR	HEPATITIS B VIKUS (SUBTYPE ADW / STRAIN OKINAWAPODW212)	133.34						
┰	NAMES OF ANTICEN PRECURSOR	IEPATITIS & VIRUS (SUBTYPE ADW / STRAIN PHILIPPINOPFOWIN)	144-372						
Т	MAINE SURFACE ANTIGEN PRECURSOR ,	IGPATITIS & VIRUS (SUBTYPE ADR)	344-372						
т-	MAKOR SURFACE ANTIGEN	ICEPATITIS B VIRUS (SUBTYPE AR)	10.98						
1	MAKOR SURFACE ANTIGEN PRECURSOR	ICEPATITIS D VIRUS (SUBTYPE ADW)	133-261						
_	REACE ANTIGEN PRECURSOR	HEPATITIS & VIRUS (SUBITPE AYW)	133-261						
7	NIAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (SUBTYPE ADYW)	133-361				-		
ī	SIAJOR SURFACE ANTIGEN PRECURSOR	WOODCIIUCK HEPATITIS VIRUS I	307-341	\$01-697					
WIIVS	MFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATHIS VIRUS SO	112.24	274-310					
+-	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCINCE HEPATITIS VIRUS 7	213-346	274-310					
ヤ¯		WOODCHUCK HEPATITIS VIRUS 6	2	•					
	PROBABLE MAJOR SURFACE ANTIGEN PRECURSOR	WOODCIIUCK IIEPATITIS VIRUS I (INFECTIOUS CLONE)	2	274-303					
-	MAJOR SURFACE ANTIGEN PRECURSOR 1	WOODCHUCK HEPATITIS VIRUS WAS (ISOLATE PW33)		İ	1		Ī	İ	ŀ
	NATRIX (M2) PROTEIN	INIT HEN'S A VIREN INTRAFF ANWHITERITY WE	-						-

					-	┞	-	ŀ	Γ
PCGINE	PDCTLZIP	AR Mentel in political and an analysis	AREAI	AREA?	AREAS	AREA 4 AP	AREAS AREAS	4 AREA?	5
CILCARAIK	PROTEIN	LICKOLIA VIBILE CETATAL ANSANNEL	Γ	141-170	Г	Γ	Г	Г	
PWILE MYXVI	M-TS PROTEIN	FILE ACRES OF SAIN CALLE ANNELS	2			$\frac{1}{1}$	-	-	l
FVRITO AIYXVL	_	INIT KONA VIKUS (STIKAIM LAUSAMAE)		Ī				 	Ī
PUNDS VACCC	_	VACCINIA VIRUS (STRAIN CONTINUES)						1	
PVN02 VACCV	PROTEIN N2	VACCINIA VIRUS (STRAIN WA)						+	Ī
PV7402 VARV	_	VARIOLA VIRUS				+		$\frac{1}{1}$	
PVN34 ROTPC	NONSTRUCTURAL PROTEIN MS)4	PORCINE ROTAVIRUS (GROUP CASTRAIN CONDEM)	700	146 401				1	Ī
PVNCA AAV3	DNA REPLICATION PROTEIN	ADEND ASSOCIATION VIRUS 7 (AAV.:)		111	167.017		<u> </u>	+	Ī
FVNCS PAVISO	PRODABLE MONCATSUP PROTEIN NSI	INDVINI: FARVOVIRUS (IIPV)				Ī		1	Ī
PVNSI AIISVA	NONSTRUCTURAL PROTEIN MS!	AFRICAN HORSE SICKNESS VIRUS (SEROI VIE 47 STRAIN VALCEAL)						+	Ī
PVNSI IAALA	NOWSTRUCTURAL PROTEIN MSI	INFLUENZA A VIRUS (STRAIN MALASKAMIT)						+	1
PVNS! IAAM	NOWSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN MANN ARBONOVO)						+	Ī
PVNSI IACHI	NONSTRUCTURAL PROTEIN MS!	INFLUENZA A VIRUS (STRAIN ACIIILE/IN))	14-14					+	1
PONCE IACKO	MONCHAIL FROTEIN MS	INFLUENZA A VIRUS (STRAIN ACHICKENCH: RAIANY MICE)	107.144						
	MANUAL PROPERTY.	INT. UENZA A VIRUS (STRAIN ACTICKEMAPANA)	₩.						
PART INCH	CONTRACTOR OF SECURITY INC.	INFLUENZA A VIRUS (STRAIN ADUCKALBERTAKO74)	107.144					-	
PVINSI IAUA	ACTUAL TROUBLE TO	INTELEBUTA A VIBILIS (CTBAIN AALIKEA TINGLANDVISE)	96:10						ĺ
PVNSI IADEI	NOWSTRUCTURAL PROTEIN PSI	THE PROPERTY A CHAIR ACTUAL ACTUAL BEALTHAND	100			\mid	-	-	Ī
PWS! IADUS	NONSTRUCTURAL PROTEIN MAI	THE DESCRIPTION AND ARCHAMOTOR CONTRACTOR OF THE PROPERTY OF T	14.144						1
PVNSI IAFON	NOWSTRUCTURAL PROTEIN INST	INFLUENCA A TRUS (STEAM ATOM FROM TOTAL TO							Ī
PVNS! IAFOW	HONSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN AFORT WARRENING)				1		+	1
PVNSI IAIPA	MONSTRUCTURAL PROTEIN NS	INFLIFUSA A VIRUS (STRAIN AFOWL PLAGUE VIRUS/RUSTOCK/14)	107-144	-					Ī
PVNSI JALEI	NONSTRUCTURAL PROTEIN NSI	INTELLENZA A VIRUS (STRAIN AL ENINGRADY) 497)	2				1		Ī
PVNCI IALEN	MONSTRIECTURAL PROTEIN NS!	INFLIENZA A VIRUS (STRAIN ALENINGRAD/SAT)							Ī
PVNKI JANIAL	NONSTRUCTURAL PROTEIN MS:	INFLUENZA A VIRUS (SIRAIN ASIALLARDVALBERTAND'S)	107-144				_		1
PVOICE TANAN	MONOTORINA PROFESSIONS	INFLUENZA A VIRIJS (STRAIN ARIALLARINNEW YORKATSOTO)	107-144			_			Ī
		INICUENZA A VIRUS (STRAIN ARIALLARIYMEN YORKABIW78)	103.146					_	
יייייייייייייייייייייייייייייייייייייי		INFILIFICA A VIRUS (STRAIN AAIYNAIMIANEDA-TIIAV76)	2.8						Ī
NAS PARTY	MONS INCLINATION HOL	INC. IELZA A VIBIG SCHRAIN APINTALI /AL DEBTA/116/261	107.144			-		 -	Ī
PVNSI JAPIO	NOWS I KINC I UKAL TRUIEIN RSI	THE LIEUTA A VIBIR STRAIN A PINTAIL AL DESTAVIORE	107.144			-		-	Ī
PVNSI IATI	MONSTRUCTURAL PROTEIN AS	TAKE THE PART AND A VINITE OF THE AND AND THE BEST APPROVED	101.144						Ī
١	NONSTRUCTURAL PROTEIN HS1	INCLUENCE A VINCE (STRAIN OF INCLUENCE AND I	7						Ī
	NONSTRUCTURAL PROTEIN NSI	INFLERCA A VIAUS (STRAIN AVIATATION CORTINATION)						+	Ī
	MONSTRUCTURAL PROTEIN MSI	INCLUENCE A VIRUS (SIRVING APOCKTO ARCORDA)						 	Ī
1	NOWSTRUCTURAL PROTEIN NSI	INTLUENCE A VIRUS (STRAIN ACTURE L'ACTURE MENTANCINALITY (1977)				1		+	T
	MONSTRUCTURAL PROTEIN NS	INTENES A VINCE CONTINUES OF THE PROPERTY OF T							1
IATRS	NONSTRUCTURAL PROTEIN NSI	INTI UENZA A VIAUS (STRAIM A) ERRASOUTH AFRICANT	3			1			1
	NOWSTRUCTURAL PROTEIN NSI	INT. UINZA A VIRUS (STRAIN ACTURACIORERICATATI)						+	Ī
_	NONSTRUCTURAL PROTEIN NST	INITUENZA A VIRUS (STRAIM AUDUMADOWIZ)						+	1
	NOHSTRUCTURAL PROTEIN MSI	INFLUENZA A VIRUS (STAAIM AUSSIU9077)						+	1
PVNS1 [AZI]	NONSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN ASWINENOWALISTIO	107-144					+	
PVNSI INBPA	MONSTRUCTURAL PROTEIN MS! F	INFLUENZA B VIRUS (SI RAIM BITALIS)	700.733						
PVNSI INCAA	NONSTRUCTURAL PROTEIN NSI	INFLUENZA C VIRUS (STRAIN CANN ARBOW)/90)	332-228					+	
PVNSI INCCA	NONSTRUCTURAL PROTEIN HS! ;	INFLUENZA C VIKUS (STRAIN CCALIFORNIA)	\$67.77					1	Ī
PVNS2 IIRSVI	NOWSTRUCTURAL PROTEIN 2	HUMAN RESMANTORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 18517)	20.49					-	
PVNS2 IIRSVA	MONSTRUCTURAL PROTEIN 2	HUNIAN RESPIRATORY SYNCYTIAL, VIRUS (STRAIN A2)	20.49					+	١
PVNS3 INBLE	NONSTRUCTURAL PROTEIN NST	INFLUENZA B VIRUS (STRAIN BALEE/40	46.33					-	ĺ
PVNS2 INBYA	HONSTRUCTURAL PROTEIN HS1	INFLUENZA B VIRUS (STRAIN BY ANIAGATA/I/I))	-					4	Ī
PVNS4 CVMS	HONSTRUCTURAL PROTEIN 4	ARJACHE CORONAVIRUS MHV (STRAM S)	378					+	1
PVNS4 CVPFS	MONSTRUCTURAL PROTEIN 4	PORCINE TRANSHISSIBLE GASTROENTENTIS CORONAVIRUS (STRAIN #577)	£.					1	
PVNS4 CVPPU	MONSTRUCTURAL PROTEIN 4	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN PUR	5					4	Ī
PVNS4 CVFRM	NONSTRUCTURAL PROTEIN 4	PORCINE RESPIRATORY COROMAVIRUS	4.30					-	
PVNST CVAAS	39 KD NONSTRUCTURAL PROTEIN	MURINE CORONAVIRUS AIIIV (STRAIN AS9)	45-80						
PVNST CVADI	NO KO NONSTRUCTURAL PROTEIN	MUNINE CORONAVIRUS BOIV (STRAIN MIN)	19.64				~		
PANKE INCO.	NONSTRUCTURAL PROTEINS MSI-MS2	INTLUENZA C VILUS (STRAIN COREAT LAKES/1167/9)	352-222						
THE DAY	HONSTRUCTURAL PROTEONS HSI-NS2	INFLUENZA C VIRUS (STRATN CZOHANNESBURG/186)	122-155						
WAST BACK	NOWSTRUCTURAL PROTEINS MS1-NS3	INFLUENZA C VIRUS (STRAIM CANISSISSIPPINO)	335-355					-	
PVNST DACYA	HONSTRUCTURAL PROTEINS NSI-NS2	INFLUENZA C VIRUS (STRAIN CYAMAGATA/1011)	111.255						
PUNIA PRVKA	PRODABILE MACLEAR ANTICEIN	FALTHYDRAINING VIRIUS (STRAIN KAPLAN) (PRV)	•			1	-	1	!
PVMIN' INIVII	NIN TO CHERT FILLS	HARMI VIRIT (SIRAIN INDIANCITI UNI) (IMM)	147.311	E 7-3		1		-	7

PCCLNE	PDCTLZIP		. 7.507		V S. V.A.V	ABEA A AREA 9	ARFAG	AREA?
		VIEWS	Т	Т	Т	Т	T	
PYMUC MOKE			354.388					
			354-388					
PYNUC INITA	MUCI EOPROTEIN	THE LIFT A VIRUS (STRAIN AFOUNETENNESSE EXIMS)	154-388					
PVNC IAITE		MARBURG VIRUS (STRAIN MUSOKE)	3					
TANK MADVE		NIANBURG VIRUS (STRAIN POPP)	97-9					
PVOOL VACCC		VACCINIA VIRUS (STRAIN COPENHAGEN	21:29	ž	1		1	
PVOD! VARV		VARIOLA VIRUS	í.					
PVON I NAV	ILL KD PROTEIN	MARCISSUS MOSAIC VIRUS (MAIV)	2	10:18	1			
PVOR! PVAR	213 KD PROTEIN	POTATO VIRUS M (STRAIN RUSSIAM) (PVM)	131.161			1		
PVOR! SAIYEA	IN KD PROTEIN	STRAWBERRY AULD YELLOW EDGE-ASSOCIATED VINUS (SATTERY)						
PVP03 11SVSA	PROBABLE MEMBRANE ANTIGEN 3	т	(A-7)				1	
PVP10 NPVAC	PIOPROTEIN							
PVP10 MPVOP	PIOPROTEIN	DRGYIA PSEUDOTSUGATA MULTICAISID POLYIEDROSIS VIKUS (UPAINTY)	196 97		Ī		 -	
PVP10 ABSOV	PROTEIN SIG	RICE BLACK STREAKED DWANG VINGS (MISON)	200	317.134				
PVP19 IISVEB		EQUINE HEIGHESVINGS 177E 1 (314ALM ABAT) (2117-1)					-	
PVP33 HChVA	PROBABLE CAPSID PROTEIN VP23	HOMAN CYTONEGALOVINOS (STRAIN ADIOV)		306.311				
PVP23 HSV6U		HERVES SIMPLEX VIRUS (1 TPE 6/3) KAIN CHANCA-1101)						
PVP23 HSVEB	PROBABLE CAPSID PROTEIN VP33	EQUINE HEILPESVIRUS TYPE I (STRAIN ABAP) (EAV-I)	56.761			+		
PVP13 VZVD	PROBABLE CAPSID PROTEIN VP33	VARCELLA ZOSTER VIRUS (STRAIM DUNIA STITUTO)	101710					
PVP2 AHSV4	OUTER CAPSID PROTEIN VP.	AFUCAN HURSE SICKNESS VINOS (SENO) TITE OF SIRVING SENO	10707					
PVP2 BTV10	OUTER CAPSID PROTEIN VP?	BLUETONGUE VIRUS (SERO) TYPE 19 (1901 A 18 USA)	116.181	649.683				
PVP3 BTVII	OUTER CAPSID PROTEIN VP1	BLUE IOMODE VIRUS (35 ROLL 17 43 OLA)						
PVP2 BTV17	OUTER CAPSID PROTEIN VP3	BLUE TONGUE VIRUS (SERU) TPE 177 (SOLATE USA)						
PVP2 BTVIA	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEKULTYPE I / 1304 ATE POLITAL APPLIAN						
PVP2 BTVIS	OUTER CAPSID PROTEIN VP2	BLUETOWGUE VIRUS (SERU) THE LY ISOURIE SOOTH AS INCH.	110.16					
PVP2 EIIDVI	OUTER CAPSID PROTEIN VP2	EPIZOOTIC HEACHQUARGE DISEASE VINOS (SENOTITES VICENOS IS	16.16	33.63	Ī			
PVP2 ROTBR	RAN-BINDING PROFEIN (*)	BOVING BOLLVINGS OF BAIN IN	134.367	\$33.53			-	
PVF1 ROTBU	ANA-BINDING PROTEIN VP	HOVING BOTACIBLIS COROLLYPE 1 STRAIN WAI	142.377	131.367				
PVP3 ROTHW	LAN-BINAMO TRO-EIN N-1	MACTINE ROTAVIRUS (GROUP C./ STRAIN CONDEN)	\$14.549	Γ	13:11			
PVF2 ROIT	MAN-MINISTER PROPERTY OF STREET	SINIAM II ROTAVIRUS (STRAIM SAIT)	115.368	933-558				
TO HOLS	OPE PROTEIN	VACCINIA VIRUS (STRAIN COFENINGEN)	178-311					
אַנוֹנְייִ	INTERNATIONAL PROFESSION POR	VACCIMIA VIRUS IS IRAIN W.R.)	116-911					
	INTRINCIPORTITION I INVESTIGATE PROTEIN P.15	VARIEN A VIRENS	119.511					
JOAN GIANA		ORGVIA ESI URDI SURIATA MULTICAPSID POLYIILDRUSIS VIRUS (UPAINPV)	107.141					
FVP) Elibvi	VT) CORE PROTEIN	EPIZODIIC HENORRHAGIC DISEASE VIRUS (SEROTYPE I) (EHOV-I)	27	134-730				
PYP) EIDVA	VPJ COAF PROTEIN	EFIZIONIC III, ANDRININGIC DISEASE VIRUS	2	734.730				
PVPI BIDV	MAKIN HAKID STRIKTITICAL PROHISM ?	RK I INVARI VIRUS (RIDV)	200			1		
PVPJ ROTSI	INNER CORE PROTEIN VP)	SINIAM II KOLAVIROS (SI KAIN SALI)	470.447					
PVP40 ERV	CAPSID PROTEIN P40	I STANTES SAINTES SAINTES IN THE STANTES OF THE STANTES OF THE SAI	119-152					
VXXII WAX	CARALLER DESIGNATION OF THE PROPERTY OF THE PR	INFLCTIOUS LARYNCOTRACHEITIS VIRUS (STRAIN THORNE VILLY) (ILTV)	5					
TALL BUT AND	VARICELLA ZOSTER VIRUS (STRAIN DURIAS) (VŽV	185-516						
TANAL FEEL	VIBAL IRANSCRIPTION REGULATOR P47	AUTOGRAPHA CALIFORNICA MUCLEAR POLYMEDROSIS VIRUS (ACMINPV)	239-270					
PVP4A VACCC	_	VACCINIA VIRUS (STRAIN COPENTIAGEN)	<u>\$</u>					
PVP4A VACCV	_	VACCIMIA VIRUS (SIRAIN WR)	22.53			+	+	$\overline{\downarrow}$
PVP4A VARV	7	VARRILA VIRUS	×-592				+	
PVP4 ROTG	_	ROTAVIRUS (GROUP B / STRAIN IDIR)	2	468-499		1		
PVP4 WTV	NONSTRUCTURAL PROTEIN PNS4	WOUND TUMOR VIRUS (WTV)						
PVPS BRD	OUTER CAPSID PROTEIN VPS	BROADITATE VIRUS (URD)		27::24			 -	
PVPS BTVIA	OUTER CAPSID PROTEIN VPS	RUE TOWARD (SERUITYE I / ISOLATE AUSTRALIA)					<u> </u>	
PVPS BIVE	CRITER CAPSID PROTEIN VPS	III III IIIWAA VIIIKAA	100					
rves nivth	INTER CAPSIN PROTEIN VPS	THE RESIDENCE OF THE STREET ST	100,135					
PVPS EIDVI	OUTER CAPSIO PROTEIN VES	WINNE HERE VALIS (WIV)	916-169			-	_	
ALA SALA	COTEX COAL PROTEIN TO	ALLY WASHINGT WINDS TO FED TO SOLATE USA)	159.107					

		All Vigure (na bacteriophoges)	П	П	П		7 7 7 7	A B F A Y
PCCENE	PDCTLZIP			3	AREAZ A	AREA LAND	Т	4
CILCAMIL	Treated and the secon	ISOCATE USA)	_	202	1			
ALL TANK	DASTRUCTURAL 36 3 KD PRO	City and Strains						
TATE STATE	_	-			1			
JAVAN LATI	AVAIOR ENVELOPE OLYCOPROTEIN PRECURSOR				1			
PLP67 MPVGN	MIAJOR ENVELOPE GLYCOPROTEIN	VIKUS (UMINEV)						
17.18	VIS PROTEIN							
TYPE BIVIN	VTS PROILIN	DIUE TONGUE VIRUS (SEROLITEE L'ABOUTE ONLY AFRICA)	1					
PV76 BIVIS	VP4 PROTEIN		111.150		-			
PVP6 BIVIA	VP6 PROTEIN	TE CONTROLL	10.200					
VIW MIV	STRUCTURAL PROTEIN PG	WOUND TORIOR VIACO (WILL)	80.20					
FVP WIN	STRUCTURAL PROTLIN PG	I VIENDOSIS VIEUS (ACKINEV)	105.462					
PVP 75 MPVAC	PAKD PROTEIN	אחרובעע נסר נוורסעספוז מועס לארייי	454-490					
PVP3 WTV	NOMSTRUCTURAL PROTEIN FINS?	WOUND TURIOR VIRUS (WIV)	11.11					
AUVAN VIEWOP	CAPSID PROTEIN PUT	-	104.110					
PUP BTVID	NONSTRUCTURAL PROTEIN PI							
PVPR RTVI	MONSTRICTURAL PROTEIN PU							
1000	MANNSTRIKE TURAL PROTEIN PS							
	MONSTRIK TITAL PROTEIN PS							
	MONSTELL TIRAL PROTEIN PE	BILUE TONGUE VIAUS (SEROTYPE I / ISOLATE AUSTIALIA)	200					
1000	NOWSTRINGTURAL PROTEIN PD					1		
	CONCLETE AT PROTEIN PS		04-67¢			1	 -	
	ACAST PACIFICATION TO		374.412		Ì			
rvri Kijy	COURS CATOLOGICAL PROPERTY OF STREET PROPERTY OF ST	()1	164-195	119-412		-		
ALM MAN	CHIER CATSOLNOIS SECTION		145-173					
PVMIE NPVAC	SE KO POLITICIDADE ENVELOR DE POLITICI	7	122-151					
PVPHE NPVOP	12 KO FUL THE DEAL ENVELOR E PROTEIN		11.14				1	
PVPR IIVIA	VAR PROTEIN		41.73				:	
FVFR HV2RE	Z == C == -		-					
LAFA HV2CA	VIR FRUITIN		41.73					
rvra sivzui	VIA PROJECIA		41.73					
PVPR 11V2D2	VAR PROTEIN		41.73					
PVPR HV2NZ	VPR PRUIEIR	,	41.73		1	-		
PVPR HV2RO	VIA PROTEIN		41.73					
FVFR 11V3SI		:	40-72					
TVFR IIV38	VIA TRUITIN		37.74				1	
PVPA SIVCZ	VPR PROTEIN	SINIAN MINIUMODEFICIENCY VIRUS (MINIALI) ISOLATE) (SIV-MIAC)	17.69			-		
PVR SIVE	VARVACE		13.69					
	VPR PROTEIN		5	,			:	
FYFR SIVAL	N. C.		12.64					
	NIN INITIAL PROPERTY OF THE PR		11-69					
FVFR SIVSP	VIATROLEIA	SOLATE	11.1					
IN DIAM	NIC TO STATE OF THE PARTY OF TH		(1)					
NA PAR	Validation 1	HINGAN BARRINGHA LICHENCY VIRUS TYPE I (HRAIN 1804, ATL) (HIV. 1)	.		_		_	
	Z-0024-123	THE THE PRINCIPLE OF THE STATE	=					
	2	HINNAN ININIUNCHIN ICHENCY VINIS TYPE I (HXB1 ISOLATE) (HVV.I)	=					
	7	HILINIAN INDIVIDUAL ICH NCY VIRUS TYPE I (IRCSF ISOLATE) (IIIV-1)		İ		<u> </u> 	1	-
1	ALCOHOL:	HINGAN MANINGHI OF HE VINIS IVIT 1 (FV.2) IVENALL STUVELL						
1 1 1 1 1 1 1	Name of the last o	SHEEP PULMONARY ALIENDALA TOSIS VIRUS	16-134					
201	XI31CE XA	LACTATE DEHYDROGEMASE-ELEVATING VIRUS (LDV)	3			1		
1000	OBE. V PROTEIN	BOVINE IMMUNODEFICIENCY VIRUS (ISOLATE 127) (BIV)	<u> </u>			-		
AND VALUE	AI PHA.A PROTEIN	BARLEY STRIPE MOSAIC VIRUS (DSMV)	2	676-703		1	+	1
THE PARTY	SCHATTELETIERAL PROTEIN NCVP2		22.20			1	1	-
2	MONETHER PROTEIN MSS	NIN COWDEN)	=	28-382				
200 200	NONSTRUCTURAL PROTEIN NEVP?	SINIAN II ROTAVIRUS (STRAIN SAII)	2.5				1	
PVSOS ROTHR	VP6 PROTEIN	BOVINE ROTAVIRUS (STRAIN IV)	2	31.		+	+	1
PVSO6 ROIBS	VP6 PROTEIN	BOVINE ROTAVIRUS (GROUP CASTRAIN SHINTORU)		2000		1		
PVCO ROTBU	VP6 PROTEIN	BOVINE ROTAVIRUS (STRAIN UK)	2000					

	PIXTIZIP	All Viruits (no betitrophegri)	A REA 1	AREA? A	AREA?	AREA4 A	AREAS IA	AREAS	ARKA
FILCYANIE	PROTEIN	CONTINUE BOTTAVIETIE (STEATH FILIA)	Γ	Г	Г				
_	VP4 PROTEIN	CIBATALL?	58-92						
VSOS ROTEH	VP6 PROTEIN	SCROTYPE (CTRAIN 1076)	25.52						
VSO6 ROTHI	VP6 PROTEIN		Ī	113-340					
PVS06 ROTHC	VP6 PROTEIN		13:52						
PVSOG ROTHS	VP6 PROTEIN		58-92	313-349					
PVSOG ROTHW	VF FROIEIN	OWDEN	64.93				1		
VSOG ROTPC	VI PROJEIN			913:34					
L SOB ROILO	VYS FAULEIN		٦	313-13		1	1		
201 80274	MONSTRUCTURAL PROTEIN MCVP4		24.30		1		1		
VSON BOTHT	GLYCOPROTEIN VP?	AS 3)			Ī				
PV509 RO1PB	GLYCOPROTEIN VP7	PORCINE ROTAVIRUS (SEROTYPE 4/STRAIN BEN-144)			T				
Т	NONSTRUCTURAL GLYCOPROTEIN NCVPS	(24)		1					
Г	HONSTRUCTURAL OLYCOPROTEIN NCYPS		25.55						
П	NONSTRUCTURAL CLYCOPROTEIN NCVPS	HUNKAN ROLAVIRUS (STRAIN AAA) CHONE 3)	200		Ī				
PVS10 ROTH?	MONSTRUCTURAL GLYCOPROTEIN M. VP3		3.55						
PVS10 ROTHS	NONSTRUCTURAL GLYCOPROTEIN PLANS	WA)	22.00						
PVSIO ROTHW	MONSTRUCTURAL OF TROPPORTED IN CONT		\$2.10						
PVSIO ROTSI	MONSTRUCTURAL OLICOROTERIA PLANS	RAIN WA)	99-130				1		
PVSII KOIHW	MINOR COLES ON THE COLES		146-184				1		
TANK DECOM	CIGNA I PROTEIN PRECURSOR		9	İ		Ì	1		
PVT CLVKA		SHOPE FIDROMA VIRUS (STRAIN KASZA) (SFV)	2		Ī				
WX AIN LLA	TIANOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECUR	MIYXOMA VIRUS (STRAIN LAUSANNE)	261-270		1	Ì			
PV12 SFVKA	TUNIOR MECROSIS FACTOR SOLUBLE RECEPTOR PRECUR	SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV)		T		1			
L	PROTEIN TIA		T	101,101	T				1
	PROBABLE DNA PACKAGING PROTEIN	HEINESVIKUS 4)	T		T	T	T		
ž	PROBABLE DNA PACKAGING PROTEIN .	ILINIAN CYTONECALOVINOS (STACINA ADIES)	26-111	Ì					
=	PROBABLE DNA PACKAGING PROTEIN	-	1	Ī		T			
	XPROTEIN		=						
660	HITCHIEF IN A 10 TAU EAST THOUSEN	H-AFRICAN ISOLATE) (MSV)	74.74						1
J	HATOINE IN ALLIANDE PROTEIN		17-59						
PYIOR WDV	INVOINTING TO PROTEIN	15V1	19-67						
Ţ	INVESTIGETICAL (19 KD PROTEIN (ONU VI)	PANICUM STREAK VIRUS	- -						
L	IIYPOTICE INCAL II KO PROTEIN IN SEGMENT SII		-			1			
L		_	79-07						
J	HYPOTHETICAL IS NO PROTEIN IN 39 RD PROTEIN SREC	AL VINEDACOSIS VINUS (ACMINYV)					1		
	HYPOTHETICAL IS 6 KD PROTEIN (OR B-166)	SULFOLDERS VIRUS-LIKE FAKTIFIE SAVI	139.00				Ī		
YJOK SSVI	HYPOTIETICAL 204 KD PROTEIN (ON E-478)	E) (NISV)	22.133						
PYZIK MSVN	HIND THE HAND ALL ALL AND THE HIND TO BE ALL ALL ALL AND ALL ALL ALL ALL ALL ALL ALL ALL ALL AL		99-137						
Y1 SOON	INVESTIGATION OF THE PROJECT OF THE	A POLYNEDROSIS VIAUS (ACMNPY)	150-211						
PVEIR COVI	HYPOTIETICAL IS 3 KD PROTEIN (OUT C-792)	_	174.312	\$43.580		1	1		
YBIS FOWPIA		FOWLPOX YIRUS (ISOLATE HP-4)4(MUNICHJ)	X :				Ī		
PYDHI HSVSC	HYPOTHETICAL 21,7 KD PROTEIN IN DHEAL STECHON (ON	HERPESYRUS SAMINI (SUBGROUP C/STRAIN)	10.41						L
PYDHJ HSVSC	HYPOTIETICAL 9 S KD PROTEIN IN DIG RESTECTOR (OR	REPUTED VIEW SAME CONTRACTOR OF STRUMENT CONT							L
PYEC4 EBV	IIYPOTHETICAL ECASA PROTEIN	ECOLOGICA VINCO (STATE OF THE S	1						
PYIOI CVBM	INTROTICE HICAL PROTEIN FOUND FOR ABOUT	BOVING COROMAVIRUS (STRAIN F13)	1.1	137.165		Π			
YIOR CVIF		BOYING COLONAVIRUS (STRAIN MEBUS)	41-14	137-165.					Ц
YOR CVBM	INVOLUE IN A PROTEIN IN NUCLEOCAPSID ON (100U)	TURKEY ENTERUC CORONAVIRUS (TCV)	41.74	137.165					
PYION CV	DAPOTASTICAL BKR52 PROTEIN	EPSTEIN BARK VIKUS (STRAIN 1995-1) (PIDMAN HERPESYIKUS 4)	67.100						1
TAME ENV	BACKS 2 PROTEIN	EPSTEIN: BALL VIRUS (STILAIN B95-4) (MURIAN HERPESVIRUS 4)	250.284						\downarrow
YOR! COYMV	INTOTIETICAL 13 KD PROTEIN (ORF!)	CONDICTION YELLOW MOTTLE YIRUS (COYMY)	07.76	K .					
VOR 2 COYAV		CONDUCTINA YELLOW MOTTLE VIRUS (COYMV)	2						
		TADTATO SELIK KICHBARKIN KINDAK	12:34						

	1			T				Ī									I		Ī					
7	MA	Ì				1	1	1	1															
	7 7717	1	1																					
_	AREAL	1																						
	ANTAL																							
	AREAL							161-65	161-65															
-	REAL	¥:3	24-33	272-711	1.4	11)-263	11-124	3	8.53	33-51	912-01	17-73	97-130	306-336	21:53	31.49	13.51	11.64	142			13		
	Alt Vieuzes (no bacterlophages)	MAUS	WHITE CLOVER MOSAIC VINOS (STRANGE MY)	WHITE CLOVER MOSAIC VIRUS (3) PAIN OF CHAM	AVIAN ADEMOVIRUS GALI	THE TANOPAOTEUS TENAX VIRUS (SILVAIN PRACTICALLY)	THERMOPROTEUS TENAX VIAUS (13 FALLER ALL VITAL)	INGRANOPACIEUS TENAX VIRUS I (SI PAIN NICA)	RICE TUNGRO BACRLIFORM VIRUS (ATBV)	RICE TUNGRO BACILLIFORM VINOS (1900-A) E FINESTA OF LIBRARY (ACAINPY	AUTOGRAPHA CALIFORNICA MUCLEAN TOLI ILLEGAZIO	HERPES SIMPLEX VIRUS (TYPE OF STRAIN VIRUS SECVIETES	EPSTEIN-BARK VIRUS (STRAIN #92-1) (NOTICE DESCRIPTION)	EPSIEN BACK VINUS (STEADY BYS-E) (TICHNA TERMS (STEADS A)	EPSTEIN BALK VIRUS (STRAIN BY-S) (HOMAN TRAINES	VACCINIA VIRUS (STIVATN COPENHANCY)	VACCINGA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN CO. 131-53	VACCORIA VIALIS (STRADA COPENHAGEN)	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN WR), AN	VACCENIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRUS (STRAIN COPENHAGEN)	L YAUTHOCYTIC CHONONENTINGTIS VIAUS (STRABA AUGS)	LYMPHOCYTIC CHONOMENINGITIS VIRUS (STIMM TASTEUM)	
		PLOCEME PLACTIZAP	PROTEIN STATE OF STAT	PYONG WOAVA HYPOTHEILAL THE PROTEIN (OF 3)	PYORS WOMEN HYPOTHETICAL IS NO BOATEN LOST SI	_	٦		PYOND TTVI HYPOTHETICAL IN THE CHEMICAS I	٦	╗	NYPOTIE ILAL VI JACIENI	YRES HSVAO HYPOTHETICAL TANKS BECOME	HYPOTHE I KAL BROKE PROTECT	HYPOTICETICAL BOAT I TROTEIN	HYPOTIE INCAL BIRT I AND LAND	YVAE VACCE HYPOTHETICAL III 7 KD PROTEST	YVAL VACCY HYPOTHETICAL 9.9 KD FIGURIA	YVBC VACCC HYPOTHETICAL 18 B KD PRUILIN	VANG VACCY HYPOTHETICAL 10 4 KD PROTEIN	WAST VACCE HYPOTIETICAL 13 9 KD PROTEDY	PYVEC VACCE HYPOTHETICAL II.6 KD PROTEIN	VA ZINC FINGER PROTEIN	PANE LYCVP ZINC FINGER PROLEIN (FINAL PROLEIN CONTRACTOR CATION CONTRACTOR PROLIFICATION CONTRAC

TABLE XV RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG CARBOXY TRUNCATIONS

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X-YTS-Z
X-YTSV-Z
X-YTSVI-Z
X-YTSVIT-Z
X-YTSVITI-Z
X-YTSVITIE-Z
X-YTSVITIEL-Z
X-YTSVITIELS-Z
X-YTSVITIELSN-Z
X-YTSVITIELSNI-Z
X-YTSVITIELSNIK-Z
X-YTSVITIELSNIKE-Z
X-YTSVITIELSNIKEN-Z
X-YTSVITIELSNIKENK-2
X-YTSVITIELSNIKENKC-Z
X-YTSVITIELSNIKENKCN-Z
X-YTSVITIELSNIKENKCNG-Z
X-YTSVITIELSNIKENKCNGT-Z
X-YTSVITIELSNIKENKCNGTD-Z
X-YTSVITIELSNIKENKCNGTDA-Z
X-YTSVITIELSNIKENKCNGTDAK-Z
X-YTSVITIELSNIKENKCNGTDAKV-Z
X-YTSVITIELSNIKENKCNGTDAKVK-Z
 X-YTSVITIELSNIKENKCNGTDAKVKL-Z
X-YTSVITIELSNIKENKCNGTDAKVKLI-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELD-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z
X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVT-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQL-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-2
 X-YTSVITIELSNIKENKCNGTDAKVKLIKOELDKYKNAVTELQLLM-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z
 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-2
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVI RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG AMINO TRUNCATIONS

```
X-QST-Z
                                                X-MQST-Z
                                               X-LMQST-Z
 5
                                              X-LLMQST-Z
                                             X-OLLMOST-Z
                                            X-LQLLMQST-Z
                                           X-ELQLLMQST-Z
                                          X-TELOLLMOST-Z
                                         X-VTELOLLMOST-Z
                                        X-AVTELQLLMQST-Z
10
                                       X-NAVTELQLLMQST-Z
                                      X-KNAVTELQLLMQST-Z
                                     X-YKNAVTELQLLMQST-Z
                                    X-KYKNAVTELQLLMQST-Z
                                 X-DKYKNAVTELQLLMQST-Z
                                 X-LDKYKNAVTELOLLMOST-Z
                                 X-ELDKYKNAVTELQLLMQST-Z
                               X-QELDKYKNAVTELQLLMQST-Z
15
                               X-KQELDKYKNAVTELQLLMQST-Z
                             X-IKQELDKYKNAVTELQLLMQST-Z
                            X-LIKQELDKYKNAVTELQLLMQST-Z
                           X-KLIKQELDKYKNAVTELQLLMQST-Z
                          X-VKLIKQELDKYKNAVTELQLLMQST-Z
                         X-KVKLIKQELDKYKNAVTELQLLMQST-Z
                        X-AKVKLIKQELDKYKNAVTELQLLMQST-Z
20
                       X-DAKVKLIKQELDKYKNAVTELQLLMQST-Z
                      X-TDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                     X-GTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                    X-NGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                   X-CNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                  X-KCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                 X-NKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
25
               X-KENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
              X-IKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
             X-NIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
            X-SNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
           X-LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
          X-ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
         X-IELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
        X-TIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
30
       X-ITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
      X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
     X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
    X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
    The one letter amino acid code is used.
```

35 Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

PCT/US95/16733

TABLE XVII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG CARBOXY TRUNCATIONS

X-FYD-Z X-FYDP-Z X-FYDPL-Z X-FYDPLV-Z X-FYDPLVF-Z X-FYDPLVFP-Z X-FYDPLVFPS-Z X-FYDPLVFPSD-Z X-FYDPLVFPSDE-Z X-FYDPLVFPSDEF-Z X-FYDPLVFPSDEFD-Z X-FYDPLVFPSDEFDA-Z X-FYDPLVFPSDEFDAS-Z X-FYDPLVFPSDEFDASI-Z X-FYDPLVFPSDEFDASIS-Z X-FYDPLVFPSDEFDASISQ-Z X-FYDPLVFPSDEFDASISQV-Z X-FYDPLVFPSDEFDASISQVN-Z X-FYDPLVFPSDEFDASISQVNE-Z X-FYDPLVFPSDEFDASISQVNEK-Z X-FYDPLVFPSDEFDASISQVNEKI-Z X-FYDPLVFPSDEFDASISOVNEKIN-Z X-FYDPLVFPSDEFDASISQVNEKINQ-Z X-FYDPLVFPSDEFDASISQVNEKINQS-Z X-FYDPLVFPSDEFDASISQVNEKINQSL-Z X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z

X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z

X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XVIII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG AMINO TRUNCATIONS

X-DELL-Z X-SDELL-Z X-KSDELL-Z 5 X-RKSDELL-Z X-IRKSDELL-Z X-FIRKSDELL-Z X-AFIRKSDELL-Z X-LAFIRKSDELL-Z X-SLAFIRKSDELL-Z X-QSLAFIRKSDELL-Z 10 X-NQSLAFIRKSDELL-Z X-INQSLAFIRKSDELL-Z X-KINQSLAFIRKSDELL-Z X-EKINQSLAFIRKSDELL-Z X-NEKINOSLAFIRKSDELL-Z X-VNEKINQSLAFIRKSDELL-Z X-QVNEKINQSLAFIRKSDELL-Z X-SQVNEKINQSLAFIRKSDELL-Z 15 X-ISQVNEKINQSLAFIRKSDELL-Z X-SISQVNEKINQSLAFIRKSDELL-Z X-ASISQVNEKINQSLAFIRKSDELL-Z X-DASISOVNEKINQSLAFIRKSDELL-Z X-FDASISQVNEKINQSLAFIRKSDELL-Z X-EFDASISQVNEKINQSLAFIRKSDELL-Z X-DEFDASISQVNEKINQSLAFIRKSDELL-Z 20 X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-LVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-DPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-YDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XIX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG CARBOXY TRUNCATIONS

X-ITL-Z X-ITLN-Z X-ITLNN-Z X-ITLNNS-Z X-ITLNNSV-Z X-ITLNNSVA-Z X-ITLNNSVAL-Z X-ITLNNSVALD-Z X-ITLNNSVALDP-Z X-ITLNNSVALDPI-Z X-ITLNNSVALDPID-Z X-ITLNNSVALDPIDI-Z X-ITLNNSVALDPIDIS-Z X-ITLNNSVALDPIDISI-Z X-ITLNNSVALDPIDISIE-Z X-ITLNNSVALDPIDISIEL-Z X-ITLNNSVALDPIDISIELN-Z X-ITLNNSVALDPIDISIELNK-Z X-ITLNNSVALDPIDISIELNKA-Z X-ITLNNSVALDPIDISIELNKAK-Z X-ITLNNSVALDPIDISIELNKAKS-Z X-ITLNNSVALDPIDISIELNKAKSD-Z X-ITLNNSVALDPIDISIELNKAKSDL-2 X-ITLNNSVALDPIDISIELNKAKSDLE-Z X-ITLNNSVALDPIDISIELNKAKSDLEE-2 X-ITLNNSVALDPIDISIELNKAKSDLEES-Z 20 X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWI-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z

The one letter amino acid code is used.

X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a

fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG AMINO TRUNCATIONS

```
X-RRS-Z
                                   X-IRRS-Z
                                 X-WIRRS-Z
5
                                X-EWIRRS-Z
                               X-KEWIRRS-Z
                               X-SKEWIRRS-Z
                             X-ESKEWIRRS-Z
                             X-EESKEWIRRS-Z
                           X-LEESKEWIRRS-Z
                          X-DLEESKEWIRRS-Z
10
                         X-SDLEESKEWIRRS-Z
                        X-KSDLEESKEWIRRS-Z
                       X-AKSDLEESKEWIRRS-Z
                      X-KAKSDLEESKEWIRRS-Z
                     X-NKAKSDLEESKEWIRRS-Z
                    X-LNKAKSDLEESKEWIRRS-Z
                   X-ELNKAKSDLEESKEWIRRS-Z
                  X-IELNKAKSDLEESKEWIRRS-2
15
                 X-SIELNKAKSDLEESKEWIRRS-Z
                X-ISIELNKAKSDLEESKEWIRRS-Z
               X-DISIELNKAKSDLEESKEWIRRS-Z
              X-IDISIELNKAKSDLEESKEWIRRS-Z
             X-PIDISIELNKAKSDLEESKEWIRRS-Z
            X-DPIDISIELNKAKSDLEESKEWIRRS-Z
           X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
20
          X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
         X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
        X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
       X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
      X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
     X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
    X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
```

The one letter amino acid code is used.

Additionally,

or carbohydrates.

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"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol,

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid

35 conjugates, polyethylene glycol, or carbohydrates.

HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG CARBOXY TRUNCATIONS

X-ALG-Z X-ALGV-Z

X-ALGVA-Z

5 X-ALGVAT-Z

X-ALGVATS-Z

X-ALGVATSA-Z

X-ALGVATSAQ-Z

X-ALGVATSAQI-Z

X-ALGVATSAQIT-Z

X-ALGVATSAQITA-Z

10 X-ALGVATSAQITAA-Z

X-ALGVATSAQITAAV-Z X-ALGVATSAOITAAVA-Z

X ALGUNISAQIIAAVA-U

X-ALGVATSAQITAAVAL-Z

X-ALGVATSAQITAAVALV-Z

X-ALGVATSAQITAAVALVE-Z

X-ALGVATSAQITAAVALVEA-Z

X-ALGVATSAQITAAVALVEAK-Z

15 X-ALGVATSAQITAAVALVEAKQ-Z

X-ALGVATSAQITAAVALVEAKQA-Z

X-ALGVATSAQITAAVALVEAKQAR-Z

X-ALGVATSAQITAAVALVEAKQARS-Z

X-ALGVATSAQITAAVALVEAKQARSD-Z

X-ALGVATSAQITAAVALVEAKQARSDI-Z

X-ALGVATSAQITAAVALVEAKQARSDIE-Z

X-ALGVATSAQITAAVALVEAKQARSDIEK-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKL-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLK-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKE-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKEA-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAI-Z

X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAIR-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a

macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG AMINO TRUNCATIONS

```
X-IRD-Z
                                   X-AIRD-Z
                                  X-EAIRD-Z
                                 X-KEAIRD-Z
                                X-LKEAIRD-Z
                              X-KLKEAIRD-Z
                              X-EKLKEAIRD-Z
                            X-IEKLKEAIRD-Z
                           X-DIEKLKEAIRD-Z
                          X-SDIEKLKEAIRD-Z
10
                         X-RSDIEKLKEAIRD-Z
                        X-ARSDIEKLKEAIRD-Z
                       X-QARSDIEKLKEAIRD-Z
                      X-KQARSDIEKLKEAIRD-Z
                     X-AKQARSDIEKLKEAIRD-Z
                    X-EAKQARSDIEŘLKEAIRD-Z
                   X-VEAKOARSDIEKLKEAIRD-Z
15
                  X-LVEAKQARSDIEKLKEAIRD-Z
                 X-ALVEAKQARSDIEKLKEAIRD-Z
                X-VALVEAKQARSDIEKLKEAIRD-Z
               X-AVALVEAKQARSDIEKLKEAIRD-Z
              X-AAVALVEAKQARSDIEKLKEAIRD-Z
             X-TAAVALVEAKQARSDIEKLKEAIRD-Z
            X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
           X-QITAAVALVEAKQARSDIEKLKEAIRD-Z
20
          X-AQITAAVALVEAKQARSDIEKLKEAIRD-Z
         X-SAQITAAVALVEAKQARSDIEKLKEAIRD-Z
        X-TSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
       X-ATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
      X-VATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
     X-GVATSAQITAAVALVEAKQARSDIEKLKEAIRD-2
    X-LGVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
25
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited

macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
- X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
- 5 X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
 - X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z
 - X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z
 - X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z
 - X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z
 - X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z
 - X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z
- X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z
 - X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-Z X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
 - X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
 - X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
 - X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
 - X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z
 - X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z
- 15 X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z
 - X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z
 - X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z
 - X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z
 - X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z
 - X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z
 - X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-2
- X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
 - X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
 - X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
 - X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
 - X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKO-Z

Anti-human parainfluenza virus 3 peptides

- 25 X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRSN-Z
 - X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRSNO-Z
 - X-NNSVALDPIDISIELNKAKSDLEESKEWIRRSNOK-Z
 - X-NSVALDPIDISIELNKAKSDLEESKEWIRRSNOKL-Z
 - X-SVALDPIDISIELNKAKSDLEESKEWIRRSNOKLD-Z
 - X-VALDPIDISIELNKAKSDLEESKEWIRRSNQKLDS-Z
 - X-ALDPIDISIELNKAKSDLEESKEWIRRSNOKLDSI-Z
- 30 X-LDPIDISIELNKAKSDLEESKEWIRRSNQKLDSIG-Z
 - X-DPIDISIELNKAKSDLEESKEWIRRSNQKLDSIGN-Z
 - X-PIDISIELNKAKSDLEESKEWIRRSNQKLDSIGNW-Z
 - X-IDISIELNKAKSDLEESKEWIRRSNOKLDSIGNWH-Z
 - X-DISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQ-Z
 - X-ISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQS-Z
 - X-SIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSS-Z X-IELNKAKSDLEESKEWIRRSNOKLDSIGNWHOSST-Z
- 35 X-ELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSSTT-Z
- X-TAAVALVEAKQARSDIEKLKEAIRDTNKAVOSVOS-Z

```
X-AVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSI-Z
X-LVEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z
X-VEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLI-Z
X-EAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIV-Z
X-AKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVA-Z
X-KQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAI-Z
X-QARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIK-Z
X-ARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKS-Z
X-RSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSV-Z
X-SDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQ-Z
X-KLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVN-Z
X-LKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
X-AIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
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Anti-simian immunodeficiency virus peptides

```
X-WQEWERKVDFLEENITALLEEAQIQQEKNMYELQK-Z
X-QEWERKVDFLEENITALLEEAQIQQEKNMYELQKL-Z
X-EWERKVDFLEENITALLEEAQIQQEKNMYELQKLN-Z
X-WERKVDFLEENITALLEEAQIQQEKNMYELQKLNS-Z
X-ERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWD-Z
X-RKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDV-Z
X-VDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF-Z
X-DFLEENITALLEEAQIQQEKNMYELQKLNSWDVF-Z
X-FLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
X-FLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
```

Anti-measles virus peptides

X-LHRIDLGPPISLERLDVGTNLGNAIAKLEAKELL-Z
X-HRIDLGPPISLERLDVGTNLGNAIAKLEAKELLE-Z
X-RIDLGPPISLERLDVGTNLGNAIAKLEAKELLES-Z
X-IDLGPPISLERLDVGTNLGNAIAKLEAKELLESS-Z
X-DLGPPISLERLDVGTNLGNAIAKLEAKELLESSD-Z
X-LGPPISLERLDVGTNLGNAIAKLEAKELLESSDQ-Z
X-GPPISLERLDVGTNLGNAIAKLEAKELLESSDQI-Z
X-PPISLERLDVGTNLGNAIAKLEAKELLESSDQIL-Z
X-PISLERLDVGTNLGNAIAKLEAKELLESSDQILR-Z
X-SLERLDVGTNLGNAIAKLEAKELLESSDQILRSM-Z
X-LERLDVGTNLGNAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. 10 Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, et al., 1989, Molecular Cloning, A 15 Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are 20 non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another 25 embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity 30 of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or tbutyloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. (See "X" in Tables I to IV,

above.) Additionally, the hydrophobic group, tbutyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

rurther, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the peptides of the invention.

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Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,

below, and assays for antiviral activity are described in Section 5.5.2, below.

5.5.1 ASSAYS FOR CELL FUSION EVENTS

Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

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standard conditions for culturing cells, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as crystal violet stain, may be used to facilitate the visualization of syncytial formation.

5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

easily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as 10 HIV-induced, syncytia formation in vitro. assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations 15 may be tested. This range should include a control culture wherein no peptide has been added. conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for 20 example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. 25 HIV as an example, such an assay would comprise CD-4+ cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4⁺ cells by cell-free HIV. Such an assay may comprise culturing an appropriate

concentration (i.e., TCID50) of virus and CD-4+ cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the present of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference 15 in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying nonretroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 20 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general 25 review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability. 30

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of 10⁴ to 10⁵ pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

5.6. USES OF THE PEPTIDES OF THE INVENTION

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The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

with respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

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As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4+ cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type 35 and subtype of virus or organism in which the specific

peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

5.5.1. SCREENING ASSAYS

As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the 15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,

above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially 25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic 35 compounds, natural products, and other sources of

potentially effective materials may be screened in a ___ variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP107 peptide for a time sufficient to allow binding of the compound to the DP107 peptide;
 - (b) removing non-bound compounds; and
 - (c) determining the presence of the compound bound to the DP107 peptide, thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;
 - (b) removing non-bound compounds; and

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(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches that may be pursued in the isolation of such DP107binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate 10 wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled, 15 either directly or indirectly. In practice, microtiter plates are conveniently utilized. anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface 20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

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In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of label immobilized on the surface indicates that

complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or DP178, whichever is appropriate for the given assay, or ab antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored complexes.

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By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two peptides to interact and bind, thus forming a complex.

In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted 15 in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire 20 reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the 25 binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

been formed. The various formats are described briefly below.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

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Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

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In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (<u>i.e.</u>, an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41\(\Delta\)178 peptides and by assaying test

compounds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41\(\Delta\)178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41\(\Delta\)178 is a maltose binding fusion protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41∆178 may be immobilized onto solid supports such as microtiter 10 wells. A series of dilutions of a test compound may then be added to each M41\Delta178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test 15 compound are removed from the wells and wells are then incubated with the DP178/M41A178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be 20 conducted. Test compounds showing an ability to disrupt DP178/M41\Delta178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to
perform a rapid, high-throughput binding assay which
is capable of directly measuring DP178 binding to
M41Δ178 for the determination of binding constants of
the ligand of inhibitory constants for competitors of
DP178 binding.

Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a solid support such as a microtiter well. DP178

binding to M41 Δ 178 is then quantitated by measuring the fraction of DP178 that is bound as ¹²⁵I-DP178 and calculating the total amount bound using a value for specific activity (dpm/ μ g peptide) determined for each labeled DP178 preparation. Specific binding to M41 Δ 178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

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5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art. 15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may 20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal, 25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline 30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

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In instances wherein intracellular administration of the peptides of the invention or other inhibitory

agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above.

Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the 15 invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-20 associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs 25 are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley 30 Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

to an HIV virus. Examples of such prophylactic use of the peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

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A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LDso (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with

little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC. (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

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The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable adjuvant in order to enhance the immunological

response. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art.

Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

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For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 pl).

would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administrated dose in the management of the oncogenic disorder of interest

will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual A program comparable to that discussed above may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be 15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion. by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated

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for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active 10 compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, 15 such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain 20 suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

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added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4⁺ cell-cell fusion and infection by cell free virus. In the 30 fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

6.1. MATERIALS AND METHODS

6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide 10 synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were 15 synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the 20 resin by treatment with trifluoracetic acid (TFA) (10ml), H_2O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were 25 chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15µ spherical) with a linear gradient; H,O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry 30 yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

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6.1.2. <u>VIRUS</u>

The HIV-11AI virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 µm filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25µl of 10 serial diluted virus was added to 75µl AA5 cells at a concentration of 2 x 105/ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post 15 infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCIDso was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497). 20 The titer of the HIV-1_{LAI} and HIV-1_{MN} stocks used for these studies, as measured on the AA5 cell line, was / approximately 1.4 x 10° and 3.8 x 10° TCID₁₀/ml, respectively.

6.1.3. CELL FUSION ASSAY

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Approximately 7 x 10⁴ Molt cells were incubated with 1 x 10⁴ CEM cells chronically infected with the HIV-1_{LAI} virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of $100\mu l$ culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of $10\mu l$ and the cell mixtures were incubated for 24 hr. at 37° C. At that time, multinucleated giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the entire well in a single field.

6.1.4. CELL FREE VIRUS INFECTION ASSAY

synthetic peptides were incubated at 37°C with either 247 TCID₅₀ (for experiment depicted in FIG. 2), or 62 TCID₅₀ (for experiment depicted in FIG.3) units of HIV-1_{LAI} virus or 25 TCID₅₀ units of HIV-2_{NHZ} and CEM CD4⁺ cells at peptide concentrations of 0, 0.04, 0.4, 4.0, and 40μg/ml for 7 days. The resulting reverse transcriptase (RT) activity in counts per minute was determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J. Hyg. 27: 493-497 for an explanation of TCID₅₀ calculations.

6.1.5. REVERSE TRANSCRIPTASE ASSAY

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The micro-reverse transcriptase (RT) assay was adapted from Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). Supernatants from virus/cell cultures are adjusted to 1% Triton-X100. A 10µl sample of supernatant was added to 50µl of RT cocktail in a 96-well U-bottom microtitre plate and the samples incubated at 37°C for 90 min. The RT cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM MgCl₂, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-radioactive dTTP, and 10µCi/ml ³²P-dTTP (Amersham, cat. No. PB.10167).

After the incubation period, $40\mu l$ of reaction mixture was applied to a Schleicher and Schuell (S+S) NA45 membrane (or DE81 paper) saturated in 2 x SSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a S+S Minifold over one sheet of GB003 (S+S) filter

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paper, with partial vacuum applied. Each well of the minifold was washed four times with 200µl 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

6.2. RESULTS

6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

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The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells 15 with chronically HIV-1 infected CEM cells. results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10µg/ml and 12.5ng/ml were tested for blockade of the 20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1 HIV-1 HIV-1 HIV-1gp, or HIV-1sF2 virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection 25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIVLAI inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study 30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of $40\mu g/ml$ (FIG. 4). These observations 35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not related to non-specific peptide/protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1_{SF2} isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at 20 peptide concentrations below lng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as $10\mu g/ml$. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates 25 an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1mediated cell fusion, but the peptide's inability to inhibit HIV-2 medicated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

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6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4+ CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an 5 experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1, isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) 10 represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad, Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each 15 concentration (0, 0.04, 0.4, 4, and $40\mu g/ml$) of peptide was incubated with 247 TCID50 units of HIV-1LAI virus and CEM cells. After 7 days of culture, cellfree supernatant was tested for the presence of RT activity as a measure of successful infection. The 20 results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated/ by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC50=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ: ID:8) and DP-118 (SEQ 25 ID:10), had over 60-fold higher IC50 concentrations of

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1_{LAI} or HIV-2_{NHZ}. 62 TCID₅₀

30 HIV-1_{LAI} or 25 GCID₅₀ HIV-2_{NHZ} were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC50 of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC50 for HIV-35 2_{NHZ}, thus making DP178 (SEQ ID:1) two logs more potent

approximately $5\mu g/ml$.

as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEO ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be noncytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

15 Approximately 3.8x10⁵ CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40μg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

7.2. RESULTS

Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40μg/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

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TABLE XXIV

% Viability
at time (hours)

w		as came (nours)			
Peptide	Peptide Concentration µg/ml	0	24	48	72
DP178 (SEQ ID:1)	40	98	97	95	97
	10	98	97	98	98
	2.5	98	93	96	96
DP116 (SEQ ID:9)	40	_98	95	98	97
AND THE RESERVE TO TH	10	98	95	93	98
	2.5	98	96	98	99
No Peptide	0	98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107
Soluble recombinant forms of gp41 used in the

25 example described below provide evidence that the
DP178 peptide associates with a distal site on gp41
whose interactive structure is influenced by the DP107
leucine zipper motif. A single mutation disrupting
the coiled-coil structure of the leucine zipper domain
transformed the soluble recombinant gp41 protein from
an inactive to an active inhibitor of HIV-1 fusion.
This transformation may result from liberation of the
potent DP178 domain from a molecular clasp with the
leucine zipper, DP107, determinant. The results also
indicate that the anti-HIV activity of various gp41
derivatives (peptides and recombinant proteins) may be

due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

8.1. MATERIALS AND METHODS

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8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of 10 gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 15 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41 Δ 107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'-25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the

30 Xmn I site of pMal-p2. Primer A and 5'ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M4135 PΔ178. All inserted sequences and mutated residues

were checked by restriction enzyme analysis and confirmed by DNA sequencing.

8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

- The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide 10 gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold, 15 or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed 20 protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.
- 25 8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY
 Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells (7 X 10⁴) were incubated with HIV-1_{mb} chronically infected CEM cells
 30 (10⁴) in 96-well flat-bottomed half-area plates (Costar) in 100 μl culture medium. Peptide and fusion proteins at various concentrations in 10 μl culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated with microscopic examination. Both M41 and M41-P did

not show cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41 Δ 178 or M41-P Δ 178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

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8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41\Delta178 or M41-P\Delta178 (5 μg/ml) in 0.1M NaHCO3, pH 8.6, were coated on 96 wells 15 Linbro ELISA plates (Flow Lab, Inc.) overnight. well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) 20 were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 > ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room 25 temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. 30 peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H2O2 were added to develop the color. reaction was stopped with an equal volume of 4.5 N H,SO, after incubation at room temperature for 10 minutes. The optical density of the stopped reaction 35 mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

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8.2. RESULTS

8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF qp41

As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic 10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because 15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (i.e., the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely 20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind 25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant 30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix 35 motif, i.e., DP107 or DP178, of the M41 fusion protein

eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

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8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, supra, synthetic peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as high as 50 µM (Table XXV, below).

TABLE XXV

DISRUPTION OF THE LEUCINE ZIPPER OF
GP41 FREES THE ANTI-HIV MOTIF

20		<u>DP107</u>	DP178	<u>M41</u>	<u>M41-P</u>	<u>Μ41-ΡΔ178</u>
	Cell fusion (IC _{so})	1 μΜ	1 nM	> 50 μM	83 nM	>50 μM
25	Fab-D binding (k _D)	-	-	3.5x10°	2.5x10 ⁻⁸	-
	HIV infectiv- ity (IC ₅₀)	iμM	80 nM	> 16 μM	66 nM	>8 μM

The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

^{- =} No detectable binding of Fab-d to the fusion proteins.

Antiviral Infectivity Assays. 20 μ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20 μ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20 μ l of CEM4 cells at 6 x 10⁵ cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO₂ incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID₅₀) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

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Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and 15 Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1 $_{\rm IIIB}$ infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical 20 sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41\Delta178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

the DP178 region, making it unavailable for anti-viral activity.

A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PΔ178, failed to reconstitute the epitope in similar mixing experiments.

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9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been 15 well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D 20 tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form 25 di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes 30 c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs 35 were tailored to the DP107 and DP178 sequences by

deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in FIG. 12. For example, the motif for GCN4 was designed as follows:

- 1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
 - 3. The PESEARCH motif would, therefore, be written as follows:
- [LMNV]-{CFGIMPTW} (2)-[LMNV]-{CFGIMPTW} (3)[LMNV]-{CFGIMPTW} (2)-[LMNV]-{CFGIMPTW} (3)[LMNV]-{CFGIMPTW} (2)-[LMNV]-{CFGIMPTW} (3)[LMNV]-{CFGIMPTW} (2)-[LMNV]-{CFGIMPTW} (3)
- position either L, M, N, or V must occur; at positions
 B and C (the next two positions) accept everything
 except C, F, G, I, M, P, T, or W; at the D position
 either L, M, N, or V must occur; at positions E, F,
 and G (the next 3 positions) accept everything except
 C, F, G, I, M, P, T, or W." This statement is
 contained four times in a 28-mer motif and five times
 in a 35-mer motif. The basic motif key then would be:
 [LMNV]-{CFGIMPTW}. The motif keys for the remaining
 well described coiled-coil sequences are summarized in
 FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also 10 possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the 15 other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of 20 the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is 25 [ILMNQTV] {CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. 15 Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the 20 fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane 25 associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the 30 proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped or glycoprotein sequences (library file PVIRUSE1).

Tables V through XIV contain lists of protein sequence names and motif hit locations for all the motifs searched.

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10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107 AND DP178-LIKE SEQUENCES IN HUMAN IMMUNODEFICIENCY VIRUS

FIG. 20 represents search results for HIV-1 BRU 10 isolate gp41 (PC/Gene protein sequence PENV_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 15 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP} {CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable 25 additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is 35

at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN RESPIRATORY SYNCYTIAL VIRUS

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FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF 20 HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids 116-202, 267-302, and 506-549. The proline-leucine zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions which share location similarities with DP-178 of HIV-35 1.

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name 5 PENV_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would 10 represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV 15 also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178 LIKE SEQUENCES IN CANINE DISTEMPER VIRUS

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Canine Distemper Virus (strain Onderstepoort) fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23). Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residues 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located 5 just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC 10 which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene 20 protein sequence name PVGLF_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

30 15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
OF DP107-LIKE AND DP178-LIKE
SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTI5 exhibit
DP107-like hits in the same region, 115-182 and 117182 respectively, of Human Parainfluenza Virus (strain
NIH 47885; PC/Gene protein sequence name PVGLF_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits nearer the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

rig. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68) at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated

PCT/US95/16733 WO 96/19495

that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

17.1 MATERIALS AND METHODS

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Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from Am using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse 20 and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

25 Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline W/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD_{450/690} was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG.

27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

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2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

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Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC50 data for each peptide represents the average of several experiments conducted utilizing that peptide.

17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, 30 T-142 to T-145 and T-334 purfied peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC, values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 to T-139, as demonstrated by their low IC₅₀ values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

The results summarized in FIG. 28A-B demonstrate
that a number of DP178-like purified peptides exhibit
a range of potent anti-viral activity. These peptides
include, for example, T-67, T-104, T-105 and T-107 to
T-119, as listed in FIG. 28A, and T-665 to T-669 and
T-671 to T-673, as listed in FIG. 28B. In addition,
some of the DP178-like peptides exhibited some level
of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV antiviral compounds.

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18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS TYPE 3 DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

- In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.
- analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of
- 30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses

35 consisted of circular dichroism (CD) studies. The CD

spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from λ_{210} using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

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Uninfected confluent monolayers of CV-1W cells

were grown in microtiter wells in 3% EMEM (Eagle

Minimum Essential Medium w/o L-glutamine (Bio

Whittaker Cat. No. 12-125F), with fetal bovine serum

(FBS; which had been heat inactivated for 30 minutes

at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented

at 3%, antibiotics/antimycotics (Gibco BRL Life

Technologies Cat. No. 15040-017) added at 1%, and

glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected CV-1W cells, then adding peptides (at the

dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, avove, in Section 17.1.

Peptides: The peptides characterized in the
study presented herein were:

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- Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid resides (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from $500\mu g/ml$ to approximately

500ng/ml. For each of the assays, a well containing no peptide was also used.

18.2 RESULTS

The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

As shown in FIG. 29A-B, a number of the HPIV3

DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC₅₀ values. In fact, peptides 201 to 205 exhibit IC₅₀ values in the nanogram/ml range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

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FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were

located at amino acid residues 156-215 and 277-289.

The peptide regions found by ALLMOTI5 were located at

amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region

(i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107

region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil 15 region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may 20 be similar to HIV in that it may contain a coiled-coil, structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined 25 structure, despite the Lupas program's prediction of a coiled-coil structure.

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20. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN EPSTEIN-BARR VIRUS

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

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FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results domonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located

at amino acid residues 193-220, as shown in FIG. 33. The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN MEASLES VIRUS

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FIG. 34 illustrates the motif search results for the fusion protein F1 of measles virus, strain Edmonston (PC Gene® protein sequence PVGLF_MEASE), successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at amino acid residues 228-262. The ALLMOTI5 search motif identifies three regions, including amino acid residues 116-184, 228-269 and 452-500. Three regions containing proline residues followed by a leucine zipper-like sequence were found beginning at proline residues 214, 286 and 451.

The Lupas program identified two regions it predicted had potential for coiled-coil structure, which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN HEPATITIS B VIRUS

FIG. 35 depicts the results of a PZIP motif search conducted on the Hepatitis B virus subtype AYW. Two regions of interest within the major surface antigen precursor S protein were identified. The first lies just C-terminal to the proposed fusion peptide of the major surface antigen (Hbs) which is found at amino acid residues 174-191. The second region is located at amino acid residues 233-267. The Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral activity of these D178/DP107 analog regions, peptides derived from area around the analog regions are synthesized, as shown in FIG. 52A-B. These peptides represent one amino acid peptide "walks" through the

putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Follwing complete synthesis, the peptide aminoterminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antivial peptides are further characterized in model systems such as wood chuck tissue culture and animal sytems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

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24. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN BACTERIAL PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

FIG. 37 depicts the search motif results for the Pseudomonas aeruginosa fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTIS. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTIS.

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Pseudomonas gonorrhoeae fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 39 depicts the search motif results for the Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTIS motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTIS search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 40 depicts the search motif results for the Staphylococcus aureus toxic shock syndrome Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTIS motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTIS motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

PIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues

55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS WITHIN VARIOUS HUMAN PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTIS motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

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26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107
ANALOGS: CD AND ANTIVIRAL
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

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26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A₂₈₀ using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (i.e., cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented—at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E). Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

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The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as described above.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

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Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

26.2 RESULTS

The data summarized in FIG. 47 represents
antiviral and structural information obtained via
"peptide walks" through the DP178-like region of the
MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC₅₀ values for such peptides were determined, as shown in FIG. 47, and ranged from $1.35\mu g/ml$ (T-257B1/C1) to $0.072\mu g/ml$ (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

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27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides

identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized
herein were as reported in Langolis et al. (Langolis,
25 A.J. et al., 1991, AIDS Research and Human
Retroviruses 7:713-720).

<u>Peptides</u>: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk
through the DP178-like region of the SIV TM protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-SIV antiviral compounds.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP-178 PEPTIDE TRUNCATIONS AND MUTATIONS

The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

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28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1.
Assays utilized HIV-1/IIIb and/or HIV-2 NIHZ isolates.
Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

<u>Peptides</u>: The peptides characterized in the study presented herein were:

1) FIGS. 49A-C present peptides derived from
the region around and containing the DP178
region of the HIV-1 BRU isolate.
Specifically, this region spanned from gp41
amino acid residue 615 to amino acid residue
717. The peptides listed contain
truncations of this region and/or mutations

which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

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28.2 RESULTS

Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

In FIG. 49A, a number of the DP178 truncations
exhibited a high level of antiviral activity, as
evidenced by their low IC₅₀ values. These include, for
example, test peptides T-50, T-624, T-636 to T-641, T645 to T-650, T-652 to T-654 and T-656. T-50
represents a test peptide which contains a point
mutation, as indicated by the residue's shaded
background. The HIV-1-derived test peptides exhibited
a distinct strain-specific antiviral activity, in that
none of the peptides tested on the HIV-2 NIHZ isolate
demonstrated appreciable antti-HIV-2 antiviral
activity.

Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ($IC_{50}>400\mu g/ml$) whereas the carboxy terminal peptide showed potent antiviral

activity (IC₅₀= $3\mu g/ml$). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

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Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by their low IC50 values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived
from the Epstein-Barr (EBV) DP-178/DP107 analog region
of the Zebra protein identified, above, in the Example
presented in Section 20 are described and tested for
anti-EBV activity. It is demonstrated that among
these peptides are ones which exhibit potential antiviral activity.

29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays (EMSA): Briefly, an EBV Zebra protein was synthesized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10 10,000 to 20,000 c.p.m. of a 32P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gelshift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-20 bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

29.2 RESULTS

The EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays 15 described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of 25 the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

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scope by the specific embodiments described which are intended as single illustrations of individual aspects

of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

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 An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.

- 2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.
- 3. The peptide of Claim 2 in which the virus is 10 HIV-1 or HIV-2.
 - 4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
- The peptide of Claim 2 in which the virus is an influenza virus.
 - 7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
- 8. The peptide of Claim 2 wherein the virus is an Epstein-Barr virus.
 - 9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide recognized by an ALLMOTIS, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
- 10. The method of Claim 9 wherein the virus is
 HIV-1 or HIV-2.

11. The method of Claim 9 wherein the virus is a respiratory syncytial virus.

- 12. The method of Claim 9 wherein the virus is a human parainfluenza virus.
 - 13. The method of Claim 9 wherein the virus is an influenza virus.
- 14. The method of Claim 9 in which the virus is a hepatitis B virus.
 - 15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

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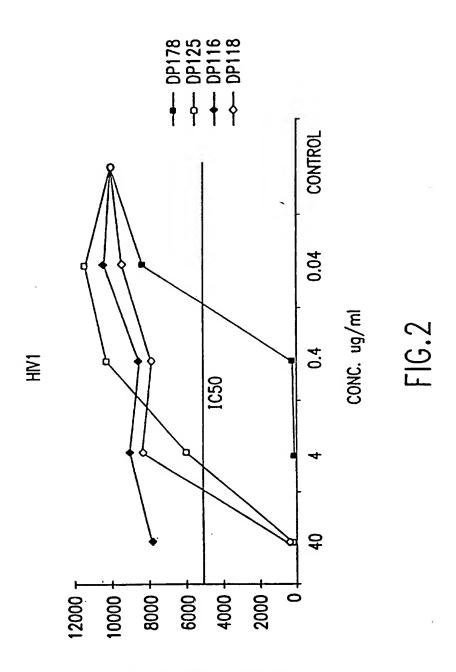
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YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNMF	YTNTIYNLLEESONQOEKNEOELLELDKWASLWNWF	YTG I I YNLLEESQNQQEKNEQELLELDKWANLWNWF	YTSL IYSLLEKSQTQQEKNEQELLELDKWASLWNWF	LEANISKSLEQAQIQQEKNAMYELQKLNSWDIFGNWF	LEANISOSLEQAQIQQEKNAYELQKLNSWDVFTNWL	SSESF TL LEGWNNWKLQL AEGWLEQ I NEKHYLED I S	QQLLDVVKRQQEMLRLTVWGTKNLQARVTA1EKYLKDQ	CGGNNLLRAIEAQCHLLOLTVWGIKQLQARILAVERYLKDQ	LOARILAVERYLKDOQO
HIV1LAI (DP-178; SEQ ID:1)	HIV1SF2 (DP-185; SEQ ID:3)	HIV1RF (SEQ ID:4)	HIVIMN (SEQ ID:5)	HIV2ROD (SEQ ID:6)	HIV2NIHZ (SEQ ID:7)	DP180 (SEQ 1D:2)	DP118 (SEQ ID:10)	DP125 (SEQ ID:8)	DP116 (SEQ 10:9)

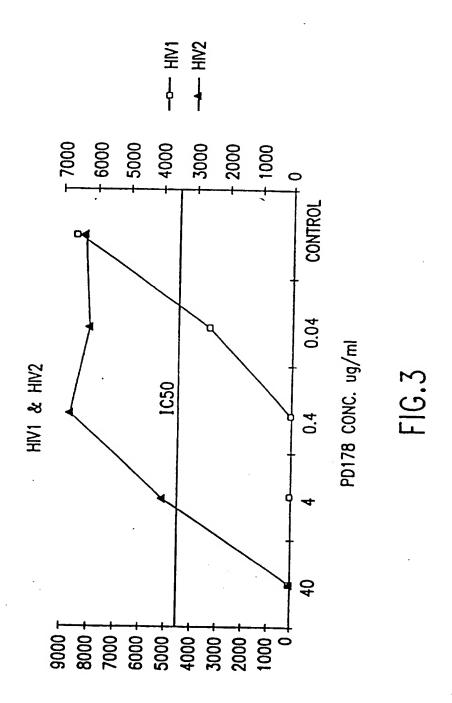
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REVERSE TRANSCRIPTASE UNITS

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Number (of Sync	<u>y</u> tio/	well:	concer	tration	in μg/n	nl (microg	grams/ml)	
DP178_	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
Syncylia				_	•	•	•	0	· ·
HIVILAL	0	0	0	0	0	0	0	0	67
HIVIM	0	0	0	0	0	ND	ND	ND	34 cs
HIVIRF	0	0	0	0	0	ND	ND	ND	65
HIVISF2	0	0	0	0	0	ND	ND	ND	58
DP125 Syncylia	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
HIVILAI	0	0	54	69	80	75	79	82	67
HIVIM	0	Ö	30	36	ND	ND	ND	ND	34
HIVIRF	0	Ö	67	63	ND	ND	ND	ND	65
HIVISF2	0	Ö	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
Syncytio			<u>·</u> -					<u></u>	
HIVILAL	75	ND	ND	ND	ND	ND	ND	ND	67
HIVIMN	35	ND	ND	ND	ND	ND	ND	ND	34
HIVIRF	81	ND	ND	ND	ND	ND	ND	ND	65
HIVISF2	81	ND	ND	ND	ND	ND	ND	МD	58

FIG.4A

40	20	10	5	2.5	1.25	0.625	0.3125	Control
50	>45	>45	>45	>45	>45	>45	>45	. 58
40	20	10	5_	2.5	1.25	0.625	0.3125	Control
0	0	0	0	0	0	0	ND	60
	50 40	50 >45 40 20	50 >45 >45 40 20 10	50 >45 >45 >45 40 20 10 5	50 >45 >45 >45 >45 40 20 10 5 2.5	50 >45 >45 >45 >45 >45 >45 40 20 10 5 2.5 1.25	50 >45 >45 >45 >45 >45 >45 40 20 10 5 2.5 1.25 0.625	50 >45 >45 >45 >45 >45 >45 >45 40 20 10 5 2.5 1.25 0.625 0.3125

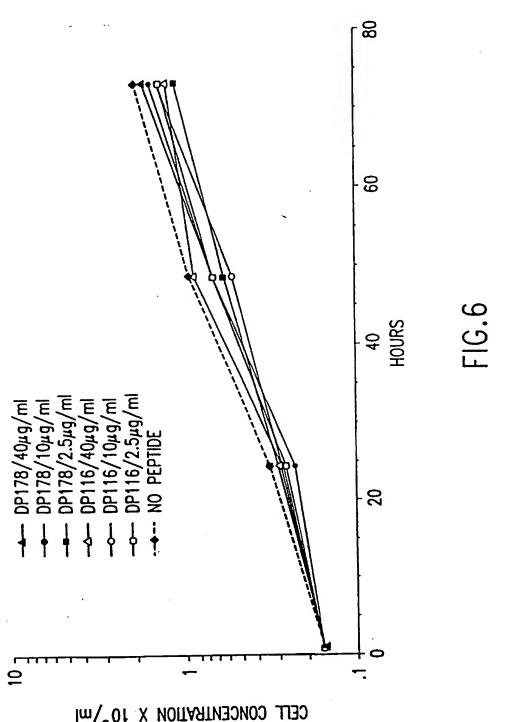
FIG.4B

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				НІVІ				
	Number	of	Syncyl	io/well:	conce	ntration	in ng/m1	(nanograms/ml)
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylio HIV1	0	0	0	0	0	14	20	48
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylia HIV1	ND .	48	ND	ND	ND	ND	ND	ND
				HIV2				
	Number	of	Syncyl	io/well:	conce	ntration	in μg/ml	(micrograms/ml)
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylio HIV2	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylia HIV2	ND	58	ND	ND	ND	ND	ND	ND

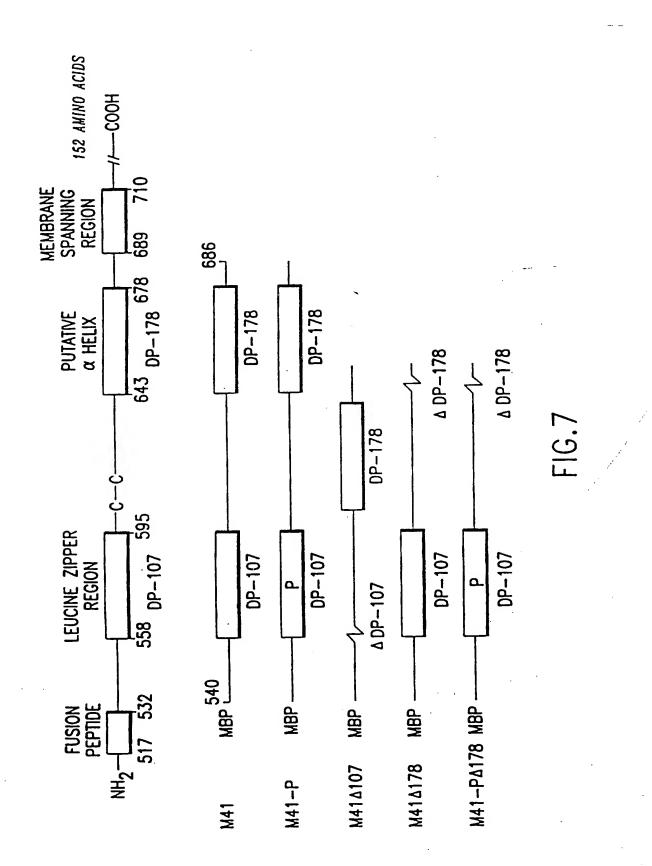
FIG.5

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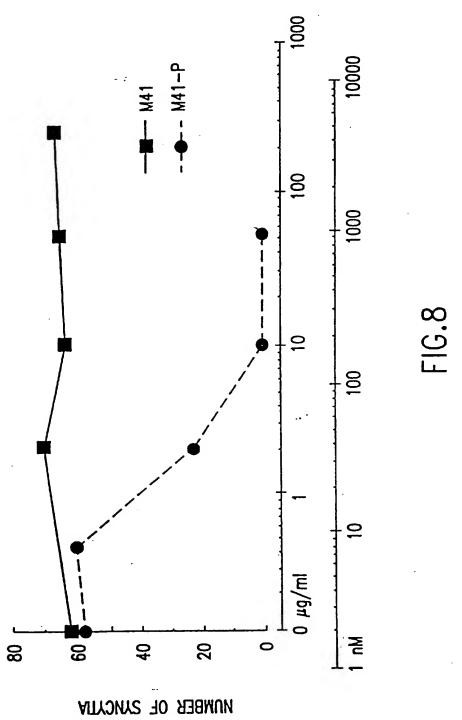


CELL CONCENTRATION X 10⁶/ml

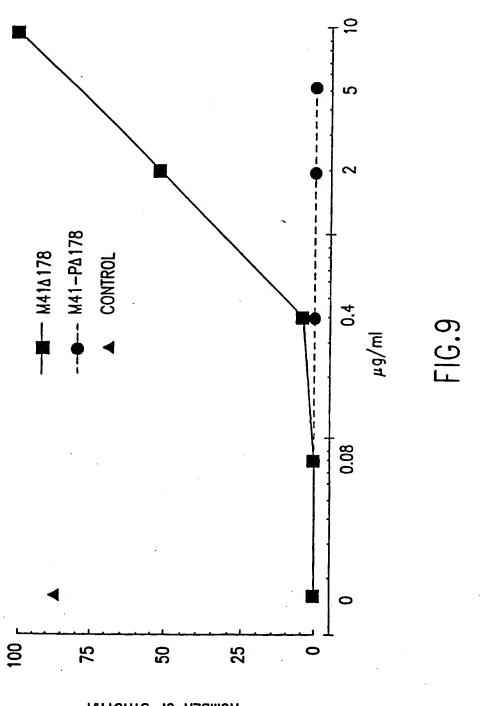
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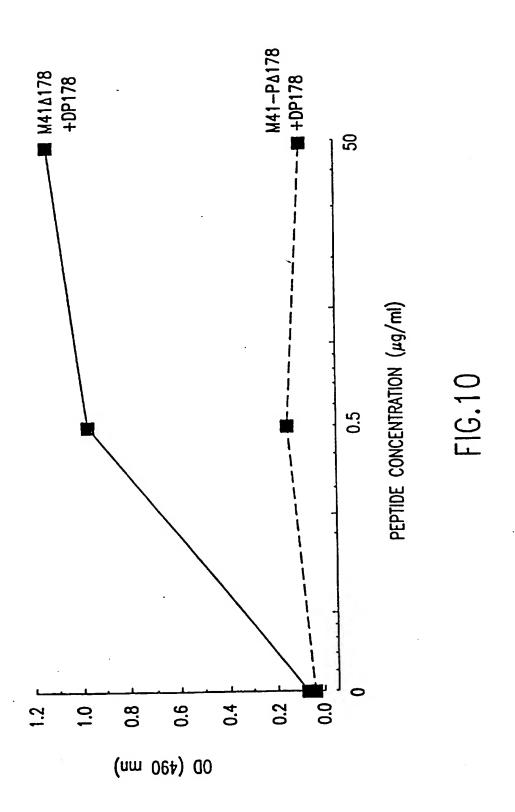


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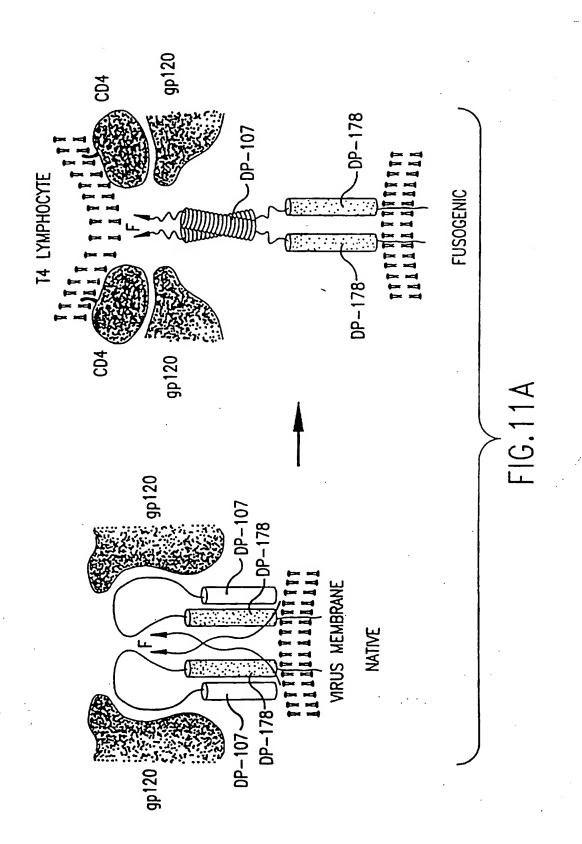


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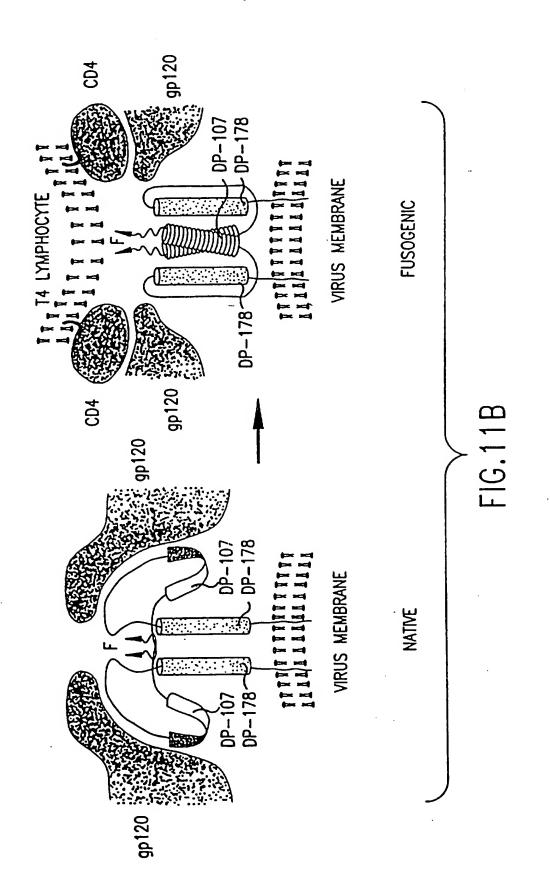
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	0	IARLIKK	ANLIK	NALRE	E OLI R N	0 0 L E K
Posilions	D A	N 3 N 3 7 H	A L 0 T E 1	N S E L A S T A	OLKHKI	FISEVEGRI
	¥	SKNY	O E K	0 A	K R R	KEFS
	0	<u> </u>	OILE	F		0
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	<u></u>			R	K	×
	A	XX	01	¥	<u>В</u>	<u></u>
	Sequence	GCN4 (acn4 veast)	C-FOS (fos human)	C-JUN (Loo! human)	C-MYC (mvo human)	FIU 100P 36

FIG. 12

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Molifs		[ILQT] {CFIMPSTY}	[10TV] (CDF IMPST)	ટ `			[EKLNOV] (CHKMPS)		[EKLOY] {ACFGWPRWMY}	[EKLOWY] {CFGNPRVY}	[EFKLOHY] {CFGNPRVY}			[ETLNOSMY] (CFGMPRVY)	[EFILNOSWY] {CFGWPRVY}	
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FIG. 13

7872-020 (SHEET 15 OF 63)

Positions Positions A D A D A D	EELLESKINYHILENEVARILKKI [LMN] (CFGINPTH)	E A O O H L L O L I I V W G I K O L O A R I L A V E R Y L [ILOTV] {CF IMPSTY} (ILMNOTV) {CF IMPT} E A O O H L L O L I I V W G I K O L O A R I L A V E R Y L [ILOTV] {COF IMPST} (ILMNOTV) {CF IMPT} E A O O H L L O L I V W G I K O L O A R I L A V E R Y L K D O [ILOTV] {COF IMPST} (ILMNOTV) {CF IMPT}	A DOHILLOLTVW GIKOLOARI A DOHILOLTVW GIKOLOARILAVERYL [EKLNOV] (CFKNOS) (EKLNOV] (CFKNOV] (CFKNOV] (CFKNOV) (CF
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6	MKOLEOKVEEL	N N N N N N N N N N N I L R A A	N N L L L R A L
Seguence	14 yeast)	DP-107 (env_hvibru)[1=0 N N L L R A I E A O O O O O O O O O O O O O O O O O O	DP-107 (env_hvlbru)L2=0 NN L L R A I E A 0 0 H DP-107 (env_hvlbru)L2=0 NN L L R A I E A 0 0 H

FIG. 17

7872-020 (SHEET 16 OF 63)

Parent Holif Hybrid Holif	' !	[LMV] {CFGIAPTW}	SILWNW [EKLOY] {ACFGNPRVWY} [EKLMNOVY] {GFGNPW}	E E SIO NOID E KINE DIELLELO KINA SLIMIN WIE E SIO NOID E KINE DIELLELO KINA SLIMIN WIE E SIO NOID E KINE DIELLELO KINA SLIMIN WIE ESIO NOID E KINE DIELLELO KINA SLIMIN WIE EFILMOSWY] (CFGWPRYY) [EFILMOSWY] (CFGWPRYY) [CFILMOSWY] (CFGWPRYY) [CFILMOSWY] (CFGWPRYY) [CFILMOSWY] (CFGWPRYY) [CFILMOSWY] (CFGWPRYYY) [CFILMOSWY] (CFGWPRYYY) [CFILMOSWYY] (CFGWPRYYY) [CFILMOSWYY] (CFGWPRYYY) [CFILMOSWYY] (CFGWPRYYY) [CFILMOSWYY] (CFGWPRYYY) [CFILMOSWYY] (CFGWPRYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
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	Sequence	GCN4 (gen4 yeast)	DP-178 (env_hvlbru)Y1=A Y DP-178 (env_hvlbru)Y1=A Y DP-178 (env_hvlbru)Y1=A Y	DP-178 (env_hvibru)Y1=0 DP-178 (env_hvibru)Y1=0 DP-178 (env_hvibru)Y1=0

FIG. 15

7872-020 (SHEET 17 OF 63)

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FIG. 16

	787	2-020	(SHEE	T 18 C
Hybrid Motil	[EFIKLMATVMY] [CFIP]	[EF1LANORSTWAY] {CFLAP}	[EFKLINOVIIY] {GFLIP}	[EF IKLANOSVAPY] [CF429]
Parent Motif	[LLAN] {CFGIAPTA!} [ILQTV] {COFIAPST} [EFKLOAY] {CFGAPRYY}	[LMNY] {GFGIMPTH} [ILOTV] {GBFIMPST} [EFILNOSMY] {GFGUPRVY}	[LIMN] {GFGILIPTW] [EKLNOV] {GFKAPS} [EFKLOMY] {GFGIAPRVY}	[LIMN] {CFGIMPTW] [EKLNOV] {CFKAPS} [EFILNOSWY] {CFGMPRVY}
	N Y H L E N E V A R L K K L L Q L T V W G T K O L Q A R I L A V E R Y L K D O O C E K N E O E L L E L D K W A S L W N W F	N Y H L E N E V A R L K K L L O L T V W G I K O L O A R I L A V E R Y L K O O S O N O O E K N E O E L L E L D K W A S L W N W F	~	NYHLENEVARLKKL OLIVWGIKOLOARILAVERYLKDO SONOOEKNEOELLELDKWASLWNWF
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و المادية	14 yeast) env_hvibru)L1=0 env_hvibru)Y1=A	GCN4 (gcn4 yeast) DP-107 (env_hv1bru)L1=D DP-178 (env_hv1bru)Y1=D	GCN4 (gcn4 yeast) DP-107 (env_hy1bru)L2=D DP-178 (env_hy1bru)Y1=A	GCN4 (gcn4 yeast) DP-107 (env_hv1bru)L2=D DP-178 (env_hv1bru)Y1=D

FIG. 1

7872-020 (SHEET 19 OF 63)

Hybrid Molif										[AEF IKLINDRSTVHY] [CFP]	=)COCHP CFP
Parent Wolif		[LIMN] [CFC]INPTH]	[ILOTV] (COF IMPST)	[EKLHOV] [CFIOLPS]	[EFKLOHY] [CFGLPRVY]	[EFILHOSMY] (OCCUPRIVY)	[IKLT] (CFGHIMPRWMY)	[AILIN] [COFCHILPWIY]	[ELR] (ACFGLPWM)	[FILTY] {ACFLIAPTW#}	*
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	Sequence	GONA (acn4 veas!)	DP-107 (env hvlbru)[1=	OP-107 (env. hv1bru)[2=	DP-178 (env. hv1bru)Y1=	DP-178 (env hylbru)Y1=	C-FOS (los human)	C-JUN (Lao! human)	C-LITC (myo human)	FLU 1000 36 E K T N E K H Q 1 E K E F	

7872-020 (SHEET 20 OF 63)

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7872-020 (SHEET 21 OF 63)

Fusion

∀ALLMOTI5∀

Peptide

4107x178x44

FLGFLG A AGSTMGARSM TLTVQARQ ALL SGIVOQO DP107-NNL

LRAIEAOOHL LOLTYWGIKO LOARILAYER YLKDO-DP107 OLLG ★ ▼ I WGC

4107x178x44

♥ALLMOTI5♥

LVS Coiled-Coil

SGKLICT TAVP ▼WNASWS NKSLEQIWNN MTWM *E ▲ WDREINN DP178-

YTSLIHSL IEESONOOEK NEOELLELDK* WASLWNWF-DP178

◆Transmembrane Region ◆

TNWLWYIK + + IF IMIYGGLYGL RIVEAVLSIY NRVRQGYS + PL

+P23LZIPC+

SFQTHLPTPR GPDR +PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL+ CL

♥ALLMOTI5♥

↑107x178x4↑

F ▼SYHRLRDLL LIVTRIVELL GRRGW ◆EALKY WWNLLOYWSO

ELKNSAVSLL NAT ↑ ALAVAEG TDRVIEVVQG A ▼ CRAIRIHPR

RIRQGLERIL L

7872-020 (SHEET 22 OF 63)

Fusion

VALLMOTISY

Peptide

4107x178x44

▼.....FLGFL LGVGSAIAS GVA ◆YSKVLHLEGEVNICIKSA

+P1&I2LZIPC+

LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ * LL +PIVNKQ

★107x178x4★

SC &SISNIETY I+ EFOOKNNRLLEITREFSYNAG & VIII'VSIMLINSELLSL

+P1&12LZIPC+

VALLMOTI5

INDM →PI →TNDQ KKLMSNNVQI V→ RQQSYSI→ MS IIKEEVLAYV

VO▼ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

+P7. 12, & 23LZIPC+

4107x178x44

VALLMOTISY

EPIINFYDPLVF +PSDE +FDASISOVNEKINOSLAF *I+ RKSDELL+

◆ Transmembrane Region ◆

HNVNA + GK STIN + IMITTI IIVIIVILLS LIAVGLLLY + C+

KARSTPVTLS KDQLSGINNI AFSN

7872-020 (SHEET 23 OF 63)

Fusion Peptide

♥ALLMOTI5♥

4107x178x44

ELGELG

♥AAGTA MGAAA ◆TALTYOSOHLLAGILOOOKNLLAAY

4107x178x44

EAQ+ QQM +LKLTIWGVKNLNARYTALEKYLEDOARLN+ AWG+ CA

LVS Coilcd-Coil

♥ALLMOTI5♥ **♦**107x178x4**♦**

WKQVCHTTVP WQWNNRTPDW VNNMT *WLE *WEROISYLEGNIT

+107x178x4+

TOLEEARAQEEKNLD* AYOKLSS* WSDFWSW* FDF *SKWLN +ILK

+Transmembrane Region +

IGFLDYLGIIGLRLLYTY+ YS. CIARVRQGYS PLSPQIHIHP WKGQPDNAEG

PGEGGDKRKN SSEPWQKESG TAEWKSNWCK RLTNWCSISS IWLYNS

∀ALLMOTI5∀

♥CLTL LVHLRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♥

ACRSAYRA IINSPRRVRQ GLEGILN

7872-020 (SHEET 24 OF 63)

Fusion

Peptide ♥ALLMOTI5♥

4107x178x44

LVS Coiled-Coil

....FAG

<u> ▼VVL</u>

AGVALGVATA AQITAGIALIIQ **SNLNAQAIQ

SLRTSLEOSNIKAIEEIREATOETYIA* VOGYODY* VNNEL* VP

YALLMOTISY

4107x178x44

+P6 & 12LZIPC+

AMOHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD *PISA *VEISIOALIYAL

GGETHKILEKLGYSGSD ↑ MIAILESRGIKTKI ▼ THVDLPGKF IILSISY

+P1 & 12LZIPC+

PTLSEVKGVIVHRLEAV SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS

ESAICSONSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil

♥ALLMOTI5♥

+P12 & 23LZIPC+

DMVYEGKVAL G *PAISLD *RL*DVGTNLGNALKKLDDAKVLI*

+Transmembrane Region +

DSS + NOILETVRRS + SFN + FGSLL SYPILSCTAL ALLLLIYCC +

K RRYOOTLKOH TKVDPAFKPD LTGTSKSYVR SL

7872-020 (SHEET 25 OF 63)

Fusion ▼ALLMOTI5▼

Peptide

▼.....FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN **▲ILRLKESITA**

TIEAVHEYTDGLSOLAYA* VG KM* QQFVNDQFNNTAQELDCIKITQQV

♥ALLMOTI5♥

GVELNLYLTELTTV FGPQTTSPAL *TQLTIQALYNAGGNMDYLLTKLGVG

+P1 & 12LZIPC+

LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTIU VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ

♥ALLMOTI5♥

4107x178x44

NYGEAVSLID RHSCN ★♥VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG

LVS Coiled-Coil

*N LDISTELGNY NNSISNALDK LEESNSKLDK VNVKLTSTSA

membrane Region +

LTAISLVCGIJ:SLV * A LACYLMY + KQKAQQKTLLWLGNNTLGQMRATTKM

7872-020 (SHEET 26 OF 63)

Fusion

♥ ALLMOTIS ♥

Peptide

+107x178x4+ *LVS Coiled-Coil*

.....FFGGV

★IG ▼TIALG *VATSAQITAAVALYEAKQARSDIEKLKE

AIRDTNIKAVOSVOSSIGNLIVAIKSVO* DYVNKE** IVPSIARLGCEAAG

YALLMOTISY

4107x178x44

LQLGIALTQH *YSELTNIFGDNIGSLQEKGIKLQGIASLYRTNITEY*

P5 & 12LZIPC

IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL +PLLTRLLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

♥ALLMOTI5♥

4107x178x44

+P6 & 23LZIPC+

NDITLNNSVALD +PIDI +SIELN +KAKSDLEESKEWI+ RRSNOKL+

+ Transmembrane Region +

DSIGNWHOSSTT

+IIIV → LIM IIILFIINVT II + ILAVKYY → R

IQKINIRVDQN DKPYVLTNK

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Fusion
Peptide
.....GLFGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

4107x178x44

YALLMOTISY

LVS Coilcd-Coil

*Q *AADLKST *QAAIDQINGKLNRVIEKTNEKFHOIEKEFSEVEGRIQ

DLEKYYEDTKIDL* WSYNAELLYALENOHTI♠ DLT♥ DSEMNKLFEKTR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

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7872-020 (SHEET 38 OF 63)

Fusion

♥ALLMOTI5♥

Peptide

★107x178x4★

......RNKRGVFVLGFLGFLATAGSAMGAAS ** XXXXAQSRTLLAGIVOOOO

LLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQAQL*NAWG* CAF

♥ALLMOTI5♥

*LVS Predicted Coiled -Coil

RQVCHTTVPWPNASLTPDW *NND *TWQEWERKVDFLEENITALLEEAQIQQ

↑107x178x4↑

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP

WQIEYIHF

7872-020 (SHEET 39 OF 63)

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSSHGDLFRFSSD

107x178x4
IQCPSFGTRENHTEGLLMVFKDNIIPYSF *KVRSYTKIVTNILIYNGWYADSVTNRHE*
EKFSVDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR
YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN
KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW
QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD
RYTKGQEAIT YFITSGGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG
STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA
RAWCLEQKRQ NMVLRELTKI NPTTVMSSIY GKAVAAKRLG DVISVSQCVP VNQATVTLRK
SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

<u>*107x178x4</u>* EIHVYNDYHH FKTIELDGIA TLQTFISLNT <u>*SLIENIDFASLELYSRDEQRASNVFD</u> *<u>LE</u>*

LVS Predicted Coiled Coil TM Potential
GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

P12LZIPC

TM Potential
LVSTVGGLFSSLVSGFISF FK N +PFGGMLILVLVAGVVILVISL+ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQKR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

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MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQGQ

**

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ <u>\$107x178x4</u> +Dimerization+

@KRY KNRVASRKCRAK *FK@ Q +LLOHYREVAAAKSSENDRLRLLLKO *

MCPSLDVD+ SI IPRTPDVLHE DLLNF

7872-020 (SHEET 41 OF 63)

Fusion

Peptide

▼ALLMOTI5**▼**

LVS Coiled-Coil

FAG

▼VVLAGAALGVATAAQITAGIALHQSML*NSQAIDNLRASLETTN

OAIEAIROAGOEMI*LAVQGVQDYINN♥ ELIPSMNQLSCDLIGQKLGLKLLRYYT

+P23LZIPC+

♣P6,12LZIPC**♣**

↑107x178x4↑

♥ALLMOTI5♥

EILSLFGPSLRD +PISA +▼EISIOALSYALGGDINKV+ LEKLGYSGGDL+

÷P1,12LZIPC÷

LGILES

A RGIKARI

▼ THVDTESYFIVLSIAY

*PTLSEIKGVIVHRLEGV

*SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

+P23LZIPC ÷

P12LZIPC

♥ALLMOTI5**♥**

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP +P →IS*LERLDVGTNLGN

◆ Transmembrane Region ◆

AIAKLEDAKELL+ ESSDOI*L+ RSMK +GLSSTSIVYILI♥ AVCLGGLIGIP

<u>ALICCC</u> ◆ RGRCNKKGEOVGMSRPGLKPDLTGTSKSYVRSL

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Pre S1 and Pre S2
MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

+P12 & 23LZIPC+

MENITSG FLG +PLL VLQAGFFLLTRILTI+ PQSLDSWWTSLNFLGGTTVCLG

*P12 & 23LZIPC *
QNSQSPTSNHSPTSCPPTC *PGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQGML *
PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

◆ <u>Transmembrane Region</u> ◆
LWEWASARFSWLS ◆ <u>LLVPFVQWFVGLSPTVWLSVI</u> ◆ WMMWYWGPSL

- ◆Transmembrane Region ◆
- +YSILSPFLPLLPIFFCLWVYI+

7872-020 (SHEET 43 OF 63)

Fusion

♥ALLMOTI5♥

▲107x178x4▲

Peptide

*LVS Coiled Coil

AIQLIPLFVG LGI ♥TTAVSTGAAGLGVS ♠IT *QYTKLSHQLISDV

OAISSTIQDLQDQVDSLAEVVLQ* NRRGLDLLTAE ↑ QGGI ▼

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT......????????????????????????......

FIG 36

7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **★ YODYTARTOVTRAVSEVSALKTAAESAILEGKEIVSSA ★** T**▼**

PK DTQYDIGFT

- ↑107x178x4↑
- **♥ALLMOTI5♥**
- **♣♥ESTLLDGSGKSOIOVTDNODGTVELVATLGKSSGS♣**AIKGAVITVSR**♥**

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

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MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

- **4107x178x44**
- **♥ALLMOTI5♥**
- **↑** ▼ KDNTSAGVASSSSIKGKYVKEVKVENGVVTAT **↑**

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLON

CDPTTANGTA NKANKVGLYF Y

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♦♥SWKNVDKENNFTLKNEQTTADYATNVNI**

QLMESNGTKAISVVGKETE

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

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MNKKLLMNFF IVSPLLLATT ATDFTPVP

- **↑107x178x4↑**
- **♥**ALLMOTI5**♥**
- **♦♥LSSNQIIKTAKASTNDNIKDLLDWYSSGSDTFTNS♦♥**

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

- **↑107x178x4↑**
- **♦DLNTKRTKKSOHTSEGTYIHFQISGVT♦**

N TEKLPTPIEL PLKVKVHGKD SPLKYG

- *P12LZIPC*
- *PKFDKKQLAISTLDFEIRHQLTQI*

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

F19. 40

7872-020 (SHEET 48 OF 63)

♥ALLMOTI5**♥**

MKKTAFILLL FIALTLTTSP L ▼VNG

- **★107x178x4★**
- *LVS Predicted Coiled-Coil*
- *S & EKSEEINEKDLRKKSELORNALSNLRQIY* YYNEKAITENKESDD &

QFLENTLL♥ FKG FFTGHPW

- **↑107x178x4**↑
- **AYNDLLVDLGSKDATNKYKGKKVDLYGAY**

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEEKKVP INLWIDGKQTTV

- +P12LZIPC+
- *PIDKVKTSKKEVTVQELDL* QARHYLHGK FGLYNSDSFGGKVQ

P12LZIPC

RGLIVF HSSEGSTVSY DLFDAQGQY +P DTLLRIYRDN KTINSENLHI+

DLYLYTT

7872-020 (SHEET Y OF 63)

♥ALLMOTI5♥

MKKTAFTLLL FIALTLTTSP L

♥VNGS

↑107x178x4↑

♠EKSEEINEKDLRKKSELOGTALGNLKQIYYYNEKAKTENKESHD♠ Q♥

FLOHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

↑107x178x4↑

♥ALLMOTI5**♥**

+P12LZIPC÷

♣P ♥L ♠ETVKTNKKNVTVQELDLQARRYL♣ QEKYNLYN♠

SDVFDGKVQR♥ GLIVF HTSTE

+P23LZIPC+

PSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHI DIYLYTS

7872-020 (SHEET 50 OF 63)

MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

- **♥ALLMOTI5♥**
- **♥QMNINLYDHARGTQTGFVRYDDGYV**
- **↑107x178x4↑**
- **♦STSLSLRSAHLAGOYILSGYSLTIYIVI** ANMFNVNDVISVY♥

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

- **▼ALLMOTI5 ▼**
- **▼ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL▼**

7872-020 (SHEET 51 OF 63)

MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM
GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA
LVSSVAPSQT RAPHPFGVPA PSAGAYSRAG VVKTMTGGRA

LVS Predicted Coiled-Coil
QSIGRRGKVE QLSPEEEEKR RIRRE *RNKMA AAK

↑107x178x4↑

- **▼ALLMOTI5 ▼**
- **♥CRNRRREL ★TDTLQAETDQLEDEKSALQTEIANLLKEKEKL♥**

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

WO 96/19495 PCT/US95/16733

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SGWESYYKTEGDEEAEEQEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNS
VNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

↑107x178x4↑

♥ALLMOTI5♥

LVS Predicted Coiled-Coil

♥LRVH *FEE &SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS DSFENPVLQQHFRNLEALALDLME

- *P12LZIPC*
- *PEQAVDLTLPKVEAMNKRL* GSLVDEFKELVYPPDYNPEGKVTKR
 KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG
 LKKQELLEALTKHFQD

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GGGALSPQHSAVTQGSIIKNKEGMDAKS

- **4107x178x4 4**
- **♥ALLMOTI5♥**
- **▼ * LTAWSRTLYTFKDYFYDFTREEWKLLDT *** AQQIVYRNV MLENYKNLVSLGYQLT ***** KPDVILRLEKGEEPWLVEREIHQETHPD SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN DLIKHQRIHVGAETYKCNQCGIIFSQNS
- +P23LZIPC+
- *PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI* RENAY

7872-020 (SHEET 54 OF 63)

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FIG. 518

7872-020 (SHEET 62 OF 63)

Domain I: 174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P₂₂₀

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-N-W-T-S-L-N-F-L-G-G-T
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-N-W-T-S-L-N-F-L-G-G-T-T
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-N-W-T-S-L-N-F-L-G-G-T-T-V
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C
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OF 63)

I.P.L.L.V.L.L.D.Y.Q.G-M-L.P.V.C.P.L.I.P.G-8-S-T-8-T-G-P-C-R-T-C-H-T-T

7872-020

Domain II:

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L-I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-8-T-8-T-G-P-C-R-T-C-H-T
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INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

			
IPC(6)	SSIFICATION OF SUBJECT MATTER :C07K 7/04,14/025, 14/16; C12N 9/94, 9/96, 9/98,	9/99	
	:530/324; 424/184.1 o International Patent Classification (IPC) or to both:	national classification and IPC	<u></u>
<u>_</u>	DS SEARCHED		
	ocumentation searched (classification system followed	by classification symbols)	
	530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1		
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Documenta	ion sericined outer than infimition decontentation as the		
Electronic d	ata base consulted during the international search (na	me of data base and, where practicable	, search terms used)
MEDLIN	E, AIDSLINE, APS		
C. DOC	UMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where ap	propriate, of the relevant passages	Relevant to claim No.
X	PROCEEDINGS OF THE NATIONAL OF THE UNITED STATES OF AMER		1-3, 9, and 10
Y	21, issued November 1992, Wild e Inhibitor of Human Immunodefic	t al, "A Synthetic Peptide	4-8 and 11-15
	Correlation Between Solution Structure		
	pages 10537-41, see entire docum	nent.	
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X Furt	ner documents are listed in the continuation of Box C	. See patent family annex.	
r	ecial entegories of cited documents:	"I" inter document published after the int date and not in conflict with the applic	ution but cited to understand the
to	cument defining the general state of the art which is not considered be of particular relovance	principle or theory underlying the in- "X" document of particular relevance; the	
	riier document published on or after the interestional filing date current which may throw doubts on priority claim(s) or which is	considered novel or cannot be considered when the document is taken alone	ared to involve an inventive step
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.O. qu	compact referring to an oral disclosure, use, exhibition or other	considered to involve an inventive combined with one or more other sec being obvious to a person skilled in t	s step when the document is the documents, such combination the art
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Date of the	actual completion of the international search	Date of mailing of the international se	arch report
28 MAR	CH 1996	09 APR 1996	
Name and a Commission Box PCT	mailing address of the ISA/US mer of Patents and Trademarks	Authorized officer	Trus for
Washingto	n, D.C. 20231	JEFFREY STUCKER	•
Ecosimile B	Ja <i>(7</i> 03) 305-3730	Telephone No. (703) 308-0196	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
Category*	CHARGE OF DOCUMERS, WAR INCLUDED, WHERE SPECIFICATION, OF the Personnel Processing	
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Y	91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	4-8 and 11-15
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